



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 132122

**TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Thursday, September 09, 2004**

Case Serial Number: 09/93800

**From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526**

david.schreiber@uspto.gov

Search Notes

THIS PAGE LEFT BLANK.

SEARCH REQUEST FORM**Scientific and Technical Information Center**

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY**Type of Search****Vendors and cost where applicable**

Searcher: D. Schreiber NA Sequence (#) 22 STN _____
 Searcher Phone #: 272-2526 AA Sequence (#) _____ Dialog _____
 Searcher Location: Remsen EOI 161 Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: _____ Bibliographic _____ Dr. Link _____
 Date Completed: 9/9 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: 18 Fulltext _____ Sequence Systems Compucon
 Clerical Prep Time: _____ Patent Family _____ WWW/Internet _____
 Online Time: 135 Other _____ Other (specify) _____

THIS PAGE LEFT BLANK

Schreiber, David

132122

From: Schultz, James
Sent: Monday, August 30, 2004 1:39 PM
To: Schreiber, David
Subject: score over length search request, 09/913,800

Hi David,

I need a score over length nucleotide sequence search on SEQ ID NOS:32 and 21 in the above entitled case, which are both 20mers. I need the lower and upper limits to be 8 and 30, respectively, I need any hits that are above 65% complementarity, and please transfer as many hits into the excel program as possible. Please do not search the interference databases at this time.

Thanks,

Doug Schultz

James Douglas Schultz, PhD

AU 1635 (Biotechnology)

Patent Examiner

United States Patent and Trademark Office

(Office) REM 2D18

(Mail) REM 2C18

(571) 272-0763

1 135.11
24 12.7
31 12.1
34 138.5 3p
4 130
4p
61

THIS PAGE LEFT BLANK

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is ____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

THIS PAGE LEFT BLANK



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



THIS PAGE LEFT BLANK

›

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:12:19 ; Search time 0.001 Seconds
(without alignments)
131.184 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18

Sequence: 1 cttgagctgttggcgac 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 331 seqs, 3644 residues

Total number of hits satisfying chosen parameters: 662

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 331 summaries

Database : rge21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.8	76.7	20	1	AX613679
C 2	13.4	74.4	20	1	AX295263
C 3	12.4	68.9	18	1	AX364018
C 4	12.2	67.8	17	1	AX327367
C 5	12	66.7	17	1	AX148915
C 6	11.8	65.6	18	1	A92619
C 7	11.8	65.6	18	1	AX228100
C 8	11.2	62.2	17	1	AX186445
C 9	11.2	62.2	17	1	AX323076
C 10	10.8	60.0	16	1	AX211614
C 11	10.4	57.8	15	1	AX10671
C 12	10	55.6	11	1	AX627141
C 13	10	55.6	13	1	AX370825
C 14	10	55.6	15	1	AX036632
C 15	10	55.6	15	1	AX079652
C 16	10	55.6	15	1	AX102415
C 17	10	55.6	15	1	AX201450
C 18	10	55.6	15	1	BD006265
C 19	10	55.6	15	1	BD061453
C 20	10	55.6	15	1	BD073159
C 21	9.8	54.4	15	1	AX133723
C 22	9.8	54.4	15	1	AX180013
C 23	9.8	54.4	15	1	AX180702
C 24	9.8	54.4	15	1	AX456767
C 25	9.4	52.2	11	1	AX470959
C 26	9.4	52.2	11	1	AX623861
C 27	9.4	52.2	11	1	AX624544
C 28	9.4	52.2	11	1	AX631282
C 29	9.4	52.2	11	1	AX631965
C 30	9.4	52.2	14	1	A42557
C 31	9.4	52.2	14	1	A89517
C 32	9.4	52.2	14	1	AX139338
C 33	9.4	52.2	14	1	BD013621

9.4	52.2	14	1	BD067030
9.4	52.2	14	1	BD197849
9.4	52.2	14	1	BD197877
9.2	51.1	14	1	AR180446
9	50.0	9	1	AX669029
9	50.0	13	1	A89162
9	50.0	13	1	BD066675
8.8	48.9	12	1	A71529
8.8	48.9	12	1	AR101077
8.8	48.9	12	1	I79840
8.8	48.9	13	1	AX306735
8.8	48.9	13	1	AX239943
8.8	46.7	10	1	BD240488
8.4	46.7	10	1	E39679
8.4	46.7	10	1	E54832
8.4	46.7	10	1	AX351706
8.4	46.7	10	1	AX152432
8.4	46.7	10	1	AX189806
8.4	46.7	10	1	AX301325
8.4	46.7	10	1	AX667177
8.4	46.7	10	1	BD007906
8.4	46.7	11	1	E16056
8.4	46.7	11	1	E16063
8.4	46.7	11	1	AX339218
8.4	46.7	11	1	AX482047
8.4	46.7	11	1	AX511286
8.4	46.7	11	1	AX623855
8.4	46.7	11	1	AX626051
8.4	46.7	11	1	AX626057
8.4	46.7	11	1	AX626089
8.4	46.7	11	1	AX627011
8.4	46.7	11	1	AX628872
8.4	46.7	11	1	AX629473
8.4	46.7	11	1	AX631276
8.4	46.7	12	1	AR224222
8.4	46.7	12	1	AR224228
8.4	46.7	12	1	AR224229
8.4	46.7	12	1	AX078111
8.4	46.7	12	1	BD209765
8	44.4	9	1	AX668703
8	44.4	9	1	AX668877
8	44.4	9	1	AX668878
8	44.4	9	1	AX815434
8	44.4	10	1	AR002177
8	44.4	10	1	BD239522
8	44.4	10	1	E39696
8	44.4	10	1	AX152377
8	44.4	10	1	AX153346
8	44.4	10	1	BD008001
8	44.4	11	1	AR049910
8	44.4	11	1	I18622
8	44.4	11	1	AX629696
8	44.4	11	1	AX630367
8	44.4	12	1	AS1502
8	44.4	12	1	BD023284
7.8	43.3	11	1	AR082362
7.8	43.3	11	1	AR120904
7.8	43.3	11	1	BD274437
7.8	43.3	11	1	I24463
7.8	43.3	11	1	I78408
7.8	43.3	11	1	I88968
7.8	43.3	11	1	I88970
7.8	43.3	11	1	I88971
7.8	43.3	11	1	I88972
7.8	43.3	11	1	I88973
7.8	43.3	11	1	I88981
7.8	43.3	11	1	I88982
7.8	43.3	11	1	I88983
7.8	43.3	11	1	AR205797
7.8	43.3	11	1	AR301664
7.8	43.3	11	1	AR301737
7.8	43.3	11	1	AR399176
7.8	43.3	11	1	AX393135

ACCESSION:BD067030
ACCESSION:BD197849
ACCESSION:BD197877
ACCESSION:AR180446
ACCESSION:AX669029
ACCESSION:A89162
ACCESSION:BD066675
ACCESSION:A71529
ACCESSION:AR101077
ACCESSION:I79840
ACCESSION:AR306735
ACCESSION:AX239943
ACCESSION:BD240488
ACCESSION:E39679
ACCESSION:E54832
ACCESSION:AR351706
ACCESSION:AX152432
ACCESSION:AX189806
ACCESSION:AX301325
ACCESSION:AX667177
ACCESSION:BD007906
ACCESSION:E16056
ACCESSION:E16063
ACCESSION:AX339218
ACCESSION:AX482047
ACCESSION:AX511286
ACCESSION:AX623855
ACCESSION:AX626051
ACCESSION:AX626057
ACCESSION:AX626089
ACCESSION:AX627011
ACCESSION:AX628872
ACCESSION:AX629473
ACCESSION:AX631276
ACCESSION:AR224222
ACCESSION:AR224228
ACCESSION:AR224229
ACCESSION:AX078111
ACCESSION:BD209765
ACCESSION:AX668703
ACCESSION:AX668877
ACCESSION:AX668878
ACCESSION:AX815434
ACCESSION:AR002177
ACCESSION:BD239522
ACCESSION:E39696
ACCESSION:AX152377
ACCESSION:AX153346
ACCESSION:BD008001
ACCESSION:AR049910
ACCESSION:I18622
ACCESSION:AX629696
ACCESSION:AX630367
ACCESSION:AS1502
ACCESSION:BD023284
ACCESSION:AR082362
ACCESSION:AR120904
ACCESSION:BD274437
ACCESSION:I24463
ACCESSION:I78408
ACCESSION:I88968
ACCESSION:I88970
ACCESSION:I88971
ACCESSION:I88972
ACCESSION:I88973
ACCESSION:I88981
ACCESSION:I88982
ACCESSION:I88983
ACCESSION:AR205797
ACCESSION:AR301664
ACCESSION:AR301737
ACCESSION:AR399176
ACCESSION:AX393135

107	7.8	43.3	11	1	AX470922	ACCESSION:AX470922	C 180	7.4	41.1	11	1	AR081183	ACCESSION:AR081183
108	7.8	43.3	11	1	AX623196	ACCESSION:AX623196	C 181	7.4	41.1	11	1	AR085380	ACCESSION:AR085380
C 109	7.8	43.3	11	1	AX623333	ACCESSION:AX623333	C 182	7.4	41.1	11	1	AR088128	ACCESSION:AR088128
110	7.8	43.3	11	1	AX623779	ACCESSION:AX623779	C 183	7.4	41.1	11	1	AR104287	ACCESSION:AR104287
111	7.8	43.3	11	1	AX625543	ACCESSION:AX625543	C 184	7.4	41.1	11	1	AR143549	ACCESSION:AR143549
C 112	7.8	43.3	11	1	AX626232	ACCESSION:AX626232	C 185	7.4	41.1	11	1	AR171455	ACCESSION:AR171455
113	7.8	43.3	11	1	AX626661	ACCESSION:AX626661	C 186	7.4	41.1	11	1	AR171626	ACCESSION:AR171626
114	7.8	43.3	11	1	AX626814	ACCESSION:AX626814	C 187	7.4	41.1	11	1	BD243216	ACCESSION:BD243216
C 115	7.8	43.3	11	1	AX628155	ACCESSION:AX628155	C 188	7.4	41.1	11	1	AR256517	ACCESSION:AR256517
C 116	7.8	43.3	11	1	AX628362	ACCESSION:AX628362	C 189	7.4	41.1	11	1	AR301456	ACCESSION:AR301456
C 117	7.8	43.3	11	1	AX628435	ACCESSION:AX628435	C 190	7.4	41.1	11	1	AR301685	ACCESSION:AR301685
118	7.8	43.3	11	1	AX628838	ACCESSION:AX628838	C 191	7.4	41.1	11	1	AR430441	ACCESSION:AR430441
119	7.8	43.3	11	1	AX628949	ACCESSION:AX628949	C 192	7.4	41.1	11	1	AX393080	ACCESSION:AX393080
C 120	7.8	43.3	11	1	AX630617	ACCESSION:AX630617	C 193	7.4	41.1	11	1	AX470739	ACCESSION:AX470739
C 121	7.8	43.3	11	1	AX630754	ACCESSION:AX630754	C 194	7.4	41.1	11	1	AX471259	ACCESSION:AX471259
C 122	7.8	43.3	11	1	AX631200	ACCESSION:AX631200	C 195	7.4	41.1	11	1	AX471804	ACCESSION:AX471804
123	7.8	43.3	11	1	AX710712	ACCESSION:AX710712	C 196	7.4	41.1	11	1	AX623471	ACCESSION:AX623471
C 124	7.8	43.3	11	1	BD124414	ACCESSION:BD124414	C 197	7.4	41.1	11	1	AX623599	ACCESSION:AX623599
C 125	7.8	43.3	11	1	BD124487	ACCESSION:BD124487	C 198	7.4	41.1	11	1	AX624037	ACCESSION:AX624037
C 126	7.8	43.3	12	1	A02238	ACCESSION:A02238	C 199	7.4	41.1	11	1	AX625216	ACCESSION:AX625216
C 127	7.8	43.3	12	1	A02242	ACCESSION:A02242	C 200	7.4	41.1	11	1	AX625287	ACCESSION:AX625287
C 128	7.8	43.3	12	1	A71468	ACCESSION:A71468	C 201	7.4	41.1	11	1	AX625755	ACCESSION:AX625755
C 129	7.8	43.3	12	1	A71530	ACCESSION:A71530	C 202	7.4	41.1	11	1	AX625897	ACCESSION:AX625897
C 130	7.8	43.3	12	1	A71545	ACCESSION:A71545	C 203	7.4	41.1	11	1	AX626004	ACCESSION:AX626004
C 131	7.8	43.3	12	1	AR012645	ACCESSION:AR012645	C 204	7.4	41.1	11	1	AX627030	ACCESSION:AX627030
C 132	7.8	43.3	12	1	AR096775	ACCESSION:AR096775	C 205	7.4	41.1	11	1	AX627103	ACCESSION:AX627103
C 133	7.8	43.3	12	1	AR100946	ACCESSION:AR100946	C 206	7.4	41.1	11	1	AX627289	ACCESSION:AX627289
134	7.8	43.3	12	1	AR167693	ACCESSION:AR167693	C 207	7.4	41.1	11	1	AX627952	ACCESSION:AX627952
135	7.8	43.3	12	1	AR167825	ACCESSION:AR167825	C 208	7.4	41.1	11	1	AX628001	ACCESSION:AX628001
136	7.8	43.3	12	1	E29577	ACCESSION:E29577	C 209	7.4	41.1	11	1	AX628607	ACCESSION:AX628607
137	7.8	43.3	12	1	E39709	ACCESSION:E39709	C 210	7.4	41.1	11	1	AX628865	ACCESSION:AX628865
138	7.8	43.3	12	1	E38683	ACCESSION:E38683	C 211	7.4	41.1	11	1	AX628883	ACCESSION:AX628883
139	7.8	43.3	12	1	E38815	ACCESSION:E38815	C 212	7.4	41.1	11	1	AX630181	ACCESSION:AX630181
140	7.8	43.3	12	1	E64109	ACCESSION:E64109	C 213	7.4	41.1	11	1	AX630892	ACCESSION:AX630892
141	7.8	43.3	12	1	E64241	ACCESSION:E64241	C 214	7.4	41.1	11	1	AX631020	ACCESSION:AX631020
142	7.8	43.3	12	1	I79841	ACCESSION:I79841	C 215	7.4	41.1	11	1	AX631458	ACCESSION:AX631458
143	7.8	43.3	12	1	AR371380	ACCESSION:AR371380	C 216	7.4	41.1	11	1	AX632637	ACCESSION:AX632637
C 144	7.4	41.1	9	1	AX669059	ACCESSION:AX669059	C 217	7.4	41.1	11	1	AX633208	ACCESSION:AX633208
C 145	7.4	41.1	10	1	A00110	ACCESSION:A00110	C 218	7.4	41.1	11	1	AX632818	ACCESSION:AX632818
C 146	7.4	41.1	10	1	A94606	ACCESSION:A94606	C 219	7.4	41.1	11	1	BD124206	ACCESSION:BD124206
C 147	7.4	41.1	10	1	AR107764	ACCESSION:AR107764	C 220	7.4	41.1	11	1	BD124435	ACCESSION:BD124435
C 148	7.4	41.1	10	1	AR107836	ACCESSION:AR107836	C 221	7.38.9	9	1	AX205218	ACCESSION:AX205218	
149	7.4	41.1	10	1	AR110398	ACCESSION:AR110398	C 222	7.38.9	9	1	AX667082	ACCESSION:AX667082	
150	7.4	41.1	10	1	AR157056	ACCESSION:AR157056	C 223	7.38.9	9	1	AX668677	ACCESSION:AX668677	
151	7.4	41.1	10	1	AR167216	ACCESSION:AR167216	C 224	7.38.9	9	1	AX668678	ACCESSION:AX668678	
152	7.4	41.1	10	1	BD239703	ACCESSION:BD239703	C 225	7.38.9	9	1	AX668679	ACCESSION:AX668679	
C 153	7.4	41.1	10	1	BD239811	ACCESSION:BD239811	C 226	7.38.9	9	1	AX668680	ACCESSION:AX668680	
154	7.4	41.1	10	1	BD240577	ACCESSION:BD240577	C 227	7.38.9	10	1	AR070982	ACCESSION:AR070982	
C 155	7.4	41.1	10	1	I12911	ACCESSION:I12911	C 228	7.38.9	10	1	AR107758	ACCESSION:AR107758	
C 156	7.4	41.1	10	1	AR266760	ACCESSION:AR266760	C 229	7.38.9	10	1	AR107840	ACCESSION:AR107840	
C 157	7.4	41.1	10	1	AR303494	ACCESSION:AR303494	C 230	7.38.9	10	1	AR161929	ACCESSION:AR161929	
C 158	7.4	41.1	10	1	AR303644	ACCESSION:AR303644	C 231	7.38.9	10	1	BD239261	ACCESSION:BD239261	
159	7.4	41.1	10	1	AR306868	ACCESSION:AR306868	C 232	7.38.9	10	1	BD240131	ACCESSION:BD240131	
160	7.4	41.1	10	1	AR351736	ACCESSION:AR351736	C 233	7.38.9	10	1	BD240425	ACCESSION:BD240425	
161	7.4	41.1	10	1	AX078107	ACCESSION:AX078107	C 234	7.38.9	10	1	BD240505	ACCESSION:BD240505	
162	7.4	41.1	10	1	AX152580	ACCESSION:AX152580	C 235	7.38.9	10	1	BD240704	ACCESSION:BD240704	
163	7.4	41.1	10	1	AX153206	ACCESSION:AX153206	C 236	7.38.9	10	1	E39676	ACCESSION:E39676	
C 164	7.4	41.1	10	1	AX301357	ACCESSION:AX301357	C 237	7.38.9	10	1	E54725	ACCESSION:E54725	
C 165	7.4	41.1	10	1	AX377146	ACCESSION:AX377146	C 238	7.38.9	10	1	E54836	ACCESSION:E54836	
166	7.4	41.1	10	1	AX667829	ACCESSION:AX667829	C 239	7.38.9	10	1	I91829	ACCESSION:I91829	
167	7.4	41.1	10	1	AX675461	ACCESSION:AX675461	C 240	7.38.9	10	1	AR222963	ACCESSION:AR222963	
168	7.4	41.1	10	1	AX716741	ACCESSION:AX716741	C 241	7.38.9	10	1	AR222966	ACCESSION:AR222966	
169	7.4	41.1	10	1	BD073892	ACCESSION:BD073892	C 242	7.38.9	10	1	AR351662	ACCESSION:AR351662	
C 170	7.4	41.1	10	1	BD161386	ACCESSION:BD161386	C 243	7.38.9	10	1	AR351737	ACCESSION:AR351737	
171	7.4	41.1	10	1	BD164453	ACCESSION:BD164453	C 244	7.38.9	10	1	AR351766	ACCESSION:AR351766	
C 172	7.4	41.1	10	1	BD167209	ACCESSION:BD167209	C 245	7.38.9	10	1	AR351771	ACCESSION:AR351771	
C 173	7.4	41.1	10	1	BD187825	ACCESSION:BD187825	C 246	7.38.9	10	1	AR351819	ACCESSION:AR351819	
C 174	7.4	41.1	10	1	BD187826	ACCESSION:BD187826	C 247	7.38.9	10	1	AR351820	ACCESSION:AR351820	
175	7.4	41.1	10	1	BD209761	ACCESSION:BD209761	C 248	7.38.9	10	1	AR382215	ACCESSION:AR382215	
C 176	7.4	41.1	11	1	A00109	ACCESSION:A00109	C 249	7.38.9	10	1	AR411415	ACCESSION:AR411415	
177	7.4	41.1	11	1	A11801	ACCESSION:A11801	C 250	7.38.9	10	1	AX152263	ACCESSION:AX152263	
178	7.4	41.1	11	1	A33068	ACCESSION:A33068	C 251	7.38.9	10	1	AX152495	ACCESSION:AX152495	
C 179	7.4	41.1	11	1	AR074503	ACCESSION:AR074503	C 252	7.38.9	10	1	AX152496	ACCESSION:AX152496	

```
C 253 7 38.9 10 1 AX152633 ACCESSION:AX152633
C 254 7 38.9 10 1 AX152997 ACCESSION:AX152997
C 255 7 38.9 10 1 AX153110 ACCESSION:AX153110
C 256 7 38.9 10 1 AX153347 ACCESSION:AX153347
C 257 7 38.9 10 1 AX153645 ACCESSION:AX153645
C 258 7 38.9 10 1 AX153621 ACCESSION:AX153621
C 259 7 38.9 10 1 AX667107 ACCESSION:AX667107
C 260 7 38.9 10 1 AX667830 ACCESSION:AX667830
C 261 7 38.9 10 1 AX667859 ACCESSION:AX667859
C 262 7 38.9 10 1 AX667864 ACCESSION:AX667864
C 263 7 38.9 10 1 AX668175 ACCESSION:AX668175
C 264 7 38.9 10 1 AX668176 ACCESSION:AX668176
C 265 7 38.9 10 1 BD007759 ACCESSION:BD007759
C 266 7 38.9 10 1 BD007902 ACCESSION:BD007902
C 267 7 38.9 10 1 BD007925 ACCESSION:BD007925
C 268 7 38.9 10 1 BD007976 ACCESSION:BD007976
C 269 7 38.9 10 1 BD083133 ACCESSION:BD083133
C 270 7 38.9 10 1 BD083215 ACCESSION:BD083215
C 271 7 38.9 10 1 BD091138 ACCESSION:BD091138
C 272 7 38.9 10 1 BD091141 ACCESSION:BD091141
C 273 7 38.9 10 1 BD167226 ACCESSION:BD167226
C 274 7 38.9 10 1 BD167253 ACCESSION:BD167253
C 275 6.8 37.8 10 1 A10261 ACCESSION:A10261
C 276 6.8 37.8 10 1 AR107864 ACCESSION:AR107864
C 277 6.8 37.8 10 1 AR167213 ACCESSION:AR167213
C 278 6.8 37.8 10 1 BD238734 ACCESSION:BD238734
C 279 6.8 37.8 10 1 BD238775 ACCESSION:BD238775
C 280 6.8 37.8 10 1 BD238782 ACCESSION:BD238782
C 281 6.8 37.8 10 1 BD238792 ACCESSION:BD238792
C 282 6.8 37.8 10 1 BD238996 ACCESSION:BD238996
C 283 6.8 37.8 10 1 BD239186 ACCESSION:BD239186
C 284 6.8 37.8 10 1 BD239228 ACCESSION:BD239228
C 285 6.8 37.8 10 1 BD239906 ACCESSION:BD239906
C 286 6.8 37.8 10 1 BD240033 ACCESSION:BD240033
C 287 6.8 37.8 10 1 BD240268 ACCESSION:BD240268
C 288 6.8 37.8 10 1 BD240555 ACCESSION:BD240555
C 289 6.8 37.8 10 1 BD240614 ACCESSION:BD240614
C 290 6.8 37.8 10 1 BD240619 ACCESSION:BD240619
C 291 6.8 37.8 10 1 BD240685 ACCESSION:BD240685
C 292 6.8 37.8 10 1 BD240705 ACCESSION:BD240705
C 293 6.8 37.8 10 1 E23590 ACCESSION:E23590
C 294 6.8 37.8 10 1 E39492 ACCESSION:E39492
C 295 6.8 37.8 10 1 E39670 ACCESSION:E39670
C 296 6.8 37.8 10 1 E54811 ACCESSION:E54811
C 297 6.8 37.8 10 1 E64721 ACCESSION:E64721
C 298 6.8 37.8 10 1 AR201710 ACCESSION:AR201710
C 299 6.8 37.8 10 1 AR266754 ACCESSION:AR266754
C 300 6.8 37.8 10 1 AR351709 ACCESSION:AR351709
C 301 6.8 37.8 10 1 AX112966 ACCESSION:AX112966
C 302 6.8 37.8 10 1 AX152364 ACCESSION:AX152364
C 303 6.8 37.8 10 1 AX153048 ACCESSION:AX153048
C 304 6.8 37.8 10 1 AX153114 ACCESSION:AX153114
C 305 6.8 37.8 10 1 AX153406 ACCESSION:AX153406
C 306 6.8 37.8 10 1 AX153433 ACCESSION:AX153433
C 307 6.8 37.8 10 1 AX153461 ACCESSION:AX153461
C 308 6.8 37.8 10 1 AX153593 ACCESSION:AX153593
C 309 6.8 37.8 10 1 AX301382 ACCESSION:AX301382
C 310 6.8 37.8 10 1 AX301388 ACCESSION:AX301388
C 311 6.8 37.8 10 1 AX301627 ACCESSION:AX301627
C 312 6.8 37.8 10 1 AX395401 ACCESSION:AX395401
C 313 6.8 37.8 10 1 AX481180 ACCESSION:AX481180
C 314 6.8 37.8 10 1 AX667180 ACCESSION:AX667180
C 315 6.8 37.8 10 1 BD007785 ACCESSION:BD007785
C 316 6.8 37.8 10 1 BD007982 ACCESSION:BD007982
C 317 6.8 37.8 10 1 BD007999 ACCESSION:BD007999
C 318 6.8 37.8 10 1 BD065146 ACCESSION:BD065146
C 319 6.8 37.8 10 1 BD083093 ACCESSION:BD083093
C 320 6.8 37.8 10 1 BD083234 ACCESSION:BD083234
C 321 6.8 37.8 10 1 BD083247 ACCESSION:BD083247
C 322 6.8 37.8 10 1 BD083273 ACCESSION:BD083273
C 323 6.8 37.8 10 1 BD083275 ACCESSION:BD083275
C 324 6.8 37.8 10 1 BD083279 ACCESSION:BD083279
```

```
C 326 6.8 37.8 10 1 BD166478 ACCESSION:BD166478
C 327 6.8 37.8 10 1 BD166531 ACCESSION:BD166531
C 328 6.8 37.8 10 1 BD166592 ACCESSION:BD166592
C 329 6.8 37.8 10 1 BD166719 ACCESSION:BD166719
C 330 6.8 37.8 10 1 BD166723 ACCESSION:BD166723
C 331 6.8 37.8 10 1 BD167013 ACCESSION:BD167013
```

RESULT 1
AX613679/c
LOCUS AX613679 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 4704 from Patent WO02072882.
ACCESSION AX613679
VERSION AX613679.1 GI:28409108
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
JOURNAL Coronary chip
PATENT: WO 02072882-A 4704 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
Location/Qualifiers
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 7.3;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTGGCGA 17
|||||
Db 19 CTTGAGGCTGTGGCGA 3

RESULT 2
AX295263/c
LOCUS AX295263 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7025 from Patent WO0179548.
ACCESSION AX295263
VERSION AX295263.1 GI:17056952
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7025 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 74.4%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 9.1;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGGCGA 17
|||||
Db 20 TGAGGCTGTGGCGA 6

RESULT 3
AR364018 AR364018 18 bp DNA linear PAT 03-SEP-2003
LOCUS
DEFINITION Sequence 14 from patent US 5245022.
ACCESSION AR364018
VERSION AR364018.1 GI:34426196
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Weis,A.L., Oakes,F.T., Hausheer,F.H., Cavanaugh,P.F. Jr. and Moskwa,P.S.
TITLE Exonuclease resistant terminally substituted oligonucleotides
JOURNAL Patent: US 5245022-A 14 SEP-1993;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGGCGA 17
|||||
Db 2 GAGGCTGTTGGCGA 15

RESULT 4
AR327367/c AR327367 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4769 from patent US 6566127.
ACCESSION AR327367
VERSION AR327367.1 GI:33713175
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4769 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 67.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTTGGCGA 17
|||||
Db 17 CTTGAGGTAGTTGGAGA 1

RESULT 5
AR148915/c AR148915 17 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 14 from patent US 6225531.
ACCESSION AR148915
VERSION AR148915.1 GI:15113005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kakitani,M., Umemoto,N., Ishida,I., Iwamatsu,A., Yoshikawa,M. and Yamaoka,N.
TITLE Glucan elicitor receptor, DNA molecule coding therefor,

fungus-resistant plants transformed with the DNA molecule and method for creating the plants
Patent: US 6225531-A 14 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 66.7%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTGGCGA 17
|||||
Db 17 TTGGKGTGTGGCGA 2
|||||

RESULT 6
A92619 A92619 18 bp DNA linear PAT 22-JAN-2000
LOCUS
DEFINITION Sequence 6 from Patent WO9808971.
ACCESSION A92619
VERSION A92619.1 GI:6741264
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Berndt,H. and Bendzko,P.
TITLE METHOD TO DETECT CLINICALLY RELEVANT MUTATIONS OF THE DNA SEQUENCE OF KI -RAS ONCOGENE, ITS USE AND A TESTKIT FOR EARLY DIAGNOSIS OF TUMOURS

JOURNAL Patent: WO 9808971-A 6 05-MAR-1998;
BERNDT HANS CHRISTOPH (DE); BENDZKO PETER (DE)

FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTGGCG 16
|||||
Db 2 TTGAGGCTGTTGGCG 16

RESULT 7
AR228100 AR228100 18 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 6 from patent US 6448002.
ACCESSION AR228100
VERSION AR228100.1 GI:27266846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Hillebrand,T., Berndt,H.-C. and Bendzko,P.
TITLE Method to detect clinically relevant mutations of the DNA sequence of ki-ras oncogene, its use and a testkit for early diagnosis of tumors

JOURNAL Patent: US 6448002-A 6 10-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY      2 TTGAGGCTGTGGCG 16
Db      2 TTGAGGCTGTGGCG 16

RESULT 8
ARI86445/c
LOCUS   ARI86445          17 bp      DNA          linear      PAT 20-APR-2002
DEFINITION   Sequence 1933 from patent US 6346398.
ACCESSION   ARI86445
VERSION     ARI86445.1  GI:20232410
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6346398-A 1933 12-FEB-2002;
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTTGAGGCTGTGGCG 16
Db      16 CTTGAGGTAGTTGGAG 1

RESULT 9
AR323076/c
LOCUS   AR323076          17 bp      RNA          linear      PAT 17-AUG-2003
DEFINITION   Sequence 478 from patent US 6566127.
ACCESSION   AR323076
VERSION     AR323076.1  GI:33708884
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 478 20-MAY-2003;
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="unknown"
           /mol_type="unassigned RNA"

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTTGAGGCTGTGGCG 16
Db      16 CTTGAGGTAGTTGGAG 1

RESULT 10
AR211614
LOCUS   AR211614          16 bp      DNA          linear      PAT 20-JUN-2002
DEFINITION   Sequence 33 from patent US 6399340.
ACCESSION   AR211614
VERSION     AR211614.1  GI:21514983
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.

Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Saito,Y., Noguchi,Y., Yoshikawa,K. and Soeda,S.
TITLE      Vector derivatives of gluconobacter plasmid pF4
JOURNAL    Patent: US 6399340-A 33 04-JUN-2002;
FEATURES   Location/Qualifiers
           source
           1..16
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      60.0%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTGAGGCTGTGGC 15
Db      3 TGGAGGCTGTAGGC 16

RESULT 11
A10671/c
LOCUS   A10671           Oligonucleotide (I2).
DEFINITION   A10671
ACCESSION   A10671
VERSION     A10671.1  GI:490797
KEYWORDS
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 15)
REFERENCE   Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
AUTHORS    Process for production of gamma-interferon
TITLE      Patent: EP 0176916-A 56 09-APR-1986;
JOURNAL    FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

Query Match      57.8%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCGAC 18
Db      14 GCTGTGGCGAC 3

RESULT 12
AX627141/c
LOCUS   AX627141          11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION   Sequence 4182 from Patent WO2053774.
ACCESSION   AX627141
VERSION     AX627141.1  GI:28455179
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conrad,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 4182 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
           source
           1..11
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      55.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
 |||||
 Db 11 AGGCTGTTGG 2

RESULT 13
 AX370825 AX370825 13 bp DNA linear PAT 01-MAR-2002
 LOCUS Sequence 9 from Patent WO0210447.
 DEFINITION AX370825
 ACCESSION AX370825
 VERSION AX370825.1 GI:19168957
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Grill,H.J., Schuetz,A. and Prix,L.
 TITLE Method for detecting nucleic acids by means of hybridization, use of this method and corresponding analysis kit and nucleic acid oligomers and use thereof
 JOURNAL Patent: WO 0210447-A 9 07-FEB-2002;
 Giesing, Michael (DE)
 FEATURES
 source 1..13
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic Oligonucleotid"

Query Match 55.6%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 34; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
 |||||
 Db 2 GCTGTTGGCG 11

RESULT 14
 AR036632/c
 LOCUS AR036632 Sequence 32 from patent US 5872242.
 DEFINITION AR036632
 ACCESSION AR036632
 VERSION AR036632.1 GI:5953300
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Monia,B.P., Cowbert,L.M. and Manoharan,M.
 TITLE Antisense oligonucleotide inhibition of ras
 JOURNAL Patent: US 5872242-A 32 16-FEB-1999;
 FEATURES
 source 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 40; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
 |||||
 Db 12 GCTGTTGGCG 3

RESULT 15
 AR079652/c
 LOCUS AR079652 Sequence 32 from patent US 5965722.
 DEFINITION AR079652
 ACCESSION AR079652

VERSION AR079652.1 GI:10006393
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Ecker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
 TITLE Antisense inhibition of ras gene with chimeric and alternating oligonucleotides
 JOURNAL Patent: US 5965722-A 32 12-OCT-1999;
 FEATURES
 source Location/Qualifiers
 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 40; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
 |||||
 Db 12 GCTGTTGGCG 3

RESULT 16
 AR102415/c
 LOCUS AR102415 15 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 40 from patent US 6083923.
 ACCESSION AR102415
 VERSION AR102415.1 GI:12813213
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and Mehta,R.C.
 TITLE Liposomal oligonucleotide compositions for modulating RAS gene expression
 JOURNAL Patent: US 6083923-A 40 04-JUL-2000;
 FEATURES
 source Location/Qualifiers
 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 40; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
 |||||
 Db 12 GCTGTTGGCG 3

RESULT 17
 AR201450/c
 LOCUS AR201450 15 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 32 from patent US 6359124.
 ACCESSION AR201450
 VERSION AR201450.1 GI:20252338
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Ecker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
 TITLE Antisense inhibition of ras gene with chimeric and alternating oligonucleotides
 JOURNAL Patent: US 6359124-A 32 19-MAR-2002;
 FEATURES
 source Location/Qualifiers
 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

```

Query Match      55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 18
BD006265/c      15 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION      Antisense inhibition of ras gene with chimeric and alternating
                  oligonucleotides.
ACCESSION      BD006265
VERSION        BD006265.1 GI:18634636
KEYWORDS       JP 2001500530-A/32.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Ecker,D.J., Cook,P.D., Monia,B.P., Freier,S.M. and Sang,Y.S.
TITLE          Antisense inhibition of ras gene with chimeric and alternating
                  oligonucleotides
JOURNAL        Patent: JP 2001500530-A 32 16-JAN-2001;
                  ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
                  PN JP 2001500530-A/32
                  PD 16-JAN-2001
                  PF 30-APR-1998 JP 1998547418
                  PR 30-APR-1997 US 08/848840
                  PI DAVID J ECKER, PHILIP DAN COOK, BRETT P MONIA, SUSAN M FREIER, PI
                     YOGESH S SANGHVI
                  PC C12Q1/68,C12P19/34,C07H19/16,C07H19/167,C07H19/173,C07H19/067,
                  PC C07H19/06,
                  PC C07H19/09,C07H21/04,A61K48/00
                  CC Key Location/Qualifiers
                  FH Key 1..15
                  FT source /organism='Artificial Sequence'.
FEATURES
source
1..15
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 19
BD061453
LOCUS
DEFINITION      Method for selectively separating living cell expressed with
                  specific gene.
ACCESSION      BD061453
VERSION        BD061453.1 GI:22607059
KEYWORDS       JP 2001286285-A/15.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Ishibashi,K. and Tsuji,A.
TITLE          Method for selectively separating living cell expressed with
                  specific gene
JOURNAL        Patent: JP 2001286285-A 15 16-OCT-2001;
                  LABORATORY OF MOLECULAR BIOPHOTONICS

```

```

OS Artificial Sequence
PN JP 2001286285-A/15
PF 16-OCT-2001
PI KANAME ISHIBASHI,AKIHIKO TSUJI
PC C12N15/09,C12N1/02,C12N5/10,C12Q1/68,G01N33/48,G01N33/53, PC
G01N33/566,
PC G01N33/58//(C12N1/02,C12R1:91),(C12Q1/68,C12R1:91),C12N15/00,
CC C12N5/00
CC Probe
FH Key Location/Qualifiers.
FEATURES
source
1..15
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 4 TGAGGCTGTT 13

RESULT 20
BD073159/c      15 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION      Antisense oligonucleotide inhibition of RAS.
ACCESSION      BD073159
VERSION        BD073159.1 GI:22618762
KEYWORDS       JP 2001509394-A/32.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Monia,B.P., Cowcert,L.M. and Manoharan,M.
TITLE          Antisense oligonucleotide inhibition of RAS
JOURNAL        Patent: JP 2001509394-A 32 24-JUL-2001;
                  ISIS PHARMACEUTICALS INC
COMMENT        OS Unidentified
                  PN JP 2001509394-A/32
                  PD 24-JUL-2001
                  PF 06-JUL-1998 JP 2000502223
                  PR 08-JUL-1997 US 08/889296
                  PI BRETT P MONIA,LEX M COWCERT,MUSIA MANOHARAN
                  PC C12N15/09,A61K31/7088,A61K48/00,A61P35/00,C12N15/00 CC
                  CC Topology: Linear;
                  CC Antisense oligonucleotide inhibition of RAS
                  FH Key Location/Qualifiers
                  FT source 1..15
FEATURES
source
1..15
/organism='Unidentified'.
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 21
AR133723
LOCUS
DEFINITION      Sequence 2148 from patent US 6194150.

```

```

ACCESSION   AR133723
VERSION     AR133723.1  GI:14122628
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE       Nucleic acid based inhibition of CD40
JOURNAL     Patent: US 6194150-A 2148 27-FEB-2001;
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  5 AGGCTGTTGGCGA 17
    |||||
Db  1 AGGCAGTTGGCCA 13

RESULT 22
LOCUS     AR180013                15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 81 from patent US 6333152.
ACCESSION AR180013
VERSION   AR180013.1  GI:20222046
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE     Gene expression profiles in normal and cancer cells
JOURNAL   Patent: US 6333152-A 81 25-DEC-2001;
FEATURES  Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  5 AGGCTGTTGGCGA 17
    |||||
Db  1 AGGCAGTTGGCCA 13

RESULT 23
LOCUS     AR180702                15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 770 from patent US 6333152.
ACCESSION AR180702
VERSION   AR180702.1  GI:20222735
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE     Gene expression profiles in normal and cancer cells
JOURNAL   Patent: US 6333152-A 770 25-DEC-2001;
FEATURES  Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  5 AGGCTGTTGGCGA 17
    |||||
Db  2 ATGCTGTTGGTGA 14

RESULT 24
LOCUS     AX456767                15 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 239 from Patent WO0218407.
ACCESSION AX456767
VERSION   AX456767.1  GI:21715654
KEYWORDS  .
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
REFERENCE  1
AUTHORS   Kurreck,J. and Erdmann,V.A.
TITLE     Antisense oligonucleotides against vrl
JOURNAL   Patent: WO 0218407-A 239 07-MAR-2002;
          Gruenenthal GmbH (DE)
FEATURES  Location/Qualifiers
             source
               1..15
               /organism="Rattus norvegicus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:10116"

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 TGAGGCTGTTGGC 15
    |||||
Db  3 TGCAGCTCTTGGC 15

RESULT 25
LOCUS     AX470959                11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 536 from Patent WO02053773.
ACCESSION AX470959
VERSION   AX470959.1  GI:22206084
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  1
AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   Patent: WO 02053773-A 536 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES  Location/Qualifiers
             source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5 AGGCTGTTGGC 15
    |||||
Db  11 ATGCTGTTGGC 1

RESULT 26
LOCUS     AX623861/c              11 bp      DNA      linear      PAT 21-FEB-2003

```



```

DEFINITION Sequence 902 from Patent WO02053774.
ACCESSION AX623861
VERSION AX623861.1 GI:28451802
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 902 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGG 13
|||
Db 11 TGGGGCTGTGG 1

RESULT 27
AX624544/c
LOCUS AX624544 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1585 from Patent WO02053774.
ACCESSION AX624544
VERSION AX624544.1 GI:28452485
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1585 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGG 13
|||
Db 11 TGGGGCTGTGG 1

RESULT 28
AX631282/c
LOCUS AX631282 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8324 from Patent WO02053774.
ACCESSION AX631282
VERSION AX631282.1 GI:28459328
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8324 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
|||
Db 11 ATGCTGTGGC 1

RESULT 29
AX631965/c
LOCUS AX631965 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9007 from Patent WO02053774.
ACCESSION AX631965
VERSION AX631965.1 GI:28467580
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9007 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
|||
Db 11 ATGCTGTGGC 1

RESULT 30
AX42557
LOCUS AX42557 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 73 from Patent WO9502051.
ACCESSION AX42557
VERSION AX42557.1 GI:2298006
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
PREVENTION AND/OR TREATMENT OF NEURAL INJURY, DEGENERATION AND
CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 73 19-JAN-1995;
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT Other publication AU 7345694 950206.
FEATURES
source
Location/Qualifiers
1. .14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

```

```
Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
Db 1 CTGTTGGCGAC 11

RESULT 31
A89517
LOCUS          A89517          14 bp      DNA          linear          PAT 22-JAN-2000
DEFINITION     Sequence 1665 from Patent WO9833904.
ACCESSION      A89517
VERSION        A89517.1 GI:6738087
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1665 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
               source
               1..14
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 3 AGGCTGTGGC 13

RESULT 32
AX139338
LOCUS          AX139338          14 bp      DNA          linear          PAT 30-MAY-2001
DEFINITION     Sequence 186 from Patent EP1076099.
ACCESSION      AX139338
VERSION        AX139338.1 GI:14275014
KEYWORDS       .
SOURCE         Mycobacterium tuberculosis
ORGANISM       Mycobacterium tuberculosis
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
               tuberculosis complex.
REFERENCE      1
AUTHORS        Suzuki,Y., Nishida,M. and Takenishi,S.
TITLE          Kit for diagnosis of tubercle bacilli
JOURNAL        Patent: EP 1076099-A 186 14-FEB-2001;
               NISSHINO INDUSTRIES, INC. (JP) ; System Research Incorporation
               (JP)
FEATURES       Location/Qualifiers
               source
               1..14
               /organism="Mycobacterium tuberculosis"
               /mol_type="unassigned DNA"
               /db_xref="taxon:1773"
               /note="capture"

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 2 GACTGTGGCG 12

RESULT 33
BD013621
LOCUS          BD013621          14 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     Diagnosis kit of tubercle bacillus.
ACCESSION      BD013621
VERSION        BD013621.1 GI:22553935
KEYWORDS       .
SOURCE         Mycobacterium tuberculosis
ORGANISM       Mycobacterium tuberculosis
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
               tuberculosis complex.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Suzuki,S., Nishida,M. and Takenishi,S.
TITLE          Diagnosis kit of tubercle bacillus
JOURNAL        Patent: JP 2001103981-A 185 17-APR-2001;
               NISSHINO IND INC.SYSTEM RESEARCH CO LTD
               OS Mycobacterium tuberculosis
               PN JP 2001103981-A/185
               PD 17-APR-2001
               PF 26-JUL-2000 JP 2000225985
               PI SADAHIKO SUZUKI,MICHIO NISHIDA,SOICHIRO TAKENISHI PC
               C12N15/09,C12N15/09,C12M1/00,C12Q1/68// (C12Q1/68,C12R1:32), PC
               (C12Q1/68,C12R1:325), (C12Q1/68,C12R1:33), C12N15/00,C12N15/00 CC
               capture
               FH Key
               FT source
               1..14
               /organism="Mycobacterium tuberculosis".
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:1773"

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 2 GACTGTGGCG 12

RESULT 34
BD067030
LOCUS          BD067030          14 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     An antisense oligonucleotide preparation method.
ACCESSION      BD067030
VERSION        BD067030.1 GI:22612633
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unidentified.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Schlingensiepen,K.H. and Brysch,W.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: JP 2001511000-A 1665 07-AUG-2001;
               BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
               OS Unknown
               PN JP 2001511000-A/1665
               PD 07-AUG-2001
               PF 30-JAN-1998 JP 1998532533
               PR 31-JAN-1997 EP 97101531.8
               PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
               PC C12N15/11,C07H21/04,A61K31/70
               CC An antisense oligonucleotide preparation method FH
               Key
               Location/Qualifiers
               source
               1..14
               /organism="Unknown".
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:1773"
               /note="capture"
```

```

/db_xref="taxon:32644"

Query Match      52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 AGGCTGTGGC 15
Db 3 AGGCTGTGGC 13

RESULT 35
BD197849
LOCUS
DEFINITION      Method and reagent for treating diseases or conditions concerning
                  14 bp RNA linear PAT 17-JUL-2003
                  molecule participating in vasculogenic response.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2002509721-A/875
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.
FEATURES
source
Query Match      52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TGAGGCTGTGG 13
Db 11 TGAGGCTGTGG 1

* RESULT 37
ARI80446
LOCUS
DEFINITION      Sequence 514 from patent US 6333152.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match      51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTCAGGCTGTGG 14
Db 1 CATGAGGATGTGG 14

RESULT 38
AX669029
LOCUS
DEFINITION      Sequence 2478 from Patent WO0242459.
ACCESSION

```

VERSION AX669029.1 GI:29292006
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 2478 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source 1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"
Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 4 GAGGCTGTT 12
|||||
Db 1 GAGGCTGTT 9
RESULT 39
A89162
LOCUS A89162 13 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1310 from Patent WO9833904.
ACCESSION A89162
VERSION A89162.1 GI:6737732
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1310 06-AUG-1998;
BIOGNOSTIK GBS (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
source 1..13
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 58; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 7 GCTGTTGGC 15
|||||
Db 3 GCTGTTGGC 11
RESULT 40
BD066675
LOCUS BD066675 13 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066675
VERSION BD066675.1 GI:22612278
KEYWORDS JP 2001511000-A/1310.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1310 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown

PN JP 2001511000-A/1310
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..13
/organism="Unknown".
FEATURES Location/Qualifiers
source 1..13
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 58; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 7 GCTGTTGGC 15
|||||
Db 3 GCTGTTGGC 11
RESULT 41
A71529/c
LOCUS A71529 12 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 88 from Patent WO9813521.
ACCESSION A71529
VERSION A71529.1 GI:4775141
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
JOURNAL Patent: WO 9813521-A 88 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES Location/Qualifiers
source 1..12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;
Qy 6 GGCTGTTGGCA 17
|||||
Db 12 GGCTGTTGGCA 1
RESULT 42
AR101077/c
LOCUS AR101077 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 47 from patent US 6083694.
ACCESSION AR101077
VERSION AR101077.1 GI:12811875
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hardy,J. and Goate,A.M.
TITLE Method for elucidation and detection of polymorphisms, splice
variants, and proximal coding mutations using intronic sequences of
the alzheimer's S182 gene
JOURNAL Patent: US 6083694-A 47 04-JUL-2000;
FEATURES Location/Qualifiers

```

source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 48.9%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTG 13
Db 12 TTGTTGCTGTTG 1

RESULT 43
I79840
LOCUS I79840 12 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 6 from patent US 5707866.
ACCESSION I79840
VERSION I79840.1 GI:3208130
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Brakier-Gingras,L., Melan.cedilla.on,P., Cote,M. and Payant,C.
TITLE DNA oligomers for inhibition of HIV by decreasing ribosomal
frameshifting
JOURNAL Patent: US 5707866-A 6 13-JAN-1998;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 48.9%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGTC 15
Db 1 GCGGCTGCTGTC 12

RESULT 44
AR306735
LOCUS AR306735 13 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 20 from patent US 6548657.
ACCESSION AR306735
VERSION AR306735.1 GI:31697060
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Burgin,A., Beigelman,L. and Bellon,L.
TITLE Method for screening nucleic acid catalysts
JOURNAL Patent: US 6548657-A 20 15-APR-2003;
FEATURES
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 48.9%; Score 8.8; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCGA 17
Db 1 GGGTGTTCACGA 12

RESULT 45
AX239943/c
LOCUS AX239943 13 bp DNA linear PAT 26-SEP-2001

```

```

DEFINITION Sequence 70 from Patent WO0164958.
ACCESSION AX239943
VERSION AX239943.1 GI:15797545
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Dempcy,R.O., Gall,A.A., Lokhov,S.G., Afonina,I.A., Singer,M.J.,
Kutyavin,I.V. and Vermeulen,N.M.
TITLE Modified oligonucleotides for mismatch discrimination
JOURNAL Patent: WO 0164958-A 70 07-SEP-2001;
Epoch Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
source
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probe sequence"

Query Match
Best Local Similarity 48.9%; Score 8.8; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTGG 14
Db 12 TGAGGCGGTTGG 1

RESULT 46
BD240488
LOCUS BD240488 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240488
VERSION BD240488.1 GI:33050258
KEYWORDS JP 2002534056-A/1906.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1906 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1906
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L. ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH key Location/Qualifiers
FT source 1. .10

```

FEATURES
source
FT Location/Qualifiers
1..10
/organism="Homo sapiens (human)"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTAGGCTGTT 12
| | | | | | | |
Db 1 TCAGGCTGTT 10

RESULT 47
E39679 LOCUS E39679 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.

ACCESSION E39679
VERSION E39679.1 GI:18621770
KEYWORDS JP 2000279181-A/212.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 212 10-OCT-2000;

COMMENT SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/212
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00

FT Key Location/Qualifiers
FT source 1..10
FT /organism="Homo sapiens (human)"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
| | | | | | | |
Db 1 CTGTGGCGA 10

RESULT 48
E54832 LOCUS E54832 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.

ACCESSION E54832
VERSION E54832.1 GI:22556315
KEYWORDS JP 2001211883-A/184.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 184 07-AUG-2001;

COMMENT SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2001211883-A/184
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA

PC C12N15/09,C07K16/18,C12P21/02,C12N15/00

CC
FH Key Location/Qualifiers.
FEATURES
source 1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
| | | | | | | |
Db 1 CTGTGGCGA 10

RESULT 49
AR351706 LOCUS AR351706 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 626 from patent US 6588746.
ACCESSION AR351706
VERSION AR351706.1 GI:33753502
KEYWORDS
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 626 08-JUL-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
| | | | | | | |
Db 1 GAGGCTGTTG 10

RESULT 50
AX152432 LOCUS AX152432 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 347 from Patent WO0138577.
ACCESSION AX152432
VERSION AX152432.1 GI:14534083
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 347 31-MAY-2001;
The Johns Hopkins University (US)

FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
|||||
Db 1 CTGTGGTGA 10

RESULT 51
AX189806
LOCUS AX189806 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 24 from Patent WO0148247.
ACCESSION AX189806
VERSION AX189806.1 GI:15143177
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Wang, S.M., Chen, J. and Rowley, J.D.
TITLE Method for generation of longer cDNA fragments from sage tags for gene identification
JOURNAL Patent: WO 0148247-A 24 05-JUL-2001;
Arch Development Corporation (US)
FEATURES
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
|||||
Db 1 CTGTGGTGA 10

RESULT 52
AX301325
LOCUS AX301325 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 39 from Patent WO0185941.
ACCESSION AX301325
VERSION AX301325.1 GI:17382408
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Versteeg, R. and Caron, H.N.
TITLE MYC targets
JOURNAL Patent: WO 0185941-A 39 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
|||||
Db 1 CTGTGGTGA 10

RESULT 53
AX667177
LOCUS AX667177 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 626 from Patent WO0242459.
ACCESSION AX667177
VERSION AX667177.1 GI:29291329
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gmn nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 626 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
|||||
Db 1 GAGGCTGTTG 10

RESULT 54
BD007906
LOCUS BD007906 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007906
VERSION BD007906.1 GI:18636279
KEYWORDS JP 2001069993-A/182.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 182 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/182
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P29/00.
PC A61P31/00, C12P21/08, C12N15/00
CC
FT source Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

/db_xref="taxon:32630"
/note="TAG sequence Hs60440"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
    ||||| |||
Db 2 AGGCTGCTGG 11

RESULT 59
AX511286
LOCUS      AX511286                11 bp    DNA          linear    PAT 27-SEP-2002
DEFINITION Sequence 24 from Patent WO02059558.
ACCESSION  AX511286
VERSION     AX511286.1 GI:23392163
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
TITLE     Means and methods for treatment evaluation
JOURNAL   Patent: WO 02059558-A 24 01-AUG-2002;
           Amsterdam Support Diagnostics B.V. (NL)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs60440"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
    ||||| |||
Db 2 AGGCTGCTGG 11

RESULT 60
AX623855/c
LOCUS      AX623855                11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 896 from Patent WO02053774.
ACCESSION  AX623855
VERSION     AX623855.1 GI:28451796
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 896 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGC 15
    ||||| |||||
Db 11 GGCTCTGGC 2

RESULT 61
AX626051
LOCUS      AX626051                11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3092 from Patent WO02053774.
ACCESSION  AX626051
VERSION     AX626051.1 GI:28454089
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3092 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
    ||||| |||
Db 1 AGGCTATTGG 10

RESULT 62
AX626057
LOCUS      AX626057                11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3098 from Patent WO02053774.
ACCESSION  AX626057
VERSION     AX626057.1 GI:28454095
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3098 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
    ||||| |||
Db 2 AGGCTGCTGG 11

RESULT 63
AX626089/c
LOCUS      AX626089                11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3130 from Patent WO02053774.
ACCESSION  AX626089
VERSION     AX626089.1 GI:28454127
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
Patent: WO 02053774-A 3130 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

5 AGGCTGTGG 14

Db

10 AGACTGTGG 1

RESULT 64

AX627011
LOCUS
DEFINITION
TITLE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
Patent: WO 02053774-A 4052 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

2 TTGAGGCTGT 11

Db

1 TTGACGCTGT 10

RESULT 65

AX628872
LOCUS
DEFINITION
TITLE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
Patent: WO 02053774-A 5913 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

8 CTGTGGCGA 17

Db

1 CTGTTGGTGA 10

RESULT 66

AX629473
LOCUS
DEFINITION
TITLE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
Patent: WO 02053774-A 6514 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1 CTTGAGGCTG 10

Db

1 CTGGAGGCTG 10

RESULT 67

AX631276/c
LOCUS
DEFINITION
TITLE
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
Patent: WO 02053774-A 8318 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

6 GGCTGTGGC 15

Db

11 GGCTCTGGC 2

RESULT 68

AR224222 LOCUS AR224222 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6440706.
ACCESSION AR224222
VERSION AR224222.1 GI:23332966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Vogelstein,B. and Kinzler,K.W.
TITLE Digital amplification
JOURNAL Patent: US 6440706-A 7 27-AUG-2002;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GCTGTTGGCG 16
Db 1 GCTGTTGGCG 10
RESULT 69
AR224228 LOCUS AR224228 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 13 from patent US 6440706.
ACCESSION AR224228
VERSION AR224228.1 GI:23332972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Vogelstein,B. and Kinzler,K.W.
TITLE Digital amplification
JOURNAL Patent: US 6440706-A 13 27-AUG-2002;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GCTGTTGGCG 16
Db 1 GCTGTTGGCG 10
RESULT 70
AR224229 LOCUS AR224229 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 14 from patent US 6440706.
ACCESSION AR224229
VERSION AR224229.1 GI:23332973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Vogelstein,B. and Kinzler,K.W.
TITLE Digital amplification
JOURNAL Patent: US 6440706-A 14 27-AUG-2002;
FEATURES
source
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GCTGTTGGCG 16
Db 1 GCTGTTGGCG 10
RESULT 71
AX078111 LOCUS AX078111 12 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 5 from Patent WO0106016.
ACCESSION AX078111
VERSION AX078111.1 GI:13157856
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS
TITLE Amplification of nucleic acids with electronic detection
JOURNAL Patent: WO 0106016-A 5 25-JAN-2001;
FEATURES
source
Location/Qualifiers
1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic."

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTTGAGGCTG 10
Db 2 CTCGAGGCTG 11
RESULT 72
BD209765 LOCUS BD209765 12 bp DNA linear PAT 17-JUL-2003
DEFINITION Electronic detection of nucleic acids using monolayers.
ACCESSION BD209765
VERSION BD209765.1 GI:33019535
KEYWORDS JP 2002513592-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 12)
AUTHORS Bammad,C. and Yu,C.
TITLE Electronic detection of nucleic acids using monolayers
JOURNAL Patent: JP 2002513592-A 5 14-MAY-2002;
COMMENT CLINICAL MICRO SENSORS INC
OS Artificial Sequence
PN JP 2002513592-A/5
PD 14-MAY-2002
PF 27-JAN-1999 JP 2000547270
PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR
17-AUG-1998 US 09/135183
PI CYNTHIA BAMDAD, CHANGYUN YU
PC C1201/68,C07F17/00,C07F19/00,C12N15/09,C12P19/34,G01N27/327,
G01N27/416,
PC G01N33/53,C12N15/00,G01N27/30,G01N27/46
CC Description of Artificial Sequence: synthetic FH Key
Location/Qualifiers
FT source 1. .12
FT Location/Qualifiers
1. .12
/organism="synthetic construct"

Db		1 CTGTTGGC 8	
RESULT 75			
AX668878			
LOCUS	9 bp DNA linear PAT 26-MAR-2003		
DEFINITION	Sequence 2327 from Patent WO0242459.		
ACCESSION	AX668878		
VERSION	AX668878.1 GI:29291855		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Liu,Q.		
TITLE	Position dependent recognition of gnn nucleotide triplets by zinc fingers		
JOURNAL	Patent: WO 0242459-A 2327 30-MAY-2002;		
FEATURES	Sangamo Biosciences Inc. (US)		
source	Location/Qualifiers		
	1..9		
	/organism="synthetic construct"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
	/note="example target DNA"		
Query Match	44.4%; Score 8; DB 1; Length 9;		
Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	8 CTGTTGGC 15		
Db	1 CTGTTGGC 8		
RESULT 76			
AX815434/c			
LOCUS	9 bp DNA linear PAT 09-DEC-2003		
DEFINITION	Sequence 9 from Patent EP1336658.		
ACCESSION	AX815434		
VERSION	AX815434.1 GI:39646135		
KEYWORDS	Nicotiana tabacum (common tobacco)		
SOURCE	Nicotiana tabacum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.		
REFERENCE	1		
AUTHORS	Chaboute,M.E., Hatzfield,Y., Reuzeau,C. and Schoonjans,R.		
TITLE	GI/s phase specific, s phase specific and meristem specific transcription control element in a transcribed region		
JOURNAL	Patent: EP 1336658-A 9 20-AUG-2003;		
FEATURES	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE DAE (FR)		
source	Location/Qualifiers		
	1..9		
	/organism="Nicotiana tabacum"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:4097"		
misc_feature	1..9		
	/note="MYB box"		
Query Match	44.4%; Score 8; DB 1; Length 9;		
Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	8 CTGTTGGC 15		
Db	8 CTGTTGGC 1		
RESULT 77			
AR002177/c			
LOCUS	10 bp DNA linear PAT 04-DEC-1999		
AR002177			

/mol_type="genomic DNA"		/db_xref="taxon:32630"	
Query Match			
46.7%; Score 8.4; DB 1; Length 12;			
Best Local Similarity 90.0%; Pred. No. 72;			
Matches 9; Conservative 0; Mismatches 0; Gaps 0;			
Qy	1 CTGAGGCTG 10		
Db	2 CTGAGGCTG 11		
RESULT 73			
AX668703			
LOCUS	9 bp DNA linear PAT 26-MAR-2003		
DEFINITION	Sequence 2152 from Patent WO0242459.		
ACCESSION	AX668703		
VERSION	AX668703.1 GI:29291678		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Liu,Q.		
TITLE	Position dependent recognition of gnn nucleotide triplets by zinc fingers		
JOURNAL	Patent: WO 0242459-A 2152 30-MAY-2002;		
FEATURES	Sangamo Biosciences Inc. (US)		
source	Location/Qualifiers		
	1..9		
	/organism="synthetic construct"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
	/note="example target DNA"		
Query Match	44.4%; Score 8; DB 1; Length 9;		
Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	9 TGTGGCG 16		
Db	2 TGTGGCG 9		
RESULT 74			
AX668877			
LOCUS	9 bp DNA linear PAT 26-MAR-2003		
DEFINITION	Sequence 2326 from Patent WO0242459.		
ACCESSION	AX668877		
VERSION	AX668877.1 GI:29291854		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Liu,Q.		
TITLE	Position dependent recognition of gnn nucleotide triplets by zinc fingers		
JOURNAL	Patent: WO 0242459-A 2326 30-MAY-2002;		
FEATURES	Sangamo Biosciences Inc. (US)		
source	Location/Qualifiers		
	1..9		
	/organism="synthetic construct"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
	/note="example target DNA"		
Query Match	44.4%; Score 8; DB 1; Length 9;		
Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	8 CTGTTGGC 15		

```
DEFINITION Sequence 31 from patent US 5741490.
ACCESSION AR002177
VERSION AR002177.1 GI:3963731
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 31 21-APR-1998;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTGCGCA 17
Db 9 GTTGCGCA 2

RESULT 78
BD239522/c
LOCUS BD239522 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239522
VERSION BD239522.1 GI:33049292
KEYWORDS JP 2002534056-A/940.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 940 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/940
PF 15-OCT-2002
PE 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111175
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1..10

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCTG 10
Db 10 TGAGGCTG 3

RESULT 79
E39696
LOCUS E39696 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39696
VERSION E39696.1 GI:18621787
KEYWORDS JP 2000279181-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 229 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/229
PD 10-OCT-2000
PE 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".
FEATURES Location/Qualifiers
source 1..10

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
Db 1 CTGTGGC 8

RESULT 80
AX152377/c
LOCUS AX152377 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 292 from Patent WO0138577.
ACCESSION AX152377
VERSION AX152377.1 GI:14534028
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 292 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
```

```
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 73;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGCTGTTG 13
      |||||
Db      9 GGCTGTTG 2

RESULT 81
AX153346
LOCUS      AX153346      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION      Sequence 1261 from Patent WO0138577.
ACCESSION      AX153346
VERSION      AX153346.1 GI:14534997
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcripomes
JOURNAL      Patent: WO 0138577-A 1261 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 73;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTTGGC 15
      |||||
Db      1 CTGTTGGC 8

RESULT 82
BD008001
LOCUS      BD008001      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION      BD008001
VERSION      BD008001.1 GI:18616374
KEYWORDS      JP 2001069993-A/277.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE      LPS activated human monocyte expressing genes
JOURNAL      Patent: JP 2001069993-A 277 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
PN JP 2001069993-A/277
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00.
PC A61P31/00,C12P21/08,C12N15/00
CC
FT Key
FT source
FT Location/Qualifiers
1. .10
/organism="Homo sapiens (human)"

FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 73;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTTGGC 15
      |||||
Db      1 CTGTTGGC 8

RESULT 83
AR049910/c
LOCUS      AR049910/c      11 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 15 from patent US 5824787.
ACCESSION      AR049910
VERSION      AR049910.1 GI:5971902
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Singer,P.A.
TITLE      Polynucleotide sizing reagent
JOURNAL      Patent: US 5824787-A 15 20-OCT-1998;
Location/Qualifiers
FEATURES
source
1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTGAGGC 8
      |||||
Db      9 CTTGAGGC 2

RESULT 84
I18622/c
LOCUS      I18622      11 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 8 from patent US 5500341.
ACCESSION      I18622
VERSION      I18622.1 GI:1598977
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Spears,P.A.
TITLE      Species-specific detection of Mycobacterium kansasii
JOURNAL      Patent: US 5500341-A 8 19-MAR-1996;
Location/Qualifiers
FEATURES
source
1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 81;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTTGGC 15
      |||||
Db      11 CTGTTGGC 4

RESULT 85
AX629696
```

LOCUS AX629696 11 bp DNA PAT 21-FEB-2003
 DEFINITION Sequence 6737 from Patent WO02053774.
 ACCESSION AX629696
 VERSION AX629696.1 GI:28457734
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
 AUTHORS Method for determining homeostasis of the skin
 TITLE Patent: WO 02053774-A 6737 11-JUL-2002;
 JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 44.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GCTGTGG 14
 Db 3 GCTGTGG 10
 RESULT 86
 AX630367
 LOCUS AX630367 11 bp DNA PAT 21-FEB-2003
 DEFINITION Sequence 7408 from Patent WO02053774.
 ACCESSION AX630367
 VERSION AX630367.1 GI:28458405
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
 AUTHORS Method for determining homeostasis of the skin
 TITLE Patent: WO 02053774-A 7408 11-JUL-2002;
 JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 44.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 CTGTGGC 15
 Db 1 CTGTGGC 8
 RESULT 87
 A91502/c
 LOCUS A91502 12 bp DNA PAT 22-JAN-2000
 DEFINITION Sequence 29 from Patent WO9824928.
 ACCESSION A91502
 VERSION A91502.1 GI:6740457
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Palliegaard,N. and Hokland,P.
 TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES

JOURNAL PATENT: WO 9824928-A 29 11-JUN-1998;
 FEATURES
 source
 1..12
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 CTGTGGC 15
 Db 12 CTGTGGC 5
 RESULT 88
 BD023284/c
 LOCUS BD023284 12 bp DNA PAT 27-AUG-2002
 DEFINITION Method for detecting abnormality in chromosome.
 ACCESSION BD023284
 VERSION BD023284.1 GI:22564507
 KEYWORDS JP 2001505428-A/29.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Parisgard,N. and Hokurando,P.
 TITLE Method for detecting abnormality in chromosome
 JOURNAL Patent: JP 2001505428-A 29 24-APR-2001;
 COMMENT NEILLS PARISGARD
 PN JP 2001505428-A/29
 PD 24-APR-2001
 PF 08-DEC-1997 JP 1998525090
 PI NEILLS PARISGARD,PATER HOKURANDO
 PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC /desc = 'DNA (synthetic)'
 FH Key Location/Qualifiers.
 FEATURES
 source
 1..12
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 CTGTGGC 15
 Db 12 CTGTGGC 5
 RESULT 89
 AR082362
 LOCUS AR082362 11 bp DNA PAT 31-AUG-2000
 DEFINITION Sequence 206 from patent US 5972704.
 ACCESSION AR082362
 VERSION AR082362.1 GI:10009088
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 unclassified.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
 Thompson,J.D.
 TITLE HIV nef targeted ribozymes
 JOURNAL Patent: US 5972704-A 206 26-OCT-1999;
 FEATURES Location/Qualifiers

```

source      1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGT 11
   |||||
Db 1 CTTGAGGAGT 11

RESULT 90
LOCUS      AR120904      11 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 206 from patent US 6159692.
ACCESSION  AR120904
VERSION     AR120904.1 GI:14104480
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
           Thompson,J.D.
TITLE     Method and reagent for inhibiting human immunodeficiency virus
           replication
JOURNAL   Patent: US 6159692-A 206 12-DEC-2000;
FEATURES   Location/Qualifiers
            source
            1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGT 11
   |||||
Db 1 CTTGAGGAGT 11

RESULT 91
LOCUS      BD274437      11 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational
           geometry.
ACCESSION  BD274437
VERSION     BD274437.1 GI:33084205
KEYWORDS   JP 2002543215-A/14.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   1 (bases 1 to 11)
AUTHORS   Manoharan,M. and Mohan,V.
TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
           geometry
JOURNAL   Patent: JP 2002543215-A 14 17-DEC-2002;
           ISIS PHARMACEUTICALS INC
COMMENT    OS Artificial Sequence
           PN JP 2002543215-A/14
           PD 17-DEC-2002
           PF 03-MAY-2000 JP 2000615638
           PR 03-MAY-1999 US 09/303586
           PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
           PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
           CC C12N15/00
           CC Oligonucleotide
           CC 2' aminolinker linkage
           FH Key Location/Qualifiers
           FT misc feature (6)..(7).
           FT Location/Qualifiers

source      1. .11
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGTGGCG 16
   |||||
Db 1 GGCTGTCTGCG 11

RESULT 92
LOCUS      I24463      11 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 7 from patent US 5543507.
ACCESSION  I24463
VERSION     I24463.1 GI:1604333
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Cook,P.D., Manoharan,M. and Bruice,T.
TITLE     Covalently cross-linked oligonucleotides
           Patent: US 5543507-A 7 06-AUG-1996;
           Location/Qualifiers
            source
            1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGTGGCG 16
   |||||
Db 1 GGCTGTCTGCG 11

RESULT 93
LOCUS      I78408      11 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 206 from patent US 5693535.
ACCESSION  I78408
VERSION     I78408.1 GI:3014562
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
           Thompson,J.D.
TITLE     HIV targeted ribozymes
           Patent: US 5693535-A 206 02-DEC-1997;
           Location/Qualifiers
            source
            1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGT 11
   |||||
Db 1 CTTGAGGAGT 11

RESULT 94
LOCUS      I88968
```


LOCUS I88968 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 10 from patent US 5719271.
ACCESSION I88968
VERSION I88968.1 GI:3408908
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 10 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

RESULT 95
LOCUS I88970 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 12 from patent US 5719271.
ACCESSION I88970
VERSION I88970.1 GI:3408910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 12 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

RESULT 96
LOCUS I88971 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 13 from patent US 5719271.
ACCESSION I88971
VERSION I88971.1 GI:3408911
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 13 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

LOCUS I88968 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 10 from patent US 5719271.
ACCESSION I88968
VERSION I88968.1 GI:3408908
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 10 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

RESULT 97
LOCUS I88972 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 14 from patent US 5719271.
ACCESSION I88972
VERSION I88972.1 GI:3408912
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 14 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

RESULT 98
LOCUS I88973 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 15 from patent US 5719271.
ACCESSION I88973
VERSION I88973.1 GI:3408913
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook, P. Dan., Manoharan, M. and Bruice, T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 15 17-FEB-1998;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

RESULT 99
LOCUS I88981 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 23 from patent US 5719271.
ACCESSION I88981
VERSION I88981.1 GI:3408921
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook,P.Dan., Manoharan,M. and Bruice,T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 23 17-FEB-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11
RESULT 100
I88982
LOCUS I88982 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 24 from patent US 5719271.
ACCESSION I88982
VERSION I88982.1 GI:3408922
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook,P.Dan., Manoharan,M. and Bruice,T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 24 17-FEB-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11
RESULT 101
I88983
LOCUS I88983 11 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 25 from patent US 5719271.
ACCESSION I88983
VERSION I88983.1 GI:3408923
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Cook,P.Dan., Manoharan,M. and Bruice,T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 25 17-FEB-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11

Db 1 GGCTGTTGGCG 11
RESULT 102
AR205797
LOCUS AR205797 11 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 14 from patent US 6369209.
ACCESSION AR205797
VERSION AR205797.1 GI:21503471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 14 09-APR-2002;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTTGGCG 16
|||||
Db 1 GGCTGTTGGCG 11
RESULT 103
AR301664/c
LOCUS AR301664 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 245 from patent US 6538173.
ACCESSION AR301664
VERSION AR301664.1 GI:31689466
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 245 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
|||||
Db 11 TTGAACCTGTT 1
RESULT 104
AR301737
LOCUS AR301737 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 318 from patent US 6538173.
ACCESSION AR301737
VERSION AR301737.1 GI:31689539
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing

```

JOURNAL Patent: US 6538173-A 318 25-MAR-2003;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GTGGTGTGG 11

RESULT 105
LOCUS AR399176 11 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6617442.
ACCESSION AR399176
VERSION AR399176.1 GI:40137665
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human Rnase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 16 09-SEP-2003;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTCTGGCG 16
Db 1 GGCTGTCTGGCG 11

RESULT 106
LOCUS AX393135 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 65 from Patent WO0210217.
ACCESSION AX393135
VERSION AX393135.1 GI:19701185
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 65 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGGCTCTGGC 11

JOURNAL Patent: US 6538173-A 318 25-MAR-2003;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GTGGTGTGG 11

RESULT 107
LOCUS AX470922 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 499 from Patent WO02053773.
ACCESSION AX470922
VERSION AX470922.1 GI:22206047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 499 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
Db 1 CTGTTGGCGAC 11

RESULT 108
LOCUS AX623196 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 237 from Patent WO02053774.
ACCESSION AX623196
VERSION AX623196.1 GI:28451137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 237 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGGCTCTGGC 11

RESULT 109
LOCUS AX623333/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 374 from Patent WO02053774.
ACCESSION AX623333
VERSION AX623333.1 GI:28451274
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 374 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 11 ACGCCGTGGC 1

RESULT 110
AX623779
LOCUS          AX623779          11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION     Sequence 820 from Patent WO02053774.
ACCESSION      AX623779
VERSION        AX623779.1 GI:28451720
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 820 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
Db 1 CTGGTGGCCAC 11

RESULT 111
AX625543
LOCUS          AX625543          11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION     Sequence 2584 from Patent WO02053774.
ACCESSION      AX625543
VERSION        AX625543.1 GI:28453484
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2584 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 374 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GAGGAGTTGG 11

RESULT 112
AX626232/c
LOCUS          AX626232          11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION     Sequence 3273 from Patent WO02053774.
ACCESSION      AX626232
VERSION        AX626232.1 GI:28454270
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3273 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGCA 17
Db 11 GGTGTGGCAA 1

RESULT 113
AX626661
LOCUS          AX626661          11 bp      DNA          linear          PAT 21-FEB-2003
DEFINITION     Sequence 3702 from Patent WO02053774.
ACCESSION      AX626661
VERSION        AX626661.1 GI:28454699
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3702 11-JUL-2002;
FEATURES     Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE       Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GAGTCTGTTCG 11

RESULT 114
```

```
AX626814
LOCUS AX626814 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3855 from Patent WO02053774.
ACCESSION AX626814
VERSION AX626814.1 GI:28454852
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3855 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGC 15
||| ||| |||
Db 1 AGGATGTGGC 11

RESULT 115
AX628155/c
LOCUS AX628155 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5196 from Patent WO02053774.
ACCESSION AX628155
VERSION AX628155.1 GI:28456193
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5196 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGC 15
||| ||| |||
Db 1 AGGATGTGGC 11

RESULT 116
AX628362/c
LOCUS AX628362 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5403 from Patent WO02053774.
ACCESSION AX628362
VERSION AX628362.1 GI:28456400
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5403 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGC 15
||| ||| |||
Db 11 AGGCTGGAGGC 1

RESULT 117
AX628435/c
LOCUS AX628435 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5476 from Patent WO02053774.
ACCESSION AX628435
VERSION AX628435.1 GI:28456473
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5476 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
||| ||| |||
Db 11 TTGAAGCAGTT 1

RESULT 118
AX628838
LOCUS AX628838 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5879 from Patent WO02053774.
ACCESSION AX628838
VERSION AX628838.1 GI:28456876
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5879 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTGG 14
||| ||| |||
Db 11 GAAGCTGCTGG 1
```

```
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5403 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
||| ||| |||
Db 11 TTGAAGCAGTT 1

RESULT 117
AX628435/c
LOCUS AX628435 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5476 from Patent WO02053774.
ACCESSION AX628435
VERSION AX628435.1 GI:28456473
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5476 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTGG 14
||| ||| |||
Db 11 GAAGCTGCTGG 1

RESULT 118
AX628838
LOCUS AX628838 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5879 from Patent WO02053774.
ACCESSION AX628838
VERSION AX628838.1 GI:28456876
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5879 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTGG 14
||| ||| |||
Db 11 GAAGCTGCTGG 1
```

```
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
Db 1 TGATGATGTTG 11

RESULT 119
AX628949
LOCUS AX628949 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5990 from Patent WO02053774.
ACCESSION AX628949
VERSION AX628949.1 GI:28456987
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5990 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTT 12
Db 1 TGGATGCTGTTT 11

RESULT 120
AX630617
LOCUS AX630617 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7658 from Patent WO02053774.
ACCESSION AX630617
VERSION AX630617.1 GI:28458655
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7658 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
Db 1 AGGCTCTGGC 11

RESULT 121
AX630754
LOCUS AX630754 11 bp DNA linear PAT 21-FEB-2003
```

```
DEFINITION Sequence 7795 from Patent WO02053774.
ACCESSION AX630754
VERSION AX630754.1 GI:28458792
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7795 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
Db 11 ACGCGGTGGC 1

RESULT 122
AX631200
LOCUS AX631200 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8242 from Patent WO02053774.
ACCESSION AX631200
VERSION AX631200.1 GI:28459244
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8242 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
Db 1 CTGTTGGCCAC 11

RESULT 123
AX710712
LOCUS AX710712 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 12 from Patent EP1288296.
ACCESSION AX710712
VERSION AX710712.1 GI:29787093
KEYWORDS Human immunodeficiency virus
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecck,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
```

```

TITLE      Method and reagent for inhibiting HBV viral replication
JOURNAL    Patent: EP 1288296-A 12 05-MAR-2003;
           RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
           source
             1..11
               /organism="Human immunodeficiency virus"
               /mol_type="unassigned RNA"
               /db_xref="taxon:12721"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CTTGAGGCTGTT 11
        |||||
Db      1 CTTGAGGAGGT 11

RESULT 124
BD124414/c
LOCUS      BD124414      11 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION  BD124414
VERSION     BD124414.1 GI:23219359
KEYWORDS    JP 2002503460-A/245.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1 (bases 1 to 11)
AUTHORS    Katz, E.H.
TITLE      Compositions and method for healing wound
JOURNAL    Patent: JP 2002503460-A 245 05-FEB-2002;
           THE WISTAR INSTITUTE
COMMENT     OS Mus musculus (mouse)
            PN JP 2002503460-A/245
            PD 05-FEB-2002
            PR 12-FEB-1999 JP 2000531545
            PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
            28-SEP-1998 US 60/102051
            PI ELLEN HEBER KATZ
            PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
            C12N5/00
            CC Compositions and method for healing wound
            FH Key Location/Qualifiers
            FT source
              1..11
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /db_xref="taxon:10090"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GAGGCTGTTGG 14
        |||||
Db      1 GTGGGTGTTGG 11

RESULT 126
A02238/c
LOCUS      A02238      12 bp      DNA      linear      PAT 26-APR-1996
DEFINITION Oligonucleotide sequence (adaptor 4) from patent EP0282042.
ACCESSION  A02238
VERSION     A02238.1 GI:488966
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 12)
AUTHORS    Doebl, H., Eggmann, B., Gentz, R., Hochuli, E. and Stueber, D.
TITLE      Fusion proteins and their purification
JOURNAL    Patent: EP 0282042-A 12 14-SEP-1988;
           F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
           source
             1..12
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 GGCTGTTGGCG 16
        |||||
Db      11 GGATCTTGGCG 1

RESULT 127
A02242/c
LOCUS      A02242      12 bp      DNA      linear      PAT 26-APR-1996
DEFINITION Oligonucleotide sequence (adaptor 6) from patent EP0282042.
ACCESSION  A02242
VERSION     A02242.1 GI:488968
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.

```

REFERENCE 1 (bases 1 to 12)
AUTHORS Doebeli,H., Eggmann,B., Gentz,R., Hochuli,E. and Stueber,D.
TITLE Fusion proteins and their purification
JOURNAL Patent: EP 0282042-A 16 14-SEP-1988;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
||| |||||
Db 11 GGGTTTGGCG 1

RESULT 128
LOCUS A71468
DEFINITION Sequence 27 from Patent WO9813521.
ACCESSION A71468
VERSION A71468.1 GI:4775080
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
JOURNAL PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
PATENT: WO 9813521-A 27 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES
source
1. .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
||| |||||
Db 2 GGACGTTGGCG 12

RESULT 129
LOCUS A71530/c
DEFINITION Sequence 89 from Patent WO9813521.
ACCESSION A71530
VERSION A71530.1 GI:4775142
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
JOURNAL PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
PATENT: WO 9813521-A 89 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES
source
1. .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCGA 17
||| |||||
Db 11 GCTGGTGACGA 1

RESULT 130
LOCUS A71545/c
DEFINITION Sequence 104 from Patent WO9813521.
ACCESSION A71545
VERSION A71545.1 GI:4775157
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
JOURNAL PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
PATENT: WO 9813521-A 104 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES
source
1. .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
||| |||||
Db 11 GGCAATTGGCG 1

RESULT 131
LOCUS AR012645/c
DEFINITION Sequence 7 from patent US 5763578.
ACCESSION AR012645
VERSION AR012645.1 GI:3970635
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fong,H.K.W.
TITLE All-trans retinaldehyde binding protein, and antibodies thereto
JOURNAL Patent: US 5763578-A 7 09-JUN-1998;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTGGCGAC 18
||| |||||
Db 12 CTGTGGGAGAC 2

RESULT 132
LOCUS AR096775/c
DEFINITION Sequence 7 from patent US 6008338.
ACCESSION AR096775

/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
||| ||| |||
Db 1 AGCTGTGGGC 11

RESULT 137

E29709 LOCUS 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, method for estimating state of
microorganism existing and method for estimating state of waste.

ACCESSION E29709.1 GI:13021212
VERSION JP 199276176-A/189.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi, I.
TITLE Method for amplifying DNA fragment, method for estimating state of
microorganism existing and method for estimating state of waste

JOURNAL Patent: JP 199276176-A 189 12-OCT-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT

OS Unidentified

PN JP 199276176-A/189

PD 12-OCT-1999

PF 31-MAR-1998 JP 1998087652

PR KOICHI INOUE

PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC

Strandedness: Single;

FH Key Location/Qualifiers

FT source 1..12 /organism='Unidentified'.

FEATURES

source
1..12
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
||| ||| |||
Db 1 AGCTGTGGGC 11

RESULT 138

E38683 LOCUS 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.

ACCESSION E38683
VERSION E38683.1 GI:18621345
KEYWORDS JP 2000270867-A/57.
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue, K.
TITLE Method and device for amplifying DNA fragment

JOURNAL Patent: JP 2000270867-A 57 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT

PN JP 2000270867-A/57

PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR KOICHI INOUE
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12 /organism='Unidentified'.

FEATURES

source
1..12
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
||| ||| |||
Db 1 AGCTGTGGGC 11

RESULT 139

E38815 LOCUS 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.

ACCESSION E38815

VERSION E38815.1 GI:18621477

KEYWORDS JP 2000270867-A/189.

SOURCE unclassified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Inoue, K.

TITLE Method and device for amplifying DNA fragment

JOURNAL Patent: JP 2000270867-A 189 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT

OS Unidentified

PN JP 2000270867-A/189

PD 03-OCT-2000

PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE

PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..12 /organism='Unidentified'.

FEATURES

source
1..12
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref="taxon:32644"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
||| ||| |||
Db 1 AGCTGTGGGC 11

RESULT 140

E64109 LOCUS 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method

for analyzing a group of microorganisms, and method for assaying contaminating substance.

ACCESSION E64109
 VERSION E64109.1 GI:13019513
 KEYWORDS JP 1999341989-A/57
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 1 (bases 1 to 12)
 Koichi, I.

Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance

Patent: JP 1999341989-A 57 14-DEC-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES

OS Artificial Sequence

PN JP 1999341989-A/57

PD 14-DEC-1999

PF 16-MAR-1999 JP 1999069694

PR

PI KOICHI INOUE

PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00

CC

FH Key Location/Qualifiers

FT source 1..12

FT Location/Qualifiers /organism='Artificial Sequence'.

FEATURES
 source

1..12 Location/Qualifiers

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 43.3%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 97;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15

|||||

1 AGCCTGTGGC 11

RESULT 141

E64241

LOCUS

DEFINITION E64241 12 bp DNA linear PAT 18-JUN-2001
 Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance.

ACCESSION E64241

VERSION E64241.1 GI:13019645

KEYWORDS JP 1999341989-A/189.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

1 (bases 1 to 12)

Koichi, I.

Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance

Patent: JP 1999341989-A 189 14-DEC-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES

OS Artificial Sequence

PN JP 1999341989-A/189

PD 14-DEC-1999

PF 16-MAR-1999 JP 1999069694

PR

PI KOICHI INOUE

PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00

CC

FEATURES
 source

1..12 Location/Qualifiers

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 43.3%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 97;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15

|||||

1 AAGCTGTGGC 11

Db

RESULT 142

I79841

LOCUS

DEFINITION I79841 12 bp DNA linear PAT 10-JUN-1998

ACCESSION I79841

VERSION I79841.1 GI:3208131

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Brakier-Gingras, L., Melan, Cedilla, on, P., Cote, M. and Payant, C.

TITLE DNA oligomers for inhibition of HIV by decreasing ribosomal

frameshifting

JOURNAL Patent: US 5707866-A 7 13-JAN-1998;

FEATURES

source

1..12 Location/Qualifiers

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 97;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14

|||||

2 GCGGCTGCTGG 12

Db

RESULT 143

AR371380

LOCUS

DEFINITION AR371380 12 bp DNA linear PAT 12-SEP-2003

ACCESSION AR371380

VERSION AR371380.1 GI:34608314

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)

AUTHORS Nandabalan, K. and Rothberg, J.M.

TITLE Identification and comparison of protein-protein interactions that

occur in populations and identification of inhibitors of these

interactors

JOURNAL Patent: US 6395478-A 34 28-MAY-2002;

FEATURES

source

1..12 Location/Qualifiers

/organism="unknown"

/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 97;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGA 17

```
Db          ||||| |||
2 GCTGCTGGTGA 12

RESULT 144
AX669059    AX669059    9 bp    DNA    linear    PAT 26-MAR-2003
LOCUS       Sequence 2508 from Patent WO0242459.
ACCESSION   AX669059
VERSION     AX669059.1 GI:29292036
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gmn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 2508 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES    source
            Location/Qualifiers
            1..9
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
    ||||| |||
Db 1 GAGGCTCTT 9

RESULT 145
A00110/c    A00110    10 bp    DNA    linear    PAT 09-MAR-1993
LOCUS       Nucleotide sequence 12 from patent number GB2180539.
ACCESSION   A00110
VERSION     A00110.1 GI:344082
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 10)
AUTHORS     .
JOURNAL     Patent: GB 2180539-A 12 01-APR-1987;
            Location/Qualifiers
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGCGGAC 18
    ||||| |||
Db 10 GTTGCGGAC 2

RESULT 146
A94606     A94606     10 bp    DNA    linear    PAT 26-JAN-2000
LOCUS       Sequence 6 from Patent EP0945462.
ACCESSION   A94606
VERSION     A94606.1 GI:6778919
KEYWORDS    .
SOURCE      unidentified
            unidentified
            ORGANISM

unclassified.
1 (bases 1 to 10)
Kumar,D. and Srivastava,B.S.
Mycrobacterium tuberculosis specific DNA fragment
Patent: EP 0945462-A 6 29-SEP-1999;
COUNCIL SCIENT IND RES (IN)
FEATURES    Location/Qualifiers
            1..10
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
    ||||| |||
Db 1 TTGAGGATG 9

RESULT 147
AR107764/c  AR107764    10 bp    DNA    linear    PAT 14-FEB-2001
LOCUS       Sequence 10 from patent US 6110667.
DEFINITION  AR107764
ACCESSION   AR107764
VERSION     AR107764.1 GI:12823251
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
            ORGANISM
            Unclassified.
            1 (bases 1 to 10)
            Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
            Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
            Patent: US 6110667-A 10 29-AUG-2000;
            Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
    ||||| |||
Db 9 TTGAGGATG 1

RESULT 148
AR107836/c  AR107836    10 bp    DNA    linear    PAT 14-FEB-2001
LOCUS       Sequence 82 from patent US 6110667.
DEFINITION  AR107836
ACCESSION   AR107836
VERSION     AR107836.1 GI:12823323
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
            ORGANISM
            Unclassified.
            1 (bases 1 to 10)
            Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
            Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
            Patent: US 6110667-A 82 29-AUG-2000;
            Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
    ||||| |||
Db 9 TTGAGGATG 1

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 10 GTTGGCGAC 18
    ||||| |||
Db 9 GTTGGTGAC 1

RESULT 149
LOCUS AR110398 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6114514.
ACCESSION AR110398
VERSION AR110398.1 GI:12826674
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Srivastava, R., Kumar, D. and Srivastava, B. Shanker.
TITLE Mycobacterium tuberculosis specific DNA fragment
JOURNAL Patent: US 6114514-A 6 05-SEP-2000;
FEATURES
    source
        1..10
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTG 10
    ||||| ||
Db 1 TTGAGGATG 9

RESULT 150
LOCUS AR157056 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242585.
ACCESSION AR157056
VERSION AR157056.1 GI:15125760
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Srivastava, R., Kumar, D. and Srivastava, B. Shanker.
TITLE Mycobacterium tuberculosis specific DNA fragment
JOURNAL Patent: US 6242585-A 6 05-JUN-2001;
FEATURES
    source
        1..10
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTG 10
    ||||| ||
Db 1 TTGAGGATG 9

RESULT 151
LOCUS AR167216 10 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 50 from patent US 6284466.
ACCESSION AR167216
VERSION AR167216.1 GI:16243725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)

AUTHORS Benson, A.
TITLE Method of detecting genetic polymorphisms using over represented
sequences
JOURNAL Patent: US 6284466-A 50 04-SEP-2001;
FEATURES
    source
        1..10
        Location/Qualifiers
        1..10
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGA 17
    ||||| |||
Db 2 TGCTGGCGA 10

RESULT 152
LOCUS BD239703 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239703
VERSION BD239703.1 GI:33049473
KEYWORDS JP 2002534056-A/1121.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1121 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1121
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089897,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090040,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/01, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source
1..10
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
    source
        1..10
        Location/Qualifiers
        1..10
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

[illegible]


```

source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCG 16
Db 10 CTCTGGCG 2

RESULT 166
LOCUS AX667829 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1278 from Patent WO0242459.
ACCESSION AX667829
VERSION AX667829.1 GI:29291366
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1278 30-MAY-2002;
Sangamo Biosciences Inc. (US)
LOCATION/Qualifiers
FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
Db 2 AGGCTGTTG 10

RESULT 167
LOCUS AX675461 10 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 185 from Patent WO0246408.
ACCESSION AX675461
VERSION AX675461.1 GI:29333527
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Li, L., Furtak, K., Perna, A., Patturajan, M., Shimkets, R.A., Guo, X.,
Casman, S.J., Burgess, C.E., Malyankar, U.M., Tchernev, V.T.,
Vernes, C.A., Spytek, K.A., Agee, M., Rastelli, L., Shenoy, S.G.,
Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Gerlach, V., Edinger, S.,
Macdougall, J.R., Peyman, J.A., Gunther, E., Stone, D.J., Ellerman, K.
and Gangolli, E.A.
TITLE Human proteins, polynucleotides encoding them and methods of using
the same
JOURNAL Patent: WO 0246408-A 185 13-JUN-2002;
Curagen Corporation (US)
LOCATION/Qualifiers
FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="SAGE library tag sequence"

source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
Db 1 AGCCTGTTG 9

RESULT 168
LOCUS AX716741 10 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 3 from Patent WO03020984.
ACCESSION AX716741
VERSION AX716741.1 GI:29890055
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Nelson, J., Fuller, C., Sood, A. and Kumar, S.
TITLE Terminal-phosphate-labeled nucleotides and methods of use
JOURNAL Patent: WO 03020984-A 3 13-MAR-2003;
Amersham Biosciences Corp. (US)
LOCATION/Qualifiers
FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA Template"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
Db 2 AGGCTGTTG 10

RESULT 169
LOCUS BD073892 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073892
VERSION BD073892.1 GI:22619495
KEYWORDS JP 2001512698-A/17.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Suishelm, K., Hosier, S. and Kubbies, M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 17 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/17
PD 28-AUG-2001
PR 05-AUG-1998 JP 2000506375
PF 08-AUG-1997 US 08/908873
PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC
C1201/68, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N15/09, PC
C12P21/02
PC C12P21/08, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Isolation of novel aging factor gene P23
FH Key Location/Qualifiers
FT source 1..10
/organism="Unidentified".
FT Location/Qualifiers
source
1..10

```

```
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
    |||||
Db 2 GAGGGTGTT 10

RESULT 170
BD161386/c
LOCUS      BD161386          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161386
VERSION    BD161386.1 GI:27867144
KEYWORDS  JP 2002186482-A/208.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE     Human activated Th1 and Th2 cell expression genes
JOURNAL   Patent: JP 2002186482-A 208 02-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002186482-A/208
          PD 02-JUL-2002
          PF 19-DEC-2000 JP 2000385816
          PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
          C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
          activated Th1 and Th2 cell expression genes FH Key
          Location/Qualifiers
          FT source      1..10
                          /organism='Homo sapiens (human)'.

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
    |||||
Db 2 GAGGGTGTT 10

RESULT 170
BD161386/c
LOCUS      BD161386          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161386
VERSION    BD161386.1 GI:27867144
KEYWORDS  JP 2002186482-A/208.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE     Human activated Th1 and Th2 cell expression genes
JOURNAL   Patent: JP 2002186482-A 208 02-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002186482-A/208
          PD 02-JUL-2002
          PF 19-DEC-2000 JP 2000385816
          PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
          C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
          activated Th1 and Th2 cell expression genes FH Key
          Location/Qualifiers
          FT source      1..10
                          /organism='Homo sapiens (human)'.

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
    |||||
Db 10 AGGCTTTG 2

RESULT 171
BD161453
LOCUS      BD161453          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161453
VERSION    BD161453.1 GI:27867211
KEYWORDS  JP 2002186482-A/275.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE     Human activated Th1 and Th2 cell expression genes
JOURNAL   Patent: JP 2002186482-A 275 02-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002186482-A/275
          PD 02-JUL-2002
          PF 19-DEC-2000 JP 2000385816
          PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
          C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
          activated Th1 and Th2 cell expression genes FH Key
          Location/Qualifiers
          FT source      1..10
                          /organism='Homo sapiens (human)'.

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
    |||||
Db 10 AGGCTTTG 2

RESULT 171
BD161453
LOCUS      BD161453          10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161453
VERSION    BD161453.1 GI:27867211
KEYWORDS  JP 2002186482-A/275.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE     Human activated Th1 and Th2 cell expression genes
JOURNAL   Patent: JP 2002186482-A 275 02-JUL-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002186482-A/275
          PD 02-JUL-2002
          PF 19-DEC-2000 JP 2000385816
          PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
          C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
          activated Th1 and Th2 cell expression genes FH Key
          Location/Qualifiers
          FT source      1..10
                          /organism='Homo sapiens (human)'.

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGCA 17
    |||||
Db 9 TGTGGGAGA 1

RESULT 173
BD187825/c
LOCUS      BD187825          10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION A method for designing a peptide nucleic acid.
ACCESSION  BD187825
VERSION    BD187825.1 GI:32997564
KEYWORDS  JP 2003009876-A/1.
SOURCE     synthetic construct
```

```

ORGANISM      synthetic construct
LOCUS          1 (bases 1 to 10)
DEFINITION    A method for designing a peptide nucleic acid
ACCESSION     Sudo, Y. and Sugimoto, N.
VERSION       A method for designing a peptide nucleic acid
KEYWORDS      Patent: JP 2003009876-A 1 14-JAN-2003;
SOURCE        FUJII PHOTO FILM CO LTD
ORGANISM      OS Artificial Sequence
REFERENCE      PN JP 2003009876-A/1
AUTHORS       PD 14-JAN-2003
TITLE         PF 02-JUL-2001 JP 2001200370
JOURNAL       PI YUKIO SUDO, NAOKI SUGIMOTO
COMMENT       PC C12N15/09, C12Q1/68, C12N15/00
              CC A method for designing a peptide nucleic acid PH Key
              Location/Qualifiers
              FT source 1..10
              FT /organism='Artificial Sequence'.
FEATURES      source
              1..10
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 9 GCTGTTAGC 1

RESULT 174
LOCUS          BD187826
DEFINITION    A method for designing a peptide nucleic acid.
ACCESSION     BD187826
VERSION       BD187826.1 GI:32997565
KEYWORDS      JP 2003009876-A/2.
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE      1 (bases 1 to 10)
AUTHORS       Sudo, Y. and Sugimoto, N.
TITLE         A method for designing a peptide nucleic acid
JOURNAL       Patent: JP 2003009876-A 2 14-JAN-2003;
COMMENT       FUJII PHOTO FILM CO LTD
              OS Artificial Sequence
              PN JP 2003009876-A/2
              PD 14-JAN-2003
              PF 02-JUL-2001 JP 2001200370
              PI YUKIO SUDO, NAOKI SUGIMOTO
              PC C12N15/09, C12Q1/68, C12N15/00
              CC A method for designing a peptide nucleic acid PH Key
              Location/Qualifiers
              FT source 1..10
              FT /organism='Artificial Sequence'.
FEATURES      source
              1..10
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 2 GCTGTTAGC 10

RESULT 175

```

```

BD209761
LOCUS          BD209761
DEFINITION    Electronic detection of nucleic acids using monolayers.
ACCESSION     BD209761
VERSION       BD209761.1 GI:33019531
KEYWORDS      JP 2002513592-A/1.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Bandad, C. and Yu, C.
TITLE         Electronic detection of nucleic acids using monolayers
JOURNAL       Patent: JP 2002513592-A 1 14-MAY-2002;
COMMENT       CLINICAL MICRO SENSORS INC
              OS Artificial Sequence
              PN JP 2002513592-A/1
              PD 14-MAY-2002
              PF 27-JAN-1999 JP 2000547270
              PR 06-MAY-1998 US 60/084425, 06-MAY-1998 US 60/084509 PR
              PI CYNTHIA BANDAD, CHANGYUN YU
              PC C12Q1/68, C07F17/00, C07F19/00, C12N15/09, C12P19/34, G01N27/327,
              PC G01N27/416
              PC G01N33/53, C12N15/00, G01N27/30, G01N27/46
              CC Description of Artificial Sequence: synthetic FH Key
              Location/Qualifiers
              FT source 1..10
              FT /organism='Artificial Sequence'.
FEATURES      source
              1..10
              Location/Qualifiers
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
Db 2 CTCGAGGCT 10

RESULT 176
LOCUS          A00109/c
DEFINITION    Nucleotide sequence 11 from patent number GB2180539.
ACCESSION     A00109
VERSION       A00109.1 GI:344081
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE      1 (bases 1 to 11)
AUTHORS       Patent: GB 2180539-A 11 01-APR-1987;
JOURNAL       Location/Qualifiers
FEATURES      source
              1..11
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
Db 10 GTTGGCGAC 2

RESULT 177
A11801

```

LOCUS A11801 11 bp DNA linear PAT 01-DEC-1993
DEFINITION Ttp-1.
ACCESSION A11801
VERSION A11801.1 GI:489391
SOURCE .
KEYWORDS unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 11)
AUTHORS Hauptmann,R., Himmler,A. and Swetly,P.
TITLE Horse gamma interferon
JOURNAL Patent: EP 0271824-A 26 22-JUN-1988;
BOHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES Location/Qualifiers
source 1..11
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
| | | | |
Db 3 TTGAGGCTG 11

RESULT 178
A33068 11 bp DNA linear PAT 11-DEC-1996
LOCUS A33068
DEFINITION ScFv PCR product BamHI insert mutagenic oligo.
ACCESSION A33068
VERSION A33068.1 GI:1926700
KEYWORDS .
SOURCE synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS .
TITLE METHODS FOR PRODUCING MEMBERS OF SPECIFIC BINDING PAIRS
JOURNAL Patent: WO 9201047-A 191 23-JAN-1992;
FEATURES Location/Qualifiers
source 1..11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
| | | | |
Db 1 GAGGCTGGYG 11

RESULT 179
AR074503/c 11 bp DNA linear PAT 28-AUG-2000
LOCUS AR074503
DEFINITION Sequence 82 from patent US 5955075.
ACCESSION AR074503
VERSION AR074503.1 GI:10001258
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 82 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..11

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 180
AR081183/c 11 bp DNA linear PAT 31-AUG-2000
LOCUS AR081183
DEFINITION Sequence 82 from patent US 5972353.
ACCESSION AR081183
VERSION AR081183.1 GI:10007911
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 5972353-A 82 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 181
AR085380 11 bp DNA linear PAT 01-SEP-2000
LOCUS AR085380
DEFINITION Sequence 82 from patent US 5981711.
ACCESSION AR085380
VERSION AR085380.1 GI:10012149
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 82 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 182
AR088128 11 bp DNA linear PAT 07-SEP-2000
LOCUS AR088128
DEFINITION Sequence 82 from patent US 5989838.
ACCESSION AR088128

LOCUS A11801 11 bp DNA linear PAT 01-DEC-1993
DEFINITION Ttp-1.
ACCESSION A11801
VERSION A11801.1 GI:489391
SOURCE .
KEYWORDS unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 11)
AUTHORS Hauptmann,R., Himmler,A. and Swetly,P.
TITLE Horse gamma interferon
JOURNAL Patent: EP 0271824-A 26 22-JUN-1988;
BOHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES Location/Qualifiers
source 1..11
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 180
AR081183/c 11 bp DNA linear PAT 31-AUG-2000
LOCUS AR081183
DEFINITION Sequence 82 from patent US 5972353.
ACCESSION AR081183
VERSION AR081183.1 GI:10007911
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 5972353-A 82 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 181
AR085380 11 bp DNA linear PAT 01-SEP-2000
LOCUS AR085380
DEFINITION Sequence 82 from patent US 5981711.
ACCESSION AR085380
VERSION AR085380.1 GI:10012149
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 82 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
| | | | |
Db 11 TGAGCCTGT 3

RESULT 182
AR088128 11 bp DNA linear PAT 07-SEP-2000
LOCUS AR088128
DEFINITION Sequence 82 from patent US 5989838.
ACCESSION AR088128

VERSION AR088128.1 GI:10014891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
Unclassified.
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 82 23-NOV-1999;
LOCATION/Qualifiers
FEATURES 1..11
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGCCTGT 11
|||||
Db 11 TGAGCCTGT 3
RESULT 183
AR104287/c
LOCUS AR104287 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 82 from patent US 6093548.
ACCESSION AR104287
VERSION AR104287.1 GI:12816995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
Unclassified.
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 82 25-JUL-2000;
LOCATION/Qualifiers
FEATURES 1..11
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGCCTGT 11
|||||
Db 11 TGAGCCTGT 3
RESULT 184
AR143549/c
LOCUS AR143549 11 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 82 from patent US 6204370.
ACCESSION AR143549
VERSION AR143549.1 GI:15104835
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
Unclassified.
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 82 20-MAR-2001;
LOCATION/Qualifiers
FEATURES 1..11
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGCCTGT 11
|||||
Db 11 TGAGCCTGT 3
RESULT 185
AR171455/c
LOCUS AR171455 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 82 from patent US 6297041.
ACCESSION AR171455
VERSION AR171455.1 GI:17910405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
Unclassified.
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 82 02-OCT-2001;
LOCATION/Qualifiers
FEATURES 1..11
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGCCTGT 11
|||||
Db 11 TGAGCCTGT 3
RESULT 186
AR171626/c
LOCUS AR171626 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 82 from patent US 6297051.
ACCESSION AR171626
VERSION AR171626.1 GI:17910576
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
Unclassified.
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297051-A 82 02-OCT-2001;
LOCATION/Qualifiers
FEATURES 1..11
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGCCTGT 11
|||||
Db 11 TGAGCCTGT 3
RESULT 187
BD243216/c
LOCUS BD243216 11 bp DNA linear PAT 17-JUL-2003
DEFINITION MN gene and protein.
ACCESSION BD243216
VERSION BD243216.1 GI:33052986
KEYWORDS JP 2002528085-A/65.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: JP 2002528085-A 65 03-SEP-2002;
INSTITUTE OF VIROLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002528085-A/65
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
JAN ZAVADA,SILVIA PASTOREKOVA,JAFOMIR PASTOREK PC
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
C07K14/47,
PC C1201/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
CC MN gene and protein
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
FEATURES
source 1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
|||||
Db 11 TGAGGCTGT 3

RESULT 188
AR256517/c
LOCUS AR256517 11 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6485901.
ACCESSION AR256517
VERSION AR256517.1 GI:27306109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gildea,B.D., Coull,J.M., Hyldig-Nielsen,J.J. and Fianadaca,M.J.
TITLE Methods, kits and compositions pertaining to linear beacons
JOURNAL Patent: US 6485901-A 3 26-NOV-2002;
FEATURES
source 1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
|||||
Db 9 GCTGTTGGC 1

RESULT 189
AR301456/c
LOCUS AR301456 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 37 from patent US 6538173.
ACCESSION AR301456
VERSION AR301456.1 GI:31689258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.

REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: JP 2002528085-A 65 03-SEP-2002;
INSTITUTE OF VIROLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002528085-A/65
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
JAN ZAVADA,SILVIA PASTOREKOVA,JAFOMIR PASTOREK PC
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
C07K14/47,
PC C1201/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
CC MN gene and protein
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
FEATURES
source 1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
|||||
Db 11 TGAGGCTGT 3

RESULT 188
AR256517/c
LOCUS AR256517 11 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6485901.
ACCESSION AR256517
VERSION AR256517.1 GI:27306109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gildea,B.D., Coull,J.M., Hyldig-Nielsen,J.J. and Fianadaca,M.J.
TITLE Methods, kits and compositions pertaining to linear beacons
JOURNAL Patent: US 6485901-A 3 26-NOV-2002;
FEATURES
source 1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
|||||
Db 9 GCTGTTGGC 1

RESULT 189
AR301456/c
LOCUS AR301456 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 37 from patent US 6538173.
ACCESSION AR301456
VERSION AR301456.1 GI:31689258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.

```

```

TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 37 25-MAR-2003;
FEATURES
source 1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
|||||
Db 11 GTTGGTGAC 3

RESULT 190
AR301685/c
LOCUS AR301685 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 266 from patent US 6538173.
ACCESSION AR301685
VERSION AR301685.1 GI:31689487
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 266 25-MAR-2003;
FEATURES
source 1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
|||||
Db 11 GTTGGTGAC 3

RESULT 191
AR430441/c
LOCUS AR430441 11 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6649349.
ACCESSION AR430441
VERSION AR430441.1 GI:40191238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gildea,B.D., Coull,J.M. and Hyldig-Nielsen,J.J.
TITLE In-situ methods for analyzing target sequences using linear beacons
JOURNAL Patent: US 6649349-A 3 18-NOV-2003;
FEATURES
source 1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
|||||
Db 9 GCTGTTGGC 1

RESULT 192

```

AX393080/c
LOCUS AX393080 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 10 from Patent WO0210217.
ACCESSION AX393080
VERSION AX393080.1 GI:19701130
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS St Croix, B., Kinzler, K.W. and Vogelstein, B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 10 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CTTGAGGCT 9
Db 11 CTTGAGGAT 3
RESULT 193
AX470739/c
LOCUS AX470739 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 316 from Patent WO02053773.
ACCESSION AX470739
VERSION AX470739.1 GI:22205864
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 316 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CTTGAGGCT 9
Db 11 CTTGAGGAT 3
RESULT 194
AX471259/c
LOCUS AX471259 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 836 from Patent WO02053773.
ACCESSION AX471259
VERSION AX471259.1 GI:22206384
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 836 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 TGAGGCTGT 11
Db 9 TGAGGATGT 1
RESULT 195
AX471804
LOCUS AX471804 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1381 from Patent WO02053773.
ACCESSION AX471804
VERSION AX471804.1 GI:22206929
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1381 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 GGCTGTGG 14
Db 2 GGCTGTGG 10
RESULT 196
AX623471/c
LOCUS AX623471 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 512 from Patent WO02053774.
ACCESSION AX623471
VERSION AX623471.1 GI:28451412
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 512 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;

```
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
Db 10 GGCTGGTGG 2
|||||

RESULT 197
AX623599/c
LOCUS AX623599 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 640 from Patent WO02053774.
ACCESSION AX623599
VERSION AX623599.1 GI:28451540
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 640 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGCC 15
Db 11 GCTGTTGCC 3
|||||

RESULT 198
AX624037/c
LOCUS AX624037 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1078 from Patent WO02053774.
ACCESSION AX624037
VERSION AX624037.1 GI:28451978
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1078 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
Db 11 TTTAGGCTG 3
|||||

RESULT 199
AX625216/c
LOCUS AX625216 11 bp DNA linear PAT 21-FEB-2003
```

```
DEFINITION Sequence 2257 from Patent WO02053774.
ACCESSION AX625216
VERSION AX625216.1 GI:28453157
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2257 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 11 GAGGCCGTT 3
|||||

RESULT 200
AX625287
LOCUS AX625287 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2328 from Patent WO02053774.
ACCESSION AX625287
VERSION AX625287.1 GI:28453228
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2328 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTTTTGG 14
Db 1 GGCTTTTGG 9
|||||

RESULT 201
AX625755/c
LOCUS AX625755 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2796 from Patent WO02053774.
ACCESSION AX625755
VERSION AX625755.1 GI:28453696
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
```



```

JOURNAL Patent: WO 02053774-A 2796 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTGG 14
Db 11 GGCTGTGG 3

RESULT 202
AX625897/c
LOCUS
DEFINITION Sequence 2938 from Patent WO02053774.
ACCESSION AX625897
VERSION AX625897.1 GI:28453935
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2938 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
Db 11 TTCAGGCTG 3

RESULT 203
AX626004/c
LOCUS
DEFINITION Sequence 3045 from Patent WO02053774.
ACCESSION AX626004
VERSION AX626004.1 GI:28454042
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3045 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1
Db 2 CCTGAGGCT 10

RESULT 206
AX627289
LOCUS
DEFINITION Sequence 4330 from Patent WO02053774.
ACCESSION AX627289

```

```

Qy 9 TGTGGCGA 17
Db 11 TGTGGAGA 3

RESULT 204
AX627030/c
LOCUS
DEFINITION Sequence 4071 from Patent WO02053774.
ACCESSION AX627030
VERSION AX627030.1 GI:28455068
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4071 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 13
Db 9 AGGCTGTGG 1

RESULT 205
AX627103
LOCUS
DEFINITION Sequence 4144 from Patent WO02053774.
ACCESSION AX627103
VERSION AX627103.1 GI:28455141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4144 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1
Db 2 CCTGAGGCT 10

RESULT 206
AX627289
LOCUS
DEFINITION Sequence 4330 from Patent WO02053774.
ACCESSION AX627289

```



```

Db      11 CGTGAGGCT 3
      1 |||||
RESULT 211
AX628883/c
LOCUS   AX628883          11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 5924 from Patent WO02053774.
ACCESSION   AX628883
VERSION     AX628883.1 GI:28456921
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5924 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 TTGAGGCTG 10
            |||||
Db      11 TTCAGGCTG 3
      1 |||||
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 TTGAGGCTG 10
            |||||
Db      11 TTCAGGCTG 3
      1 |||||
RESULT 212
AX630181
LOCUS   AX630181          11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 7222 from Patent WO02053774.
ACCESSION   AX630181
VERSION     AX630181.1 GI:28458219
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7222 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 TTGAGGCTG 10
            |||||
Db      11 TTCAGGCTG 3
      1 |||||
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 TTGAGGCTG 10
            |||||
Db      2 TTGGGCTG 10
      2 TTGGGCTG 10
      1 |||||
RESULT 213
AX630892/c
LOCUS   AX630892          11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 7933 from Patent WO02053774.
ACCESSION   AX630892
VERSION     AX630892.1 GI:28458932
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8500 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      2 TTGAGGCTG 10
            |||||
Db      2 TTGGGCTG 10
      2 TTGGGCTG 10
      1 |||||

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7933 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      6 GGCTGTTGG 14
            |||||
Db      10 GGCTGTTGG 2
      10 GGCTGTTGG 2
      1 |||||
RESULT 214
AX631020/c
LOCUS   AX631020          11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 8061 from Patent WO02053774.
ACCESSION   AX631020
VERSION     AX631020.1 GI:28459062
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8061 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      7 GCTGTGGC 15
            |||||
Db      11 GCTGTGGC 3
      11 GCTGTGGC 3
      1 |||||
RESULT 215
AX631458/c
LOCUS   AX631458          11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 8500 from Patent WO02053774.
ACCESSION   AX631458
VERSION     AX631458.1 GI:28459524
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 8500 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

```

```

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
Db 11 TTTAGGCTG 3

RESULT 216
AX632637/c
LOCUS
DEFINITION Sequence 9679 from Patent WO02053774.
ACCESSION AX632637
VERSION AX632637.1 GI:28468252
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9679 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 11 GAGGCGGTT 3

RESULT 217
AX632708
LOCUS
DEFINITION Sequence 9750 from Patent WO02053774.
ACCESSION AX632708
VERSION AX632708.1 GI:28468323
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9750 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GCGCTGTTGG 14
Db 1 GCGTTTGG 9

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18

```

```

RESULT 218
AX632818
LOCUS
DEFINITION Sequence 9860 from Patent WO02053774.
ACCESSION AX632818
VERSION AX632818.1 GI:28468433
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9860 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 2 TGAGGCTTT 10

RESULT 219
BD124206/c
LOCUS
DEFINITION Compositions and method for healing wound.
ACCESSION BD124206
VERSION BD124206.1 GI:23219151
KEYWORDS JP 2002503460-A/37.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 37 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/37
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
/organism="Mus musculus"
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18

```

```

Db      11 GTTGGTGAC 3
||||| |||
Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 220
BD124435/c
LOCUS      BD124435      11 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION  BD124435
VERSION     BD124435.1 GI:23219380
KEYWORDS    JP 2002503460-A/266.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1 (bases 1 to 11)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL     Katz, E.H.
COMMENT     Compositions and method for healing wound
PATENT: JP 2002503460-A 266 05-FEB-2002;
THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PN JP 2002503460-A/266
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FT key
FT source 1..11
FT Location/Qualifiers
          /organism="Mus musculus"
          /mol_type="genomic DNA"
          /db_xref="taxon:10090"
FEATURES
source 1..11
          Location/Qualifiers
          /organism="Mus musculus (mouse)"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      10 GTTGGCGAC 18
||||| |||
Db      11 GTTGGTGAC 3

RESULT 221
AX205218
LOCUS      AX205218      9 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION Sequence 110 from Patent WO0155369.
ACCESSION  AX205218
VERSION     AX205218.1 GI:15394473
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 9)
AUTHORS     Mauro,V.P., Edelman,G.M., Chappell,G.M., Owens,G., Pinkstaff,J.K.,
TITLE       Krushel,L. and Zhou,W.
JOURNAL     Synthetic internal ribosome entry sites and methods of identifying
same
PATENT: WO 0155369-A 110 02-AUG-2001;
The Scripps Research Institute (US) ; The Neurosciences Institute
FEATURES
source 1..9
          Location/Qualifiers
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
          /note="random 9 nt sequence"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6 GGCTGTT 12
||||| |||
Db      2 GGCTGTT 8

RESULT 222
AX667082
LOCUS      AX667082      9 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 531 from Patent WO0242459.
ACCESSION  AX667082
VERSION     AX667082.1 GI:29291232
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL     fingers
COMMENT     Patent: WO 0242459-A 531 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source 1..9
          Location/Qualifiers
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
          /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      8 CTGTGG 14
||||| |||
Db      2 CTGTGG 8

RESULT 223
AX668677
LOCUS      AX668677      9 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 2126 from Patent WO0242459.
ACCESSION  AX668677
VERSION     AX668677.1 GI:29291652
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL     fingers
COMMENT     Patent: WO 0242459-A 2126 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source 1..9
          Location/Qualifiers
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
          /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 AGGCTGT 11
||||| |||
Db      2 AGGCTGT 8

```

```
RESULT 224
AX668678          AX668678          9 bp  DNA  linear  PAT 26-MAR-2003
DEFINITION  Sequence 2127 from Patent WO0242459.
ACCESSION   AX668678
VERSION     AX668678.1  GI:29291653
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 2127 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
            1..9
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
    |||||
Db 2 AGGCTGT 8

RESULT 225
AX668679          AX668679          9 bp  DNA  linear  PAT 26-MAR-2003
DEFINITION  Sequence 2128 from Patent WO0242459.
ACCESSION   AX668679
VERSION     AX668679.1  GI:29291654
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 2128 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
            1..9
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
    |||||
Db 2 AGGCTGT 8

RESULT 226
AX668680          AX668680          9 bp  DNA  linear  PAT 26-MAR-2003
DEFINITION  Sequence 2129 from Patent WO0242459.
ACCESSION   AX668680
VERSION     AX668680.1  GI:29291655
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 2129 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
            1..9
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
    |||||
Db 2 AGGCTGT 8
```

```
artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 2129 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..9
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
    |||||
Db 1 GAGGCTG 7

RESULT 227
AR070982/c        AR070982          10 bp  DNA  linear  PAT 18-FEB-2000
LOCUS          AR070982
DEFINITION  Sequence 16 from patent US 5908978.
ACCESSION   AR070982
VERSION     AR070982.1  GI:7221870
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Ameron,H.V., Wilcox,P., Sederoff,R.R., Kuhlman,E.George.,
            O'Malley,D.M. and Grattapaglia,D.
TITLE       Methods for within family selection of disease resistance in woody
            perennials using genetic markers
JOURNAL     Patent: US 5908978-A 16 01-JUN-1999;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
    |||||
Db 7 AGGCTGT 1

RESULT 228
AR107758/c        AR107758          10 bp  DNA  linear  PAT 14-FEB-2001
LOCUS          AR107758
DEFINITION  Sequence 4 from patent US 6110667.
ACCESSION   AR107758
VERSION     AR107758.1  GI:12823245
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE       Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
JOURNAL     Patent: US 6110667-A 4 29-AUG-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
```

```

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 7 GCTGTTG 1

RESULT 229
LOCUS AR107840 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6110667.
ACCESSION AR107840
VERSION AR107840.1 GI:12823327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 86 29-AUG-2000;
FEATURES
source
1..10
Location/Qualifiers
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 8 GCTGTTG 2

RESULT 230
LOCUS AR161929 10 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6258537.
ACCESSION AR161929
VERSION AR161929.1 GI:16228959
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keinath,A.P., Somai,B.M. and Dean,R.A.
TITLE Method of diagnosing gummy stem blight in plants using a polymerase
chain reaction assay
JOURNAL Patent: US 6258537-A 2 10-JUL-2001;
FEATURES
source
1..10
Location/Qualifiers
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 4 AGGCTGT 10

RESULT 231
LOCUS BD239261 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239261
VERSION BD239261.1 GI:33049031

```

```

KEYWORDS JP 2002534056-A/679.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 679 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/679
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)"

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/db_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGG 14
Db 2 CTGTTGG 8

RESULT 232
LOCUS BD240131 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240131
VERSION BD240131.1 GI:33049901
KEYWORDS JP 2002534056-A/1549.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1549 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1549
PD 15-OCT-2002

```

```

PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/111715
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
|||||
Db 3 AGGCTGT 9

RESULT 233
BD240425/c
LOCUS BD240425 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240425.1 GI:33050195
VERSION JP 2002534056-A/1843.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1843 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1843
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/111715
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
|||||
Db 3 AGGCTGT 9

RESULT 233
BD240425/c
LOCUS BD240425 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240425.1 GI:33050195
VERSION JP 2002534056-A/1843.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1843 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1843
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/111715
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGT 13
|||||
Db 8 GCTGTGT 2

RESULT 234
BD240505
LOCUS BD240505 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240505
BD240505.1 GI:33050275
VERSION JP 2002534056-A/1923.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1923 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1923
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/111715
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGT 13
|||||
Db 8 GCTGTGT 2

```



```
FEATURES
  source
    Location/Qualifiers
      1. .10
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.9%; Score 7; DB 1; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
Db 2 GAGGCTG 8

RESULT 235
BD240704/c
LOCUS BD240704 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240704
VERSION BD240704.1 GI:33050474
KEYWORDS JP 2002534056-A/2122.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 200279181-A 209 10-OCT-2000;
  SCIENCE & TECH AGENCY
COMMENT
  OS Homo sapiens (human)
  PN JP 200279181-A/209
  PD 10-OCT-2000
  PR 01-APR-1999 JP 1999095481
  PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
  C12N15/09,C07K14/475,C07K16/18,C12N15/00
  CC
  FH Key Location/Qualifiers
  FT source 1. .10 /organism="Homo sapiens (human)".
  FEATURES
    source
      Location/Qualifiers
        1. .10
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTG 13
Db 1 GCTGTTG 7

RESULT 237
E54725/c
LOCUS E54725 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54725
VERSION E54725.1 GI:22556208
KEYWORDS JP 2001211883-A/77.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  Human normal liver cell expression genes
  Patent: JP 2001211883-A 77 07-AUG-2001;
  SCIENCE & TECH AGENCY
COMMENT
  OS Homo sapiens (human)
  PN JP 2001211883-A/77
  PD 07-AUG-2001
  PR 31-JAN-2000 JP 2000023170
  PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
  YAMASHITA
  PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
  CC
  FH Key Location/Qualifiers
  FT source 1. .10 /organism="Homo sapiens"
  FEATURES
    source
      Location/Qualifiers
        1. .10
          /organism="Homo sapiens"
          /mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGG 7
Db 9 CTTGAGG 3
```

/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||
Db 10 AGGCTGT 4

RESULT 238
E54836/c

LOCUS Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
DEFINITION E54836
ACCESSION E54836
VERSION E54836.1 GI:22556319
KEYWORDS JP 2001211883-A/188.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes

JOURNAL Patent: JP 2001211883-A 188 07-AUG-2001;
SCIENCE & TECH AGENCY

COMMENT OS Homo sapiens (human)

PN JP 2001211883-A/188

PD 07-AUG-2001

PF 31-JAN-2000 JP 2000023170

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA

PC C12N15/09, C07K16/18, C12P21/02, C12N15/00

CC

FH Key Location/Qualifiers.

source 1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||
Db 7 AGGCTGT 1

RESULT 239

LOCUS 191829 10 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 20 from patent US 5726038.
ACCESSION I91829
VERSION I91829.1 GI:3936299
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)
AUTHORS Christiansen,L. and Petersen,J Gunner,Litake.
TITLE DNA construct encoding the YAP3 signal peptide

JOURNAL Patent: US 5726038-A 20 10-MAR-1998;
FEATURES Location/Qualifiers

source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGCGAC 18
|||||
Db 3 TGGCGAC 9

RESULT 240

LOCUS AR222963 10 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 16 from patent US 6432640.
ACCESSION AR222963
VERSION AR222963.1 GI:23330801
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)

AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.

TITLE P53-induced apoptosis

JOURNAL Patent: US 6432640-A 16 13-AUG-2002;

FEATURES Location/Qualifiers

source 1. .10

/organism="unknown"

/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11

|||||

Db 1 AGGCTGT 7

RESULT 241

LOCUS AR222966/c 10 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from patent US 6432640.
ACCESSION AR222966
VERSION AR222966.1 GI:23330804
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)

AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.

TITLE P53-induced apoptosis

JOURNAL Patent: US 6432640-A 19 13-AUG-2002;

FEATURES Location/Qualifiers

source 1. .10

/organism="unknown"

/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGC 15

|||||

Db 10 TGTGGC 4

RESULT 242

LOCUS AR351662 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 556 from patent US 6589746.
ACCESSION AR351662
VERSION AR351662.1 GI:33753458
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)

AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 556 08-JUL-2003;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGC 15
|||||
Db 2 TGTGGC 8
RESULT 243
AR351737
LOCUS AR351737 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1279 from patent US 6588746.
ACCESSION AR351737
VERSION AR351737.1 GI:33753533
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1279 08-JUL-2003;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
|||||
Db 4 GAGGCTG 10
RESULT 244
AR351766
LOCUS AR351766 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1308 from patent US 6588746.
ACCESSION AR351766
VERSION AR351766.1 GI:33753562
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1308 08-JUL-2003;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
|||||
Db 4 GAGGCTG 10

Db 4 GAGGCTG 10
RESULT 245
AR351771
LOCUS AR351771 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1313 from patent US 6588746.
ACCESSION AR351771
VERSION AR351771.1 GI:33753567
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1313 08-JUL-2003;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
|||||
Db 4 GAGGCTG 10
RESULT 246
AR351819
LOCUS AR351819 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1624 from patent US 6588746.
ACCESSION AR351819
VERSION AR351819.1 GI:33753615
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1624 08-JUL-2003;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
|||||
Db 4 GAGGCTG 10
RESULT 247
AR351820
LOCUS AR351820 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1625 from patent US 6588746.
ACCESSION AR351820
VERSION AR351820.1 GI:33753616
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.


```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 411 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
Db 2 GAGGCTG 8

RESULT 253
AX152633/c
LOCUS AX152633 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 548 from Patent WO0138577.
ACCESSION AX152633
VERSION AX152633.1 GI:14534284
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 548 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
Db 8 CTTGAGG 2

RESULT 254
AX152997/c
LOCUS AX152997 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 912 from Patent WO0138577.
ACCESSION AX152997
VERSION AX152997.1 GI:14534648
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 912 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 411 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 9 GCTGTTG 3

RESULT 255
AX153110
LOCUS AX153110 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION AX153110
VERSION AX153110.1 GI:14534761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1025 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 1 GCTGTTG 7

RESULT 256
AX153347/c
LOCUS AX153347 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1262 from Patent WO0138577.
ACCESSION AX153347
VERSION AX153347.1 GI:14534998
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1262 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 1 GCTGTTG 7

RESULT 257
AX153347/c
LOCUS AX153347 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1262 from Patent WO0138577.
ACCESSION AX153347
VERSION AX153347.1 GI:14534998
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1262 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
Db 9 TGAGGCT 3

RESULT 257
```

AX153645/c
LOCUS AX153645 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1560 from Patent WO0138577.
ACCESSION AX153645
VERSION AX153645.1 GI:14535296
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1560 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCT 9
Db 9 TGAGGCT 3
RESULT 258
AX362611/c
LOCUS AX362611 10 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 45 from Patent WO0208425.
ACCESSION AX362611
VERSION AX362611.1 GI:18694755
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Finkel,K. and Koshy,B.
TITLE Haplotypes of the adrb3 gene
JOURNAL Patent: WO 0208425-A 45 31-JAN-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 7 GAGGCTG 1
RESULT 259
AX667107
LOCUS AX667107 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 556 from Patent WO0242459.
ACCESSION AX667107
VERSION AX667107.1 GI:29291257
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.

AX153645/c
LOCUS AX153645 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1560 from Patent WO0138577.
ACCESSION AX153645
VERSION AX153645.1 GI:14535296
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1560 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCT 9
Db 9 TGAGGCT 3
RESULT 258
AX362611/c
LOCUS AX362611 10 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 45 from Patent WO0208425.
ACCESSION AX362611
VERSION AX362611.1 GI:18694755
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Finkel,K. and Koshy,B.
TITLE Haplotypes of the adrb3 gene
JOURNAL Patent: WO 0208425-A 45 31-JAN-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 7 GAGGCTG 1
RESULT 259
AX667107
LOCUS AX667107 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 556 from Patent WO0242459.
ACCESSION AX667107
VERSION AX667107.1 GI:29291257
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.

TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 556 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGC 15
Db 2 TGTGGC 8
RESULT 260
AX667830
LOCUS AX667830 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1279 from Patent WO0242459.
ACCESSION AX667830
VERSION AX667830.1 GI:29291367
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1279 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 4 GAGGCTG 10
RESULT 261
AX667859
LOCUS AX667859 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1308 from Patent WO0242459.
ACCESSION AX667859
VERSION AX667859.1 GI:29291396
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1308 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 4 GAGGCTG 10

RESULT 262
 AX667864
 LOCUS AX667864 10 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 1313 from Patent WO0242459.
 ACCESSION AX667864
 VERSION AX667864.1 GI:29291401
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 1313 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 4 GAGGCTG 10

RESULT 263
 AX668175
 LOCUS AX668175 10 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 1624 from Patent WO0242459.
 ACCESSION AX668175
 VERSION AX668175.1 GI:29291454
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 1624 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 4 GAGGCTG 10

RESULT 264
 AX668176
 LOCUS AX668176 10 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 1625 from Patent WO0242459.
 ACCESSION AX668176
 VERSION AX668176.1 GI:29291455
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Liu, Q.
 TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
 JOURNAL Patent: WO 0242459-A 1625 30-MAY-2002;
 Sangamo Biosciences Inc. (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 4 GAGGCTG 10

RESULT 265
 BD007759/c
 LOCUS BD007759/c 10 bp DNA linear PAT 31-JAN-2002
 DEFINITION LPS activated human monocyte expressing genes.
 ACCESSION BD007759
 VERSION BD007759.1 GI:18636132
 KEYWORDS JP 2001069993-A/35.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S. and Suzuki, T.
 TITLE LPS activated human monocyte expressing genes
 JOURNAL Patent: JP 2001069993-A 35 21-MAR-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 FN JP 2001069993-A/35
 PD 21-MAR-2001
 PF 28-APR-2000 JP 2000131079
 PR PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
 C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
 A61P29/00,
 PC A61P31/00, C12P21/08, C12N15/00
 CC
 FH Key Location/Qualifiers
 FT source 1..10
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

FEATURES Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      6 GGCTGTT 12
      1111111
Db      8 GGCTGTT 2

RESULT 266
BD007902/c
LOCUS      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007902
VERSION     BD007902.1 GI:18636275
KEYWORDS   JP 2001069993-A/178.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE     LPS activated human monocyte expressing genes
JOURNAL   Patent: JP 2001069993-A 178 21-MAR-2001;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2001069993-A/178
          PD 21-MAR-2001
          PF 28-APR-2000 JP 2000131079
          PR PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            CC A61P31/00,C12P21/08,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..10
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'

FEATURES             source
     Query Match      38.9%; Score 7; DB 1; Length 10;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      1111111
Db      1 GCTGTGG 7

RESULT 268
BD007976
LOCUS      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007976
VERSION     BD007976.1 GI:18636349
KEYWORDS   JP 2001069993-A/252.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE     LPS activated human monocyte expressing genes
JOURNAL   Patent: JP 2001069993-A 252 21-MAR-2001;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2001069993-A/252
          PD 21-MAR-2001
          PF 28-APR-2000 JP 2000131079
          PR PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            CC A61P31/00,C12P21/08,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..10
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'

FEATURES             source
     Query Match      38.9%; Score 7; DB 1; Length 10;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGCTGT 11
      1111111
Db      4 AGGCTGT 10

RESULT 269
BD083133/c
LOCUS      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083133
VERSION     BD083133.1 GI:22628743
KEYWORDS   JP 2001327293-A/54.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
```

```
PC      A61P31/00,C12P21/08,C12N15/00
CC
FH      Key Location/Qualifiers
FT      source 1..10
        /organism='Homo sapiens (human)'.

FEATURES             source
     Query Match      38.9%; Score 7; DB 1; Length 10;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      1111111
Db      1 GCTGTGG 7

RESULT 268
BD007976
LOCUS      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007976
VERSION     BD007976.1 GI:18636349
KEYWORDS   JP 2001069993-A/252.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE     LPS activated human monocyte expressing genes
JOURNAL   Patent: JP 2001069993-A 252 21-MAR-2001;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2001069993-A/252
          PD 21-MAR-2001
          PF 28-APR-2000 JP 2000131079
          PR PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            CC A61P31/00,C12P21/08,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..10
              /organism='Homo sapiens (human)'.

FEATURES             source
     Query Match      38.9%; Score 7; DB 1; Length 10;
     Best Local Similarity 100.0%; Pred. No. 1.2e+02;
     Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGCTGT 11
      1111111
Db      4 AGGCTGT 10

RESULT 269
BD083133/c
LOCUS      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083133
VERSION     BD083133.1 GI:22628743
KEYWORDS   JP 2001327293-A/54.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
```



```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Matsushina,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE
Human matured/activated dendritic cell expression genes
JOURNAL
Patent: JP 2001327293-A 54 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
OS Homo sapiens (human)
PN JP 2001327293-A/54
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
|||||
Db 9 TGAGGCT 3

RESULT 270
BD083215
LOCUS
BD083215 10 bp DNA linear PAT 27-AUG-2002
DEFINITION
Human matured/activated dendritic cell expression genes.
ACCESSION
BD083215
VERSION
BD083215.1 GI:22628825
KEYWORDS
JP 2001327293-A/136.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Matsushina,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE
Human matured/activated dendritic cell expression genes
JOURNAL
Patent: JP 2001327293-A 136 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
OS Homo sapiens (human)
PN JP 2001327293-A/136
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGG 14
|||||
Db 2 CTGTGG 8

RESULT 271
BD091138

```

```

LOCUS
BD091138 10 bp DNA linear PAT 27-AUG-2002
DEFINITION
P53-induced apoptosis.
ACCESSION
BD091138
VERSION
BD091138.1 GI:22636748
KEYWORDS
JP 2001523441-A/16.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE
P53-induced apoptosis
JOURNAL
Patent: JP 2001523441-A 16 27-NOV-2001;
THE JOHNS HOPKINS UNIVERSITY
COMMENT
OS Homo sapiens (human)
PN JP 2001523441-A/16
PD 27-NOV-2001
PF 17-SEP-1998 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
apoptosis
FH Key Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
1..10
Location/Qualifiers
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
|||||
Db 1 AGGCTGT 7

RESULT 272
BD091141/c
LOCUS
BD091141/c 10 bp DNA linear PAT 27-AUG-2002
DEFINITION
P53-induced apoptosis.
ACCESSION
BD091141
VERSION
BD091141.1 GI:22636751
KEYWORDS
JP 2001523441-A/19.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE
P53-induced apoptosis
JOURNAL
Patent: JP 2001523441-A 19 27-NOV-2001;
THE JOHNS HOPKINS UNIVERSITY
COMMENT
OS Homo sapiens (human)
PN JP 2001523441-A/19
PD 27-NOV-2001
PF 17-SEP-1998 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
apoptosis
FH Key Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
1..10
Location/Qualifiers

```

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGC 15
| | | | |
Db 10 TGTGGC 4

RESULT 273
BD167226/c
LOCUS Human liver disease-expressing genes.
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167226
VERSION BD167226.1 GI:27873038
KEYWORDS JP 2002209591-A/771.
SOURCE unidentified
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 771 30-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/771
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
| | | | |
Db 7 AGGCTGT 1

RESULT 275
A10261
LOCUS Synthetic nucleotide sequence fragment encoding part of the
DEFINITION glucagon polypeptide residues within pMT290.
ACCESSION A10261
VERSION A10261.1 GI:489122
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Norris,K., Thim,L., Norris,F., Hansen,M.T. and Moody,A.J.
TITLE A process for preparing glucagon or derivatives thereof in a
JOURNAL transormed yeast strain
Patent: EP 0189998-A 12 06-AUG-1986;
NOVO-NORDISK A/S

FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGCTG 10
| | | | |
Db 1 CTTGAGAGTG 10

RESULT 276
AR107864
LOCUS Sequence 110 from patent US 6110667.
DEFINITION Sequence 110 from patent US 6110667.
ACCESSION AR107864
VERSION AR107864.1 GI:12823351
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigan,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 110 29-AUG-2000;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
| | | | |
Db 7 AGGCTGT 1

RESULT 275
A10261
LOCUS Synthetic nucleotide sequence fragment encoding part of the
DEFINITION glucagon polypeptide residues within pMT290.
ACCESSION A10261
VERSION A10261.1 GI:489122
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Norris,K., Thim,L., Norris,F., Hansen,M.T. and Moody,A.J.
TITLE A process for preparing glucagon or derivatives thereof in a
JOURNAL transormed yeast strain
Patent: EP 0189998-A 12 06-AUG-1986;
NOVO-NORDISK A/S

FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGCTG 10
| | | | |
Db 1 CTTGAGAGTG 10

RESULT 276
AR107864
LOCUS Sequence 110 from patent US 6110667.
DEFINITION Sequence 110 from patent US 6110667.
ACCESSION AR107864
VERSION AR107864.1 GI:12823351
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigan,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 110 29-AUG-2000;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"


```
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
    ||| ||| |||
Db 10 TGAAGCAGTT 1

RESULT 280
BD238782/c
LOCUS          10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Preparation and use of superior vaccines.
ACCESSION     BD238782
VERSION       BD238782.1 GI:33048552
KEYWORDS      JP 2002534056-A/200.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 10)
              Roberts,B.L. and Shankara,S.
              Preparation and use of superior vaccines
              Patent: JP 2002534056-A 210 15-OCT-2002;
              GENZYME CORP
              OS Homo sapiens (human)
              PN JP 2002534056-A/200
              PD 15-OCT-2002
              PF 18-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
              PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
              19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
              19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
              19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
              19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
              19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
              19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
              19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
              19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
              19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
              19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
              08-DEC-1998 US 60/111715
              PI BRUCE L ROBERTS,SRINIVAS SHANKARA
              PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
              PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
              PC C12N15/00,C12N5/00,C12N15/00
              CC Preparation and use of superior vaccines
              FH Key Location/Qualifiers
              FT source 1..10
              /organism="Homo sapiens (human)".

FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGC 15
    ||| ||| |||
Db 1 GGCACTAGGC 10

RESULT 282
BD238996
LOCUS          10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Preparation and use of superior vaccines.
ACCESSION     BD238996
VERSION       BD238996.1 GI:33048766
KEYWORDS      JP 2002534056-A/414.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 10)
              Roberts,B.L. and Shankara,S.

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGC 15
    ||| ||| |||
Db 10 GGCCCTTGGC 1
```



```

GOIN37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
        1..10
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.8%; Score 6.8; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCTGTTGG 13
Db 10 GAGCTGTTGG 1

RESULT 285
BD239906
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239906
VERSION BD239906.1 GI:33049676
KEYWORDS JP 2002534056-A/1324.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
AUTHORS Preparation and use of superior vaccines
TITLE Patent: JP 2002534056-A 1324 15-OCT-2002;
JOURNAL GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1324
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
        1..10
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.8%; Score 6.8; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGG 14
Db 1 AGGCTGTTGG 10

RESULT 287
BD240268
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240268

```

```

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGG 14
Db 1 AGGCTGTTGG 10

RESULT 286
BD240033
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240033
VERSION BD240033.1 GI:33049803
KEYWORDS JP 2002534056-A/1451.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
AUTHORS Preparation and use of superior vaccines
TITLE Patent: JP 2002534056-A 1451 15-OCT-2002;
JOURNAL GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1451
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
        1..10
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 37.8%; Score 6.8; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGG 14
Db 1 AGGCTGTTGG 10

RESULT 287
BD240268
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240268

```

```

VERSION BD240268.1 GI:33050038
KEYWORDS JP 2002534056-A/1686.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1686 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1686
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GCTGCTGCGC 16
Db 1 GCTGTAGGGG 10
RESULT 289
BD240614/c
LOCUS BD240614 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240614
VERSION BD240614.1 GI:33050384
KEYWORDS JP 2002534056-A/2032.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2032 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/2032
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTTG 13
Db 1 GAGGCTTTG 10
RESULT 288
BD240555
LOCUS BD240555 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240555
VERSION BD240555.1 GI:33050325
KEYWORDS JP 2002534056-A/1973.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1973 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1973

```

```
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
|||||
Db 10 TGAGGATCTT 1

RESULT 290
BD240619/c
LOCUS BD240619 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240619
VERSION BD240619.1 GI:33050389
KEYWORDS JP 2002534056-A/2037.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2037 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/2037
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090044 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
|||||
Db 10 TGAGGATCTT 1

RESULT 291
BD240685
LOCUS BD240685 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240685
VERSION BD240685.1 GI:33050455
KEYWORDS JP 2002534056-A/2103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2103 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/2103
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090044 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
|||||
```

```
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
|||||
```



```

Db 1 GGGGCTGTGG 10

RESULT 292
BD240705/c
LOCUS BD240705 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240705
VERSION BD240705.1 GI:33050475
KEYWORDS JP 2002534056-A/2123.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 10)
AUTHORS Atsushi.M.
TITLE Method for distinguishing hop variety
JOURNAL Patent: JP 1999103895-A 13 20-APR-1999;
KIRIN BREWERY CO LTD
COMMENT OS Unidentified
PN JP 1999103895-A/13
PD 20-APR-1999
PF 03-OCT-1997 JP 1997271771
PR
PI ATSUSHI MURAKAMI
PC C1201/68,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..10
/organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..10
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGTGTGGGAC 18
Db 10 TGACGGGCGAC 1

RESULT 294
E39492
LOCUS E39492 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39492
VERSION E39492.1 GI:18621583
KEYWORDS JP 2000279181-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 25 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/25
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGC 15
Db 1 GGCTGGGGGC 10

Db 1 GGGGCTGTGG 10

RESULT 293
E23590/c
LOCUS E23590 10 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for distinguishing hop variety.
ACCESSION E23590
VERSION E23590.1 GI:13024456
KEYWORDS JP 1999103895-A/13.
SOURCE unidentified
ORGANISM unclassified.

```

```
RESULT 295
E39670/c      E39670      10 bp      DNA      linear      PAT 31-JAN-2002
LOCUS
DEFINITION   Genes with human dendritic cell expression.
ACCESSION    E39670
VERSION      E39670.1 GI:18621761
KEYWORDS     JP 2000279181-A/203.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE    1 (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 203 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/203
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR
            PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            CC C12N15/09,C07K14/475,C07K16/18,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..10
            FT /organism='Homo sapiens (human)'.

FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14
    ||| ||| ||
Db 10 AGGTTGTGG 1

RESULT 296
E54811
LOCUS
DEFINITION   Human normal liver cell expression genes.
ACCESSION    E54811
VERSION      E54811.1 GI:22556294
KEYWORDS     JP 2001211883-A/163.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE    1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE       Human normal liver cell expression genes
JOURNAL     Patent: JP 2001211883-A 163 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2001211883-A/163
            PD 07-AUG-2001
            PF 31-JAN-2000 JP 2000023170
            PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            CC C12N15/09,C07K16/18,C12P21/02,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..10
            FT /organism="Homo sapiens"
            FT /mol_type="genomic DNA"
            FT /db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14
    ||| ||| ||
Db 10 AGGTTGTGG 1

RESULT 297
E64721
LOCUS
DEFINITION   Method for distinguishing rice variety.
ACCESSION    E64721
VERSION      E64721.1 GI:18623016
KEYWORDS     JP 2000287691-A/7.
SOURCE       unidentified
ORGANISM     unclassified.

REFERENCE    1 (bases 1 to 10)
AUTHORS     Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
TITLE       Method for distinguishing rice variety
JOURNAL     Patent: JP 2000287691-A 7 17-OCT-2000;
            NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
COMMENT     OS Unidentified
            PN JP 2000287691-A/7
            PD 17-OCT-2000
            PF 09-APR-1999 JP 1999102709
            PR
            PI KENICHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI
            CC C12N15/09,C12Q1/68,G01N33/10,C12N15/00
            FH Key Location/Qualifiers
            FT source 1..22
            FT /organism='Unidentified'.

FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGTGGCGAC 18
    ||| ||| |||
Db 10 TGACGGCGAC 1

RESULT 298
AR201710/c
LOCUS
DEFINITION   Sequence 42 from patent US 6361937.
ACCESSION    AR201710
VERSION      AR201710.1 GI:20256249
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.

REFERENCE    1 (bases 1 to 10)
AUTHORS     Stryer,L.
TITLE       Computer-aided nucleic acid sequencing
JOURNAL     Patent: US 6361937-A 42 26-MAR-2002;
            Location/Qualifiers
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
```



```
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
| | | | | |
Db 1 GGGGCTGTGG 10

RESULT 304
AX153048/c
LOCUS AX153048 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 963 from Patent WO0138577.
ACCESSION AX153048
VERSION AX153048.1 GI:14534699
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 963 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGTGGCGAC 18
| | | | | |
Db 10 TGATGGCGC 1

RESULT 305
AX153114
LOCUS AX153114 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1029 from Patent WO0138577.
ACCESSION AX153114
VERSION AX153114.1 GI:14534765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1029 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGC 15
| | | | | |
Db 1 AGGATGTGG 10

RESULT 306
AX153406
LOCUS AX153406 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1321 from Patent WO0138577.
ACCESSION AX153406
VERSION AX153406.1 GI:14535057
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1321 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGC 15
| | | | | |
Db 1 GGCTCTGGC 10

RESULT 307
AX153433
LOCUS AX153433 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1348 from Patent WO0138577.
ACCESSION AX153433
VERSION AX153433.1 GI:14535084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1348 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTGG 14
| | | | | |
Db 1 AGGATGTGG 10

RESULT 308
AX153461/c
LOCUS AX153461 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1376 from Patent WO0138577.
ACCESSION AX153461
VERSION AX153461.1 GI:14535112
KEYWORDS
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1376 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
|||||
Db 10 TGAAGCAGTT 1

RESULT 309
AX153593
LOCUS AX153593 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1508 from Patent WO0138577.
ACCESSION AX153593
VERSION AX153593.1 GI:14535244
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1508 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
|||||
Db 1 GGCTGGGGC 10

RESULT 310
AX301382
LOCUS AX301382 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 96 from Patent WO0185941.
ACCESSION AX301382
VERSION AX301382.1 GI:17382465
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 96 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/mol_type="Homo sapiens"

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 341 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
|||||
Db 1 GGCTGGGGC 10
```

```
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
|||||
Db 1 GGCTCTGGC 10

RESULT 311
AX301388/c
LOCUS AX301388 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 102 from Patent WO0185941.
ACCESSION AX301388
VERSION AX301388.1 GI:17382471
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 102 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
|||||
Db 10 TGAAGCAGTT 1

RESULT 312
AX301627
LOCUS AX301627 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 341 from Patent WO0185941.
ACCESSION AX301627
VERSION AX301627.1 GI:17382710
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 341 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
|||||
Db 1 GGCTGGGGC 10
```

RESULT 313
AX395401/c
LOCUS AX395401 10 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 38 from Patent WO0206495.
ACCESSION AX395401
VERSION AX395401.1 GI:21066376
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Chamberlain,J.S. and Hauschka,S.D.
TITLE Mutant muscle-specific enhancers
JOURNAL Patent: WO 0206495-A 38 24-JAN-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES
Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
||| |||||
Db 10 TGCAGCTGTT 1

RESULT 314
AX481180
LOCUS AX481180 10 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 240 from Patent WO0246412.
ACCESSION AX481180
VERSION AX481180.1 GI:22217647
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Rebar,E.; Jamieson,A., Liu,Q., Liu,P.Q., Wolffe,A., Eisenberg,S.P.
and Jarvis,E.
TITLE Regulation of angiogenesis with zinc finger proteins
JOURNAL Patent: WO 0246412-A 240 13-JUN-2002;
Sangamo Biosciences Inc. (US)
FEATURES
Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="target"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
||| |||||
Db 1 GCTGGGCGCG 10

RESULT 315
AX667180
LOCUS AX667180 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 629 from Patent WO0242459.
ACCESSION AX667180
VERSION AX667180.1 GI:29291332
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 629 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
||| |||||
Db 1 GGTGTTGGAG 10

RESULT 316
BD007785
LOCUS BD007785 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007785
VERSION BD007785.1 GI:18636158
KEYWORDS JP 2001069993-A/61.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 61 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/61
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGT 11
||| |||||
Db 1 TTGAAGCTTT 10

RESULT 317
BD007982/c
LOCUS BD007982 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007982
VERSION BD007982.1 GI:18636355

```
KEYWORDS JP 2001069993-A/258.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 258 21-MAR-2001,
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/258
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
CC A61P31/00,C12P21/08,C12N15/00
FH Key Location/Qualifiers
FT 1..10 /organism='Homo sapiens (human)'.
FEATURES source
LOCATION/Qualifiers
1..10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTT 12
Db 10 TGTGGCTGGT 1
RESULT 318
BD007999/c
LOCUS BD007999 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007999
VERSION BD007999.1 GI:18636372
KEYWORDS JP 2001069993-A/275.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 275 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/275
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
CC A61P31/00,C12P21/08,C12N15/00
FH Key Location/Qualifiers
FT 1..10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
FEATURES source
LOCATION/Qualifiers
1..10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTT 12
Db 10 TGTGGCTGGT 1
RESULT 319
BD065146
LOCUS BD065146 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065146
VERSION BD065146.1 GI:22610749
KEYWORDS JP 2001509017-A/82.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 82 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/82
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT 1..10 /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES source
LOCATION/Qualifiers
1..10 /organism='Saccharomyces cerevisiae'
/mol_type='genomic DNA'
/db_xref='taxon:4932'
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GCTGTTGGCG 16
Db 1 GGTGTTGGCG 10
RESULT 320
BD083093
LOCUS BD083093 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083093
VERSION BD083093.1 GI:22628703
KEYWORDS JP 2001327293-A/14.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 14 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/14
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI
```

PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGC 15
Db 1 GGCTGGGGC 10

RESULT 321
BD083234
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083234
VERSION BD083234.1 GI:22628844
KEYWORDS JP 2001327293-A/155.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 155 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/155
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGC 15
Db 1 GGCTGGGGC 10

RESULT 322
BD083247/c
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083247
VERSION BD083247.1 GI:22628857
KEYWORDS JP 2001327293-A/168.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 168 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/168
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGC 15
Db 1 GGCTGGGGC 10

RESULT 323
BD083273
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083273
VERSION BD083273.1 GI:22628883
KEYWORDS JP 2001327293-A/194.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 194 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/194
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGA 17
Db 1 CTGCTGGAGA 10

RESULT 324
BD083275
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083275
VERSION BD083275.1 GI:22628885
KEYWORDS JP 2001327293-A/196.
SOURCE Homo sapiens (human)

JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/168
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
Db 10 AAGCTGCTGG 1

RESULT 323
BD083273
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083273
VERSION BD083273.1 GI:22628883
KEYWORDS JP 2001327293-A/194.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 194 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/194
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGA 17
Db 1 CTGCTGGAGA 10

RESULT 324
BD083275
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083275
VERSION BD083275.1 GI:22628885
KEYWORDS JP 2001327293-A/196.
SOURCE Homo sapiens (human)


```
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
    ||| |||
Db 10 TGAAGCAGTT 1

RESULT 328
BD166592/c
LOCUS      BD166592      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166592
VERSION     BD166592.1 GI:27872404
KEYWORDS   JP 2002209591-A/137.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 137 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/137
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            CC Human liver disease-expressing genes
            FH Key Location/Qualifiers
            FT source 1..10
            /organism='Homo sapiens (human)'.

FEATURES             source
    source            1..10
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGCGCTGT 11
    ||| |||
Db 10 TTGCCGCTGT 1

RESULT 330
BD166723/c
LOCUS      BD166723      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166723
VERSION     BD166723.1 GI:27872535
KEYWORDS   JP 2002209591-A/268.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 268 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/268
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            CC Human liver disease-expressing genes
            FH Key Location/Qualifiers
            FT source 1..10
            /organism='Homo sapiens (human)'.

FEATURES             source
    source            1..10
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
    ||| |||
Db 10 GGAGTTGGC 1

RESULT 329
BD166719/c
LOCUS      BD166719      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166719
VERSION     BD166719.1 GI:27872531
KEYWORDS   JP 2002209591-A/264.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 264 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/264
            PD 30-JUL-2002
```

```
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES             source
    source            1..10
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGCGCTGT 11
    ||| |||
Db 10 TTGCCGCTGT 1

RESULT 330
BD166723/c
LOCUS      BD166723      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166723
VERSION     BD166723.1 GI:27872535
KEYWORDS   JP 2002209591-A/268.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 268 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/268
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            CC Human liver disease-expressing genes
            FH Key Location/Qualifiers
            FT source 1..10
            /organism='Homo sapiens (human)'.

FEATURES             source
    source            1..10
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
    ||| |||
Db 10 TGAAGCAGTT 1

RESULT 331
BD167013/c
LOCUS      BD167013      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167013
```

VERSION BD167013.1 GI:27872825
KEYWORDS JP 2002209591-A/558.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushita,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 558 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/558
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHITA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GGCTGTTGGC 15
Db 10 GGGTGTAGC 1
Search completed: September 9, 2004, 11:12:20
Job time : 1 secs

4.7

C 107	9.4	52.2	13	1	ABC81895	Oligonucleotide SE	C 180	8.8	48.9	13	1	ABH32317	Oligonucleotide SE
C 108	9.4	52.2	13	1	ABC70901	Oligonucleotide SE	181	8.8	48.9	13	1	ABC30166	Oligonucleotide SE
C 109	9.4	52.2	13	1	ABC70900	Oligonucleotide SE	C 182	8.8	48.9	13	1	ABF27833	Oligonucleotide SE
C 110	9.4	52.2	13	1	ABF30190	Oligonucleotide SE	C 183	8.8	48.9	13	1	ABF36581	Oligonucleotide SE
C 111	9.4	52.2	13	1	ABCA4422	Oligonucleotide SE	C 184	8.8	48.9	13	1	ABH11623	Oligonucleotide SE
C 112	9.4	52.2	13	1	ABQ84081	Tubercle bacillus	C 185	8.8	48.9	13	1	ABF29703	Oligonucleotide SE
C 113	9.4	52.2	13	1	ADC33633	M. tuberculosis ol	186	8.8	48.9	13	1	ABH32316	Oligonucleotide SE
C 114	9.4	52.2	13	1	AAQ83339	ub-B antisense ol	187	8.8	48.9	13	1	ABC19814	Oligonucleotide SE
C 115	9.4	52.2	14	1	AAAL7677	Aryl hydrocarbon n	188	8.8	48.9	13	1	ABF02122	Oligonucleotide SE
C 116	9.4	52.2	14	1	AAAL7649	Human A-raf target	C 189	8.8	48.9	13	1	ABF09481	Oligonucleotide SE
C 117	9.4	52.2	14	1	AAV92817	Human A-raf target	C 190	8.8	48.9	13	1	ABF27831	Oligonucleotide SE
C 118	9.4	52.2	14	1	AAF95192	Oligonucleotide: s	191	8.8	48.9	13	1	ABF37604	Oligonucleotide SE
C 119	9.4	52.2	14	1	ABX05551	Secondary pentamer	192	8.8	48.9	13	1	ABC21254	Oligonucleotide SE
C 120	9.4	52.2	14	1	ABX05593	Simplified recomb	193	8.8	48.9	13	1	ABF09480	Oligonucleotide SE
C 121	9.4	52.2	14	1	ABX05569	Secondary pentamer	194	8.8	48.9	13	1	ABF23512	Oligonucleotide SE
C 122	9.4	52.2	14	1	ABX05603	Simplified recomb	195	8.8	48.9	13	1	ABF27832	Oligonucleotide SE
C 123	9.4	52.2	14	1	ABZ58027	Adaptor A3 blockin	196	8.8	48.9	13	1	ABF36580	Oligonucleotide SE
C 124	9.2	51.1	14	1	AA331459	Tag sequence of a	197	8.8	48.9	13	1	ABF44122	Oligonucleotide SE
C 125	9.2	51.1	14	1	AAA26152	Oestrogen receptor	C 198	8.8	48.9	13	1	ABC17883	Oligonucleotide SE
C 126	9.2	51.1	14	1	ABK32413	Human colon cancer	C 199	8.8	48.9	13	1	ABC89243	Oligonucleotide SE
C 127	9	50.0	9	1	ABQ27180	zinc finger protei	C 200	8.8	48.9	13	1	ABF23513	Oligonucleotide SE
C 128	9	50.0	9	1	ADA64507	zinc finger target	C 201	8.8	48.9	13	1	ABF48775	Oligonucleotide SE
C 129	9	50.0	10	1	AAF40252	Yeast NORF gene SA	C 202	8.8	48.9	13	1	ABF02123	Oligonucleotide SE
C 130	9	50.0	12	1	AAF56191	Microarray capture	C 203	8.8	48.9	13	1	ABC52205	Oligonucleotide SE
C 131	9	50.0	12	1	AAI65972	Synthetic k-ras co	C 204	8.8	48.9	13	1	ABC03601	Oligonucleotide SE
C 132	9	50.0	13	1	ABF62110	Oligonucleotide SE	C 205	8.8	48.9	13	1	ABC59512	Oligonucleotide SE
C 133	9	50.0	13	1	ABC47060	Oligonucleotide SE	C 206	8.8	48.9	13	1	ABF27830	Oligonucleotide SE
C 134	9	50.0	13	1	ABF67043	Oligonucleotide SE	C 207	8.8	48.9	13	1	ABF27831	Oligonucleotide SE
C 135	9	50.0	13	1	ABF62114	Oligonucleotide SE	C 208	8.8	48.9	13	1	ABC20131	Oligonucleotide SE
C 136	9	50.0	13	1	ABF87323	Oligonucleotide SE	C 209	8.8	48.9	13	1	ABC17882	Oligonucleotide SE
C 137	9	50.0	13	1	ABC47061	Oligonucleotide SE	C 210	8.8	48.9	13	1	ABF48774	Oligonucleotide SE
C 138	9	50.0	13	1	ABF62111	Oligonucleotide SE	C 211	8.8	48.9	13	1	ABF60659	Human DNA represen
C 139	9	50.0	13	1	ABH49553	Oligonucleotide SE	C 212	8.4	46.7	10	1	AAZ79478	Human dendritic ce
C 140	9	50.0	13	1	ABF67042	Oligonucleotide SE	C 213	8.4	46.7	10	1	AAZ82953	Metastatic breast
C 141	9	50.0	13	1	ABF62115	Oligonucleotide SE	C 214	8.4	46.7	10	1	AAZ84008	Metastatic breast
C 142	9	50.0	13	1	ABH49552	Oligonucleotide SE	C 215	8.4	46.7	10	1	AAZ82804	Metastatic breast
C 143	9	50.0	13	1	ABF87322	Oligonucleotide SE	C 216	8.4	46.7	10	1	AAZ82395	Metastatic breast
C 144	8.8	48.9	12	1	AAT03074	E. coli small ribo	C 217	8.4	46.7	10	1	AAC74125	Human monocyte and
C 145	8.8	48.9	12	1	AAV04827	Antisense DNA olig	C 218	8.4	46.7	10	1	AAAS6499	Human macrophage g
C 146	8.8	48.9	12	1	ABI66024	Oligonucleotide pr	C 219	8.4	46.7	10	1	AAAS6499	Human monocyte gen
C 147	8.8	48.9	12	1	ABI46177	Oligonucleotide pr	C 220	8.4	46.7	10	1	AAAS6442	Human macrophage g
C 148	8.8	48.9	12	1	ABI19567	Oligonucleotide pr	C 221	8.4	46.7	10	1	AAAS6393	Human macrophage g
C 149	8.8	48.9	12	1	ABH71852	Oligonucleotide pr	C 222	8.4	46.7	10	1	AAAS99860	Prokaryote RT-PCR
C 150	8.8	48.9	12	1	ABI63920	Oligonucleotide pr	C 223	8.4	46.7	10	1	AAH633507	Human ubiquitously
C 151	8.8	48.9	12	1	ABH75017	Oligonucleotide pr	C 224	8.4	46.7	10	1	AAH32809	LPS activated huma
C 152	8.8	48.9	12	1	ABH95746	Oligonucleotide pr	C 225	8.4	46.7	10	1	ABA06207	Human normal hepat
C 153	8.8	48.9	12	1	ABH79948	Oligonucleotide pr	C 226	8.4	46.7	10	1	AAF38690	Yeast NORF gene SA
C 154	8.8	48.9	12	1	ABH86298	Oligonucleotide pr	C 227	8.4	46.7	10	1	AAF37013	Yeast NORF gene SA
C 155	8.8	48.9	12	1	ABH12194	Oligonucleotide pr	C 228	8.4	46.7	10	1	AAF39203	Yeast NORF gene SA
C 156	8.8	48.9	12	1	ABH48872	Oligonucleotide pr	C 229	8.4	46.7	10	1	AAF36787	Yeast NORF gene SA
C 157	8.8	48.9	12	1	ABIS2064	Oligonucleotide pr	C 230	8.4	46.7	10	1	AAH42233	Nucleotide sequenc
C 158	8.8	48.9	12	1	ABH75412	Oligonucleotide pr	C 231	8.4	46.7	10	1	ABQ71507	Zinc finger protei
C 159	8.8	48.9	12	1	ABIS32027	Oligonucleotide pr	C 232	8.4	46.7	10	1	ABK23412	Transcript tag DNA
C 160	8.8	48.9	12	1	ABI33770	Oligonucleotide pr	C 233	8.4	46.7	10	1	ADA26780	Human rhophilin-11
C 161	8.8	48.9	12	1	ABH75018	Oligonucleotide pr	C 234	8.4	46.7	10	1	ACA94457	DNA tag from human
C 162	8.8	48.9	12	1	ABIS32026	Oligonucleotide pr	C 235	8.4	46.7	10	1	ABT14083	Nucleic acid sequ
C 163	8.8	48.9	12	1	AAZ55093	ShDN256 primer #2	C 236	8.4	46.7	10	1	ADA62655	Zinc finger target
C 164	8.8	48.9	13	1	AAQ33394	Liver RNA fingerpr	C 237	8.4	46.7	11	1	AAV29723	Probe used to exem
C 165	8.8	48.9	13	1	AAV11064	Human ribozyme tar	C 238	8.4	46.7	11	1	AAV29730	Probe used to exem
C 166	8.8	48.9	13	1	AAV11109	Human ribozyme tar	C 239	8.4	46.7	11	1	AAV72648	K-ras SW480 UDG-di
C 167	8.8	48.9	13	1	ABF37605	Oligonucleotide SE	C 240	8.4	46.7	11	1	AAV65344	Human skin EST 313
C 168	8.8	48.9	13	1	ABC59513	Oligonucleotide SE	C 241	8.4	46.7	11	1	ABV63110	Human skin EST 896
C 169	8.8	48.9	13	1	ABH11622	Oligonucleotide SE	C 242	8.4	46.7	11	1	ABV68127	Human skin EST 591
C 170	8.8	48.9	13	1	ABC30167	Oligonucleotide SE	C 243	8.4	46.7	11	1	ABV70531	Human skin EST 831
C 171	8.8	48.9	13	1	ABC30169	Oligonucleotide SE	C 244	8.4	46.7	11	1	ABV66286	Human skin EST 405
C 172	8.8	48.9	13	1	ABF44123	Oligonucleotide SE	C 245	8.4	46.7	11	1	ABV65312	Human skin EST 309
C 173	8.8	48.9	13	1	ABC19815	Oligonucleotide SE	C 246	8.4	46.7	11	1	ABV65306	Human skin EST 309
C 174	8.8	48.9	13	1	ABC20130	Oligonucleotide SE	C 247	8.4	46.7	11	1	ABV68728	Human skin EST 651
C 175	8.8	48.9	13	1	ABC21255	Oligonucleotide SE	C 248	8.4	46.7	11	1	AAZ27549	Human p21WAF1 CCGG
C 176	8.8	48.9	13	1	ABC03600	Oligonucleotide SE	C 249	8.4	46.7	11	1	AQZ81874	Kaposi's Sarcoma S
C 177	8.8	48.9	13	1	ABC89242	Oligonucleotide SE	C 250	8.4	46.7	12	1	AAZ47119	K-ras exon 1 varia
C 178	8.8	48.9	13	1	ABC52204	Oligonucleotide SE	C 251	8.4	46.7	12	1	AAT47118	K-ras exon 1 wild
C 179	8.8	48.9	13	1	ABC30168	Oligonucleotide SE	C 252	8.4	46.7	12	1	AAT47116	K-ras exon 1 wild

253	8.4	46.7	12	1	AAV06831	Amino derivatised	326	7.8	43.3	11	1	AAQ48927	Cross-linking olig
254	8.4	46.7	12	1	AAV32277	Random primed reve	327	7.8	43.3	11	1	AAQ48918	Cross-linking olig
255	8.4	46.7	12	1	AAV32276	Random primed reve	328	7.8	43.3	11	1	AAQ48919	Cross-linking olig
256	8.4	46.7	12	1	AB105176	Oligonucleotide pr	329	7.8	43.3	11	1	AAV06685	Oligonucleotide us
257	8.4	46.7	12	1	ABH96455	Oligonucleotide pr	330	7.8	43.3	11	1	AAV06675	Modified oligonucleu
258	8.4	46.7	12	1	ABH73096	Oligonucleotide pr	c 331	7.8	43.3	11	1	AAZ18935	Marine MRL SAGE ta
259	8.4	46.7	12	1	ABH77672	Oligonucleotide pr	332	7.8	43.3	11	1	AAZ19008	Marine MRL SAGE ta
260	8.4	46.7	12	1	AB143686	Oligonucleotide pr	333	7.8	43.3	11	1	AAZ95239	Sequence used in t
261	8.4	46.7	12	1	AB153337	Oligonucleotide pr	334	7.8	43.3	11	1	AAA88944	3',5'-linked oligo
262	8.4	46.7	12	1	AB174401	Oligonucleotide pr	335	7.8	43.3	11	1	AAA88945	3',5'-linked oligo
263	8.4	46.7	12	1	AB163160	Oligonucleotide pr	336	7.8	43.3	11	1	AAA88946	3',5'-linked oligo
264	8.4	46.7	12	1	AB161963	Oligonucleotide pr	c 337	7.8	43.3	11	1	AAZ31260	GC-rich template c
265	8.4	46.7	12	1	ABH82840	Oligonucleotide pr	338	7.8	43.3	11	1	AAH25736	Human type II RNas
266	8.4	46.7	12	1	ABH92756	Oligonucleotide pr	339	7.8	43.3	11	1	ABQ86744	Human skin stress/
267	8.4	46.7	12	1	AB108514	Oligonucleotide pr	340	7.8	43.3	11	1	ABV67690	Human skin EST 547
268	8.4	46.7	12	1	AB145227	Oligonucleotide pr	c 341	7.8	43.3	11	1	ABV67410	Human skin EST 519
269	8.4	46.7	12	1	AB155785	Oligonucleotide pr	342	7.8	43.3	11	1	ABV62451	Human skin EST 237
270	8.4	46.7	12	1	ABH78619	Oligonucleotide pr	343	7.8	43.3	11	1	ABV66069	Human skin EST 385
271	8.4	46.7	12	1	AB131077	Oligonucleotide pr	344	7.8	43.3	11	1	ABV68093	Human skin EST 587
272	8.4	46.7	12	1	ABH86170	Oligonucleotide pr	345	7.8	43.3	11	1	ABV69872	Human skin EST 765
273	8.4	46.7	12	1	ABH69405	Oligonucleotide pr	346	7.8	43.3	11	1	ABV65916	Human skin EST 370
274	8.4	46.7	12	1	ABH92262	Oligonucleotide pr	347	7.8	43.3	11	1	ABV63034	Human skin EST 820
275	8.4	46.7	12	1	AB174119	Oligonucleotide pr	c 348	7.8	43.3	11	1	ABV67617	Human skin EST 540
276	8.4	46.7	12	1	AB163944	Oligonucleotide pr	c 349	7.8	43.3	11	1	ABV62588	Human skin EST 374
277	8.4	46.7	12	1	AB124997	Oligonucleotide pr	350	7.8	43.3	11	1	ABV65487	Human skin EST 327
278	8.4	46.7	12	1	ABH97506	Oligonucleotide pr	351	7.8	43.3	11	1	ABV70455	Human skin EST 824
279	8.4	46.7	12	1	AB101343	Oligonucleotide pr	352	7.8	43.3	11	1	ABV68204	Human skin EST 599
280	8.4	46.7	12	1	ABZ58912	Human JAM3 intron	c 353	7.8	43.3	11	1	ABV70009	Human skin EST 779
281	8.4	46.7	12	1	ACA61780	Sample preparation	354	7.8	43.3	11	1	ABV64798	Human skin EST 258
282	8.4	46.7	12	1	ACA61760	Sample preparation	355	7.8	43.3	11	1	ABL51967	Human Pan-Endothel
283	8	44.4	8	1	AAA80787	A. thaliana primer	356	7.8	43.3	11	1	AAAL49633	DNA mismatch ident
284	8	44.4	9	1	ABQ72029	Zinc finger protei	357	7.8	43.3	11	1	AAAL49632	DNA mismatch ident
285	8	44.4	9	1	ABO72029	Zinc finger protei	358	7.8	43.3	11	1	AAAL49632	pWB plasmid DNA ha
286	8	44.4	9	1	ABO71854	Zinc finger protei	359	7.8	43.3	11	1	AAD32705	DNA tag used to id
287	8	44.4	9	1	ADA64355	Zinc finger target	c 360	7.8	43.3	11	1	ABX71892	Nucleic acid cloni
288	8	44.4	9	1	ADA64356	Zinc finger target	361	7.8	43.3	12	1	ACD82358	E. coli small ribo
289	8	44.4	9	1	ADA64356	Zinc finger target	362	7.8	43.3	12	1	AAV03078	Antisense DNA olig
290	8	44.4	10	1	AAQ97101	HIV-1 NL4-3 LTR nu	c 363	7.8	43.3	12	1	AAV32292	Random primed reve
291	8	44.4	10	1	AAQ97100	HIV-1 NL4-3 LTR nu	364	7.8	43.3	12	1	AAV05439	Primer used in pro
292	8	44.4	10	1	AAQ97102	HIV-1 NL4-3 LTR nu	365	7.8	43.3	12	1	AAZ41828	Organic material d
293	8	44.4	10	1	AAZ78512	Human dendritic ce	366	7.8	43.3	12	1	AAZ41696	Organic material d
294	8	44.4	10	1	AAZ82715	Metastatic breast	367	7.8	43.3	12	1	AAZ41612	Microbe detection
295	8	44.4	10	1	AAZ83636	Metastatic breast	368	7.8	43.3	12	1	AAZ41480	Microbe detection
296	8	44.4	10	1	AAZ74142	Human monocyte and	369	7.8	43.3	12	1	AAAS5875	Human retinaldehyd
297	8	44.4	10	1	AAAS6180	Human macrophage g	c 370	7.8	43.3	12	1	AAZ55846	Yeast PCR primer #
298	8	44.4	10	1	AAAS6502	Human macrophage g	371	7.8	43.3	12	1	AAZ73387	Primer used to ill
299	8	44.4	10	1	AAH64421	Human ubiquitously	372	7.8	43.3	12	1	AAZ97831	Primer used to ill
300	8	44.4	10	1	AAH63452	Human ubiquitously	373	7.8	43.3	12	1	AAZ97963	Mu oploid receptor
301	8	44.4	10	1	AAH32904	LPS activated huma	374	7.8	43.3	12	1	AAZ26620	Oligonucleotide pr
302	8	44.4	10	1	AAZ43753	Yeast NORF gene SA	375	7.8	43.3	12	1	ABH94426	Oligonucleotide pr
303	8	44.4	10	1	AAZ25887	Primer #9 to detec	c 376	7.8	43.3	12	1	ABH70592	Oligonucleotide pr
304	8	44.4	10	1	AAZ95181	UDP glycosyltransf	c 377	7.8	43.3	12	1	ABH70592	Oligonucleotide pr
305	8	44.4	10	1	AAZ95963	Primer-extension o	c 378	7.8	43.3	12	1	ABH70592	Oligonucleotide pr
306	8	44.4	10	1	AAZ95967	Human CALML gene a	c 379	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
307	8	44.4	11	1	AAZ18106	M. kansasii specie	c 380	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
308	8	44.4	11	1	AAV61928	Molecular weight m	381	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
309	8	44.4	11	1	AAV61928	Human prothrombin	c 382	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
310	8	44.4	11	1	ABV68951	Human skin EST 673	c 383	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
311	8	44.4	11	1	ABV68951	Human skin EST 740	c 384	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
312	8	44.4	11	1	AAV40927	Primer APX1.70L12	385	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
313	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 386	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
314	8	44.4	12	1	ABH71139	Oligonucleotide pr	387	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
315	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 388	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
316	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 389	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
317	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 390	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
318	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 391	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
319	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 392	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
320	8	44.4	12	1	ABH71139	Oligonucleotide pr	c 393	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
321	7.8	43.3	11	1	AAQ48916	Cross-linking olig	394	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
322	7.8	43.3	11	1	AAQ48917	Cross-linking olig	395	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
323	7.8	43.3	11	1	AAQ48917	Cross-linking olig	c 396	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
324	7.8	43.3	11	1	AAQ48925	Cross-linking olig	397	7.8	43.3	12	1	ABH88200	Oligonucleotide pr
325	7.8	43.3	11	1	AAQ48914	Cross-linking olig	398	7.8	43.3	12	1	ABH88200	Oligonucleotide pr

399	7.8	43.3	12	1	ABI12111	Oligonucleotide pr	c 472	7.8	43.3	12	1	ABI06804	Oligonucleotide pr
400	7.8	43.3	12	1	ABI129816	Oligonucleotide pr	473	7.8	43.3	12	1	ABI132404	Oligonucleotide pr
c 401	7.8	43.3	12	1	ABI169520	Oligonucleotide pr	c 474	7.8	43.3	12	1	ABI134318	Oligonucleotide pr
402	7.8	43.3	12	1	ABI163921	Oligonucleotide pr	475	7.8	43.3	12	1	ABI10235	Oligonucleotide pr
c 403	7.8	43.3	12	1	ABI193328	Oligonucleotide pr	c 476	7.8	43.3	12	1	ABH90677	Oligonucleotide pr
c 404	7.8	43.3	12	1	ABI120414	Oligonucleotide pr	477	7.8	43.3	12	1	ABI144144	Oligonucleotide pr
c 405	7.8	43.3	12	1	ABI100728	Oligonucleotide pr	478	7.8	43.3	12	1	ABI145715	Oligonucleotide pr
c 406	7.8	43.3	12	1	ABI125879	Oligonucleotide pr	479	7.8	43.3	12	1	ABI177158	Oligonucleotide pr
c 407	7.8	43.3	12	1	ABH86026	Oligonucleotide pr	c 480	7.8	43.3	12	1	ABH75413	Oligonucleotide pr
c 408	7.8	43.3	12	1	ABI141864	Oligonucleotide pr	481	7.8	43.3	12	1	ABI125639	Oligonucleotide pr
c 409	7.8	43.3	12	1	ABI155024	Oligonucleotide pr	c 482	7.8	43.3	12	1	ABI03816	Oligonucleotide pr
c 410	7.8	43.3	12	1	ABI161270	Oligonucleotide pr	c 483	7.8	43.3	12	1	ABI05325	Oligonucleotide pr
c 411	7.8	43.3	12	1	ABI172728	Oligonucleotide pr	c 484	7.8	43.3	12	1	ABI133073	Oligonucleotide pr
c 412	7.8	43.3	12	1	ABH70295	Oligonucleotide pr	c 485	7.8	43.3	12	1	ABI57771	Oligonucleotide pr
c 413	7.8	43.3	12	1	ABH95346	Oligonucleotide pr	486	7.8	43.3	12	1	ABI58136	Oligonucleotide pr
c 414	7.8	43.3	12	1	ABH70593	Oligonucleotide pr	487	7.8	43.3	12	1	ABI180801	Oligonucleotide pr
c 415	7.8	43.3	12	1	ABH71521	Oligonucleotide pr	c 488	7.8	43.3	12	1	ABI18449	Oligonucleotide pr
c 416	7.8	43.3	12	1	ABI124777	Oligonucleotide pr	489	7.8	43.3	12	1	ABH71196	Oligonucleotide pr
c 417	7.8	43.3	12	1	ABI104440	Oligonucleotide pr	c 490	7.8	43.3	12	1	ABH99938	Oligonucleotide pr
c 418	7.8	43.3	12	1	ABI132952	Oligonucleotide pr	c 491	7.8	43.3	12	1	ABH76685	Oligonucleotide pr
c 419	7.8	43.3	12	1	ABH83921	Oligonucleotide pr	c 492	7.8	43.3	12	1	ABH91623	Oligonucleotide pr
c 420	7.8	43.3	12	1	ABI110328	Oligonucleotide pr	c 493	7.8	43.3	12	1	ABH36223	Oligonucleotide pr
c 421	7.8	43.3	12	1	ABH90076	Oligonucleotide pr	c 494	7.8	43.3	12	1	ABH86970	Oligonucleotide pr
c 422	7.8	43.3	12	1	ABI141857	Oligonucleotide pr	c 495	7.8	43.3	12	1	ABI113617	Oligonucleotide pr
c 423	7.8	43.3	12	1	ABI172757	Oligonucleotide pr	c 496	7.8	43.3	12	1	ABI146100	Oligonucleotide pr
c 424	7.8	43.3	12	1	ABI160455	Oligonucleotide pr	c 497	7.8	43.3	12	1	ABI160184	Oligonucleotide pr
c 425	7.8	43.3	12	1	ABI163529	Oligonucleotide pr	c 498	7.8	43.3	12	1	ABI174204	Oligonucleotide pr
c 426	7.8	43.3	12	1	ABI130747	Oligonucleotide pr	c 499	7.8	43.3	12	1	ABH97217	Oligonucleotide pr
c 427	7.8	43.3	12	1	ABI131406	Oligonucleotide pr	c 500	7.8	43.3	12	1	ABI123341	Oligonucleotide pr
c 428	7.8	43.3	12	1	ABH84137	Oligonucleotide pr	c 501	7.8	43.3	12	1	ABH98713	Oligonucleotide pr
c 429	7.8	43.3	12	1	ABH84138	Oligonucleotide pr	c 502	7.8	43.3	12	1	ABI126688	Oligonucleotide pr
c 430	7.8	43.3	12	1	ABI123179	Oligonucleotide pr	c 503	7.8	43.3	12	1	ABI13755	Oligonucleotide pr
c 431	7.8	43.3	12	1	ABI123530	Oligonucleotide pr	c 504	7.8	43.3	12	1	ABH88565	Oligonucleotide pr
c 432	7.8	43.3	12	1	ABI125770	Oligonucleotide pr	c 505	7.8	43.3	12	1	ABH89193	Oligonucleotide pr
c 433	7.8	43.3	12	1	ABI09805	Oligonucleotide pr	c 506	7.8	43.3	12	1	ABH75818	Oligonucleotide pr
c 434	7.8	43.3	12	1	ABI150807	Oligonucleotide pr	c 507	7.8	43.3	12	1	ABI129229	Oligonucleotide pr
c 435	7.8	43.3	12	1	ABI169356	Oligonucleotide pr	c 508	7.8	43.3	12	1	ABH82959	Oligonucleotide pr
c 436	7.8	43.3	12	1	ABI158359	Oligonucleotide pr	c 509	7.8	43.3	12	1	ABI11722	Oligonucleotide pr
c 437	7.8	43.3	12	1	ABI122393	Oligonucleotide pr	c 510	7.8	43.3	12	1	ABI114453	Oligonucleotide pr
c 438	7.8	43.3	12	1	ABH98561	Oligonucleotide pr	c 511	7.8	43.3	12	1	ABI147069	Oligonucleotide pr
c 439	7.8	43.3	12	1	ABH05081	Oligonucleotide pr	c 512	7.8	43.3	12	1	ABI169559	Oligonucleotide pr
c 440	7.8	43.3	12	1	ABI09990	Oligonucleotide pr	c 513	7.8	43.3	12	1	AD45478	Oligonucleotide pr
c 441	7.8	43.3	12	1	ABI148685	Oligonucleotide pr	c 514	7.8	43.3	12	1	ABZ58916	Human JAM3 intron
c 442	7.8	43.3	12	1	ABI148873	Oligonucleotide pr	c 515	7.4	41.1	9	1	AAA33403	Low adenosine anti
c 443	7.8	43.3	12	1	ABI152599	Oligonucleotide pr	c 516	7.4	41.1	9	1	AAAF19525	Human ELAM-1 polyn
c 444	7.8	43.3	12	1	ABI158547	Oligonucleotide pr	c 517	7.4	41.1	9	1	ABQ72210	Zinc finger protei
c 445	7.8	43.3	12	1	ABH92986	Oligonucleotide pr	c 518	7.4	41.1	9	1	ABZ95219	Human ELAM-1 anti
c 446	7.8	43.3	12	1	ABH69192	Oligonucleotide pr	c 519	7.4	41.1	9	1	ADA64537	Zinc finger target
c 447	7.8	43.3	12	1	ABI20668	Oligonucleotide pr	c 520	7.4	41.1	10	1	AAQ57343	Enzymatic RNA mole
c 448	7.8	43.3	12	1	ABI129816	Oligonucleotide pr	c 521	7.4	41.1	10	1	AAQ96476	HIV-1 NL4-3 nef ge
c 449	7.8	43.3	12	1	ABH84367	Oligonucleotide pr	c 522	7.4	41.1	10	1	AAQ96477	HIV-1 NL4-3 nef ge
c 450	7.8	43.3	12	1	ABI138138	Oligonucleotide pr	c 523	7.4	41.1	10	1	AAAT29279	5'-primer for mamm
c 451	7.8	43.3	12	1	ABH90077	Oligonucleotide pr	c 524	7.4	41.1	10	1	AAAT29345	5'-primer for mamm
c 452	7.8	43.3	12	1	ABI116474	Oligonucleotide pr	c 525	7.4	41.1	10	1	AAV35919	Primer used in RAP
c 453	7.8	43.3	12	1	ABI116577	Oligonucleotide pr	c 526	7.4	41.1	10	1	AAAI19477	Human senescence f
c 454	7.8	43.3	12	1	ABH67250	Oligonucleotide pr	c 527	7.4	41.1	10	1	AAAX99946	Human parkin gene
c 455	7.8	43.3	12	1	ABI50913	Oligonucleotide pr	c 528	7.4	41.1	10	1	AAAX99945	Human parkin gene
c 456	7.8	43.3	12	1	ABI175469	Oligonucleotide pr	c 529	7.4	41.1	10	1	AAAX32315	Non-activating con
c 457	7.8	43.3	12	1	ABI162231	Oligonucleotide pr	c 530	7.4	41.1	10	1	AAAX32306	Radiactivator iso
c 458	7.8	43.3	12	1	ABH67447	Oligonucleotide pr	c 531	7.4	41.1	10	1	AAAX32312	Radiactivator iso
c 459	7.8	43.3	12	1	ABI19569	Oligonucleotide pr	c 532	7.4	41.1	10	1	AAZ79567	Human dendritic ce
c 460	7.8	43.3	12	1	ABI121552	Oligonucleotide pr	c 533	7.4	41.1	10	1	AAZ78693	Human dendritic ce
c 461	7.8	43.3	12	1	ABI125472	Oligonucleotide pr	c 534	7.4	41.1	10	1	AAZ78801	Human dendritic ce
c 462	7.8	43.3	12	1	ABH78395	Oligonucleotide pr	c 535	7.4	41.1	10	1	AAZ84279	Metastatic breast
c 463	7.8	43.3	12	1	ABI114003	Oligonucleotide pr	c 536	7.4	41.1	10	1	AAZ81150	Metastatic breast
c 464	7.8	43.3	12	1	ABH89602	Oligonucleotide pr	c 537	7.4	41.1	10	1	AAZ82196	Metastatic breast
c 465	7.8	43.3	12	1	ABI157686	Oligonucleotide pr	c 538	7.4	41.1	10	1	AAZ81306	Metastatic breast
c 466	7.8	43.3	12	1	ABI19012	Oligonucleotide pr	c 539	7.4	41.1	10	1	AAZ83439	Metastatic breast
c 467	7.8	43.3	12	1	ABI19356	Oligonucleotide pr	c 540	7.4	41.1	10	1	AAZ85795	Metastatic breast
c 468	7.8	43.3	12	1	ABI126910	Oligonucleotide pr	c 541	7.4	41.1	10	1	AAZ85917	Metastatic breast
c 469	7.8	43.3	12	1	ABH77690	Oligonucleotide pr	c 542	7.4	41.1	10	1	AAZ83130	Metastatic breast
c 470	7.8	43.3	12	1	ABH79279	Oligonucleotide pr	c 543	7.4	41.1	10	1	AAZ81087	Metastatic breast
c 471	7.8	43.3	12	1	ABI131459	Oligonucleotide pr	c 544	7.4	41.1	10	1	AAZ81916	Metastatic breast

545	7.4	41.1	10	1	AAZ82660	Metastatic breast	c 618	7.4	41.1	11	1	AAA16604	Human MN gene 3' a
546	7.4	41.1	10	1	AAZ83470	Metastatic breast	c 619	7.4	41.1	11	1	AAA52523	Human MN gene intr
547	7.4	41.1	10	1	AAZ84169	Metastatic breast	c 620	7.4	41.1	11	1	AAF77709	KTF-1 binding sequ
548	7.4	41.1	10	1	AAA56272	Human macrophage g	c 621	7.4	41.1	11	1	ABQ87081	Human skin stress/
549	7.4	41.1	10	1	AAA14152	E. coli K-12 leadi	c 622	7.4	41.1	11	1	ABQ86561	Human skin stress/
550	7.4	41.1	10	1	AAH63655	Human ubiquitously	c 623	7.4	41.1	11	1	ABQ87626	Human skin stress/
551	7.4	41.1	10	1	AAH64281	Human ubiquitously	c 624	7.4	41.1	11	1	ABV62854	Human skin EST 640
552	7.4	41.1	10	1	AAH41710	Anti-PEP gene cons	c 625	7.4	41.1	11	1	ABV69436	Human skin EST 722
553	7.4	41.1	10	1	AAF34448	Yeast NORF gene SA	c 626	7.4	41.1	11	1	ABV64542	Human skin EST 232
554	7.4	41.1	10	1	AAF41885	Yeast NORF gene SA	c 627	7.4	41.1	11	1	ABV66285	Human skin EST 407
555	7.4	41.1	10	1	AAF42672	Yeast NORF gene SA	c 628	7.4	41.1	11	1	ABV67862	Human skin EST 564
556	7.4	41.1	10	1	AAF40816	Yeast NORF gene SA	c 629	7.4	41.1	11	1	ABV70275	Human skin EST 806
557	7.4	41.1	10	1	AAF34965	Yeast NORF gene SA	c 630	7.4	41.1	11	1	ABV70713	Human skin EST 849
558	7.4	41.1	10	1	AAF40673	Yeast NORF gene SA	c 631	7.4	41.1	11	1	ABV62726	Human skin EST 512
559	7.4	41.1	10	1	AAF35576	Yeast NORF gene SA	c 632	7.4	41.1	11	1	ABV65010	Human skin EST 279
560	7.4	41.1	10	1	AAF37348	Yeast NORF gene SA	c 633	7.4	41.1	11	1	ABV71892	Human skin EST 967
561	7.4	41.1	10	1	AAF37799	Yeast NORF gene SA	c 634	7.4	41.1	11	1	ABV67255	Human skin EST 504
562	7.4	41.1	10	1	AAF36479	Yeast NORF gene SA	c 635	7.4	41.1	11	1	ABV65152	Human skin EST 293
563	7.4	41.1	10	1	AAF39653	Yeast NORF gene SA	c 636	7.4	41.1	11	1	ABV66544	Human skin EST 433
564	7.4	41.1	10	1	AAF33951	Yeast NORF gene SA	c 637	7.4	41.1	11	1	ABV70147	Human skin EST 793
565	7.4	41.1	10	1	AAF36315	Yeast NORF gene SA	c 638	7.4	41.1	11	1	ABV67207	Human skin EST 499
566	7.4	41.1	10	1	AAF40655	Yeast NORF gene SA	c 639	7.4	41.1	11	1	ABV72073	Human skin EST 985
567	7.4	41.1	10	1	AAF33950	Yeast NORF gene SA	c 640	7.4	41.1	11	1	ABV63292	Human skin EST 107
568	7.4	41.1	10	1	AAF33162	Yeast NORF gene SA	c 641	7.4	41.1	11	1	ABV64471	Human skin EST 225
569	7.4	41.1	10	1	AAF39237	Yeast NORF gene SA	c 642	7.4	41.1	11	1	ABV71963	Human skin EST 974
570	7.4	41.1	10	1	AAF43110	Yeast NORF gene SA	c 643	7.4	41.1	11	1	ABV65259	Human skin EST 304
571	7.4	41.1	10	1	AAF36967	Yeast NORF gene SA	c 644	7.4	41.1	11	1	ABV68120	Human skin EST 590
572	7.4	41.1	10	1	AAF39593	Yeast NORF gene SA	c 645	7.4	41.1	11	1	ABV68138	Human skin EST 592
573	7.4	41.1	10	1	AAF42943	Yeast NORF gene SA	c 646	7.4	41.1	11	1	ABV66358	Human skin EST 414
574	7.4	41.1	10	1	AAF40433	Yeast NORF gene SA	c 647	7.4	41.1	11	1	ABL91912	Human Pan-Endothel
575	7.4	41.1	10	1	AAF42050	Yeast NORF gene SA	c 648	7.4	41.1	11	1	ABX71837	DNA tag used to id
576	7.4	41.1	10	1	AAF36317	Yeast NORF gene SA	c 649	7.4	41.1	11	1	ABQ71829	Zinc finger protei
577	7.4	41.1	10	1	AAF43031	Yeast NORF gene SA	c 650	7.4	41.1	9	1	ABQ71831	Zinc finger protei
578	7.4	41.1	10	1	AAF43054	Yeast NORF gene SA	c 651	7.4	41.1	9	1	ABQ71412	Zinc finger protei
579	7.4	41.1	10	1	AAF37820	Yeast NORF gene SA	c 652	7.4	41.1	9	1	ABQ71830	Zinc finger protei
580	7.4	41.1	10	1	AAF35067	Yeast NORF gene SA	c 653	7.4	41.1	9	1	ABQ71828	Zinc finger protei
581	7.4	41.1	10	1	AAF35976	Yeast NORF gene SA	c 654	7.4	41.1	9	1	ADA64155	Zinc finger target
582	7.4	41.1	10	1	AAF33787	Yeast NORF gene SA	c 655	7.4	41.1	9	1	ADA64157	Zinc finger target
583	7.4	41.1	10	1	AAF36067	Yeast NORF gene SA	c 656	7.4	41.1	9	1	ADA64156	Zinc finger target
584	7.4	41.1	10	1	ABK67942	Human ADH7 gene al	c 657	7.4	41.1	9	1	ADA62560	Zinc finger target
585	7.4	41.1	10	1	ABS64903	Primer-extension o	c 658	7.4	41.1	9	1	ADA64158	Zinc finger target
586	7.4	41.1	10	1	ABK24270	Retinaldehyde-bind	c 659	7.4	41.1	10	1	AAQ97103	HIV-1 NL4-3 LTR nu
587	7.4	41.1	10	1	ABK14252	Human RRS3B2 gene	c 660	7.4	41.1	10	1	AAQ97099	HIV-1 NL4-3 LTR nu
588	7.4	41.1	10	1	RA595514	Human HSD3 gene	c 661	7.4	41.1	10	1	AAQ99832	Eucalyptus grandis
589	7.4	41.1	10	1	AAD32507	Human ORG1 gene p	c 662	7.4	41.1	10	1	AAT29349	5'-primer for mam
590	7.4	41.1	10	1	ABK96383	Human SA homologue	c 663	7.4	41.1	10	1	AAT29273	5'-primer for mam
591	7.4	41.1	10	1	ABK34224	Human interleukin	c 664	7.4	41.1	10	1	AAK39938	Human parkin gene
592	7.4	41.1	10	1	ABL52257	Human PHK2 prefer	c 665	7.4	41.1	10	1	AAK86216	SAGE tag used to i
593	7.4	41.1	10	1	ABQ71544	Zinc finger protei	c 666	7.4	41.1	10	1	AAK86213	SAGE tag used to i
594	7.4	41.1	10	1	ABA96083	CYP8B1 primer-exte	c 667	7.4	41.1	10	1	AAK59805	Primer Y3 for ampl
595	7.4	41.1	10	1	ABQ72349	Human CYP2D6 gene	c 668	7.4	41.1	10	1	AAZ22662	T7 primer for ampl
596	7.4	41.1	10	1	ABV78564	Human Th2 cell pre	c 669	7.4	41.1	10	1	AAZ79415	Human dendritic ce
597	7.4	41.1	10	1	ABV78497	Human Th1 cell pre	c 670	7.4	41.1	10	1	AAZ79495	Human dendritic ce
598	7.4	41.1	10	1	ABV84944	Human HCC highly e	c 671	7.4	41.1	10	1	AAZ79121	Human dendritic ce
599	7.4	41.1	10	1	ABK23444	Transcript tag DNA	c 672	7.4	41.1	10	1	AAZ79694	Human dendritic ce
600	7.4	41.1	10	1	ABL52030	Human SLC18A2 pref	c 673	7.4	41.1	10	1	AAZ78251	Human dendritic ce
601	7.4	41.1	10	1	AA519861	Oligonucleotide #4	c 674	7.4	41.1	10	1	AAZ82381	Metastatic breast
602	7.4	41.1	10	1	ABK70762	Primer-extension o	c 675	7.4	41.1	10	1	AAZ86113	Metastatic breast
603	7.4	41.1	10	1	AA40878	Zinc finger protei	c 676	7.4	41.1	10	1	AAZ82142	Metastatic breast
604	7.4	41.1	10	1	ABS64281	Tachykinin recepto	c 677	7.4	41.1	10	1	AAZ84467	Metastatic breast
605	7.4	41.1	10	1	RA595472	Interleukin 5 (IL5	c 678	7.4	41.1	10	1	AAZ83486	Metastatic breast
606	7.4	41.1	10	1	ABI19135	Human PCDH2 ASO PC	c 679	7.4	41.1	10	1	AAZ84078	Metastatic breast
607	7.4	41.1	10	1	ABN85917	Gamma tocopherol	c 680	7.4	41.1	10	1	AAZ84666	Metastatic breast
608	7.4	41.1	10	1	ACC57793	DNA template. Syn	c 681	7.4	41.1	10	1	AAZ84940	Metastatic breast
609	7.4	41.1	10	1	ABZ75761	C. purpureum RAPD1	c 682	7.4	41.1	10	1	AAZ84022	Metastatic breast
610	7.4	41.1	10	1	ACC41745	Zinc finger protei	c 683	7.4	41.1	10	1	AAZ86522	Metastatic breast
611	7.4	41.1	10	1	ABT14331	Nucleic acid PCR a	c 684	7.4	41.1	10	1	AAZ85103	Metastatic breast
612	7.4	41.1	10	1	ABT14343	Nucleic acid PCR a	c 685	7.4	41.1	10	1	AAZ85221	Metastatic breast
613	7.4	41.1	10	1	ADA63307	Zinc finger target	c 686	7.4	41.1	10	1	AAZ86089	Metastatic breast
614	7.4	41.1	10	1	ADB67173	PNA related bindin	c 687	7.4	41.1	10	1	AAZ83028	Metastatic breast
615	7.4	41.1	11	1	AAZ18956	Murine MRL SAGE ta	c 688	7.4	41.1	10	1	AAZ84058	Metastatic breast
616	7.4	41.1	11	1	AAZ18727	Murine C57BL/6 SAG	c 689	7.4	41.1	10	1	AAZ82188	Metastatic breast
617	7.4	41.1	11	1	AAK82053	DNA probe sequence	c 690	7.4	41.1	10	1	AAZ82729	Metastatic breast

c 691	7	38.9	10	1	AAZ82373	Metastatic breast	764	7	38.9	10	1	ABL99032	Mouse neuronal reg
c 692	7	38.9	10	1	AAZ85270	Metastatic breast	c 765	7	38.9	10	1	ABK92584	Primer-extension o
c 693	7	38.9	10	1	AAZ85752	Metastatic breast	c 766	7	38.9	10	1	ABK96378	Human SA homologue
c 694	7	38.9	10	1	AAZ82359	Metastatic breast	767	7	38.9	10	1	ABQ71632	Zinc finger protei
c 695	7	38.9	10	1	AAZ84231	Metastatic breast	768	7	38.9	10	1	ABQ71579	Zinc finger protei
c 696	7	38.9	10	1	AAZ85767	Metastatic breast	769	7	38.9	10	1	ABQ71633	Zinc finger protei
c 697	7	38.9	10	1	AAZ81283	Metastatic breast	770	7	38.9	10	1	ABQ71574	Zinc finger protei
c 698	7	38.9	10	1	AAZ82557	Metastatic breast	771	7	38.9	10	1	ABQ71545	Zinc finger protei
c 699	7	38.9	10	1	AAZ84862	Metastatic breast	772	7	38.9	10	1	ABQ71437	Zinc finger protei
c 700	7	38.9	10	1	AAZ85638	Metastatic breast	773	7	38.9	10	1	AAD25211	Human homeo box D3
c 701	7	38.9	10	1	AAZ82011	Metastatic breast	c 774	7	38.9	10	1	AAD25216	Human homeo box D3
c 702	7	38.9	10	1	AAZ83742	Metastatic breast	c 775	7	38.9	10	1	ABV84961	Human complement c
c 703	7	38.9	10	1	AAZ83255	Metastatic breast	c 776	7	38.9	10	1	ABV84988	Human multiple HCC
c 704	7	38.9	10	1	AAZ85439	Metastatic breast	c 777	7	38.9	10	1	AAD43438	Human CYP3A5 gene
c 705	7	38.9	10	1	AAZ85480	Metastatic breast	c 778	7	38.9	10	1	AAZ85571	Human IL8RB gene a
c 706	7	38.9	10	1	AAZ85719	Metastatic breast	779	7	38.9	10	1	ABK16678	Human AGTRL1 gene
c 707	7	38.9	10	1	AAZ74122	Human monocyte and	c 780	7	38.9	10	1	ABK11494	Oligonucleotide pr
c 708	7	38.9	10	1	AAZ56554	Human macrophage g	781	7	38.9	10	1	AAAL43012	Human cerberus 1 (
c 709	7	38.9	10	1	AAZ79818	Human breast/lung	782	7	38.9	10	1	AAD43794	Human AGTR2 gene p
c 710	7	38.9	10	1	AAZ79781	Human breast prefe	783	7	38.9	10	1	ABS64260	Tachykinin recepto
c 711	7	38.9	10	1	AAD15400	Tag #1 used in SAG	c 784	7	38.9	10	1	AAK98601	Human enolase 3 ge
c 712	7	38.9	10	1	AAI67358	Human FKBP8 gene p	785	7	38.9	10	1	ABK32812	Human APPBP1 gene,
c 713	7	38.9	10	1	AAH63708	Human ubiquitously	786	7	38.9	10	1	AAZ5697	Human cyclin-depen
c 714	7	38.9	10	1	AAH63571	Human ubiquitously	787	7	38.9	10	1	AAZ59395	Aldehyde dehydroge
c 715	7	38.9	10	1	AAH64720	Human highly expre	788	7	38.9	10	1	ABK29949	Cyclin D1 promoter
c 716	7	38.9	10	1	AAH64185	Human ubiquitously	c 789	7	38.9	10	1	ACA94575	DNA tag from human
c 717	7	38.9	10	1	AAH64422	Human melanocyte s	c 790	7	38.9	10	1	ABT14302	Nucleic acid PCR a
c 718	7	38.9	10	1	AAH63338	Human ubiquitously	c 791	7	38.9	10	1	ABT14310	Nucleic acid PCR a
c 719	7	38.9	10	1	AAH63570	Human ubiquitously	c 792	7	38.9	10	1	ABT14266	Nucleic acid PCR a
c 720	7	38.9	10	1	AAH64072	Human ubiquitously	793	7	38.9	10	1	ABZ81289	Small proline-rich
c 721	7	38.9	10	1	AAH20543	Human MTR1 intron7	794	7	38.9	10	1	ADA63337	Zinc finger target
c 722	7	38.9	10	1	AAD20726	Primer #18 used to	795	7	38.9	10	1	ADA63653	Zinc finger target
c 723	7	38.9	10	1	AAH32828	LPS activated huma	796	7	38.9	10	1	ADA62585	Zinc finger target
c 724	7	38.9	10	1	AAH32662	LPS activated huma	797	7	38.9	10	1	ADA63654	Zinc finger target
c 725	7	38.9	10	1	AAH32879	LPS activated huma	798	7	38.9	10	1	ADA63308	Zinc finger target
c 726	7	38.9	10	1	AAH32805	LPS activated huma							
c 727	7	38.9	10	1	ABA06211	Human normal hepat							
c 728	7	38.9	10	1	ABA06100	Human normal hepat							
c 729	7	38.9	10	1	RAF74038	Human SLC6A4 allel							
c 730	7	38.9	10	1	AAF35143	Yeast NORF gene SA							
c 731	7	38.9	10	1	AAF37041	Yeast NORF gene SA							
c 732	7	38.9	10	1	AAF41905	Yeast NORF gene SA							
c 733	7	38.9	10	1	AAF39747	Yeast NORF gene SA							
c 734	7	38.9	10	1	AAF40492	Yeast NORF gene SA							
c 735	7	38.9	10	1	AAF43211	Yeast NORF gene SA							
c 736	7	38.9	10	1	AAF42714	Yeast NORF gene SA							
c 737	7	38.9	10	1	AAF43979	Yeast NORF gene SA							
c 738	7	38.9	10	1	AAF34385	Yeast NORF gene SA							
c 739	7	38.9	10	1	AAF39293	Yeast NORF gene SA							
c 740	7	38.9	10	1	AAF42400	Yeast NORF gene SA							
c 741	7	38.9	10	1	AAF43251	Yeast NORF gene SA							
c 742	7	38.9	10	1	AAF34637	Yeast NORF gene SA							
c 743	7	38.9	10	1	AAF39100	Yeast NORF gene SA							
c 744	7	38.9	10	1	AAF42420	Yeast NORF gene SA							
c 745	7	38.9	10	1	AAF43780	Yeast NORF gene SA							
c 746	7	38.9	10	1	AAF35242	Yeast NORF gene SA							
c 747	7	38.9	10	1	AAF41021	Yeast NORF gene SA							
c 748	7	38.9	10	1	AAF39592	Yeast NORF gene SA							
c 749	7	38.9	10	1	AAF34894	Yeast NORF gene SA							
c 750	7	38.9	10	1	AAF35393	Yeast NORF gene SA							
c 751	7	38.9	10	1	AAF41531	Yeast NORF gene SA							
c 752	7	38.9	10	1	AAF43549	Yeast NORF gene SA							
c 753	7	38.9	10	1	AAF37385	Yeast NORF gene SA							
c 754	7	38.9	10	1	AAF40582	Yeast NORF gene SA							
c 755	7	38.9	10	1	AAF43159	Yeast NORF gene SA							
c 756	7	38.9	10	1	ABK24251	Retinaldehyde-bind							
c 757	7	38.9	10	1	AAZ59280	Human F12 gene all							
c 758	7	38.9	10	1	ABL52179	Human PER1 preferr							
c 759	7	38.9	10	1	ABL52208	Human PER1 preferr							
c 760	7	38.9	10	1	ABL39607	SSTR4 gene polymor							
c 761	7	38.9	10	1	ABL01179	Human AKR1B1 gene							
c 762	7	38.9	10	1	ABL42680	Human maturation/a							
c 763	7	38.9	10	1	ABL42762	Human maturation/a							

ALIGNMENTS

RESULT 1

AAA08468
ID AAA08468 standard; DNA; 18 BP.

XX AC AAA08468;

XX AC 17-JUL-2000 (first entry)

DT Human Akt-2 phosphorothioate antisense oligonucleotide SEQ ID NO:21.

DR WPI; 2000-270345/23.

XX Antisense compound for diagnosis and treatment of infection, inflammation

PT and tumor formation is targeted towards the nucleic acid encoding a

PT member of serine/threonine family of kinases.

XX Claim 3; Col 38; 30pp; English.

XX The present invention describes antisense compounds of about 8-30

CC nucleotides in length targeted to the 5' UTR (untranslated region), 3'

CC UTR or coding region of the nucleic acid encoding human Akt-2, which

CC inhibits the expression of human Akt-2. Human Akt-2 is a member of the

CC Akt/PKB family of serine/threonine kinases. The antisense compounds have

CC antiinflammatory, cytostatic and antitumorigenic activities, and can be

CC used in gene therapy. They are useful in inhibiting the expression of

CC human Akt-2 by contacting the cells or the tissues in vitro. They can

CC also be used for diagnosis and treatment of infection, inflammation and

CC tumor formation, and for prophylaxis. The present sequence represents a

CC human Akt-2 phosphorothioate antisense oligonucleotide used in the

CC exemplification of the present invention

XX SQ Sequence 18 BP; 2 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGGCTGTGGCGAC 18

Db 1 CTTGAGGCTGTGGCGAC 18

RESULT 2

AAT08592

ID AAT08592 standard; DNA; 19 BP.

XX AC AAT08592;

XX 25-MAR-2003 (revised)

DT 27-JUN-1996 (first entry)

XX K-ras protooncogene exon 12 capture probe #7.

DE Capture probe; quantitative; qualitative; covalent bond; solid surface;

XX organosilane; immobilisation; enzyme conjugate; antibody; reporter;

KW K-ras; proto-oncogene; point mutation; ss.

XX OS Synthetic.

XX DE19518217-A1.

XX 30-NOV-1995.

XX 10-MAY-1995; 95DE-01018217.

XX 11-MAY-1994; 94DE-04416802.

XX (INTE-) IMTEC IMMUNDIAGNOSTIKA GMBH.

PA Bernd H, Schoessler W, Bebenroth M, Oehlschlaegel K, Hiepe F;

PI Schroeder G;

XX WPI; 1996-012002/02.

XX Determn of DNA after capture by probe immobilised on solid phase - useful

PT in diagnosis and monitoring of viral infections and cancer.

XX Example 2; Page 5; 13pp; German.

XX The sequences AAT08580-95 are examples of probes and capture probes used

CC in a novel method for the quantitative and qualitative determination of

CC DNA sequences. The method involves covalently bonding a capture probe to

CC a solid surface which has been chemically activated by an alcoholic soln.

CC of organosilane and heat. The probe or target sequence then binds to the

CC immobilised capture probe and can be detected by a marker present on the

CC target sequence or using an enzyme conjugate, anti-nucleic acid antibody

CC or second reporter probe. The capture probes AAT08586-92 can be used to

CC detect point mutations in the K-ras proto-oncogene exon 12 sequence, as

CC exemplified by the oligonucleotide AAT08585. (Updated on 25-MAR-2003 to

XX correct PR field.)

XX SQ Sequence 19 BP; 3 A; 2 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 22;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGGCG 16

Db 2 TTGAGGCTGTGGCG 16

RESULT 3

ABI95305/c

ID ABI95305 standard; DNA; 20 BP.

XX AC ABI95305;

XX 16-FEB-2002 (first entry)

XX Capture oligonucleotide Zip ID#2392 oligo #9.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;

KW ligase detection reaction; LDR; p53; BRCA2; infectious disease;

KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;

KW oncogene; tumour suppressor; human papillomavirus; forensic;

KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX WO200179548-A2.

XX 25-OCT-2001.

XX 04-APR-2001; 2001WO-USO10958.

XX 14-APR-2000; 2000US-0197271P.

XX (CORR) CORNELL RES FOUND INC.

PA Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX WPI; 2002-034366/04.

XX Designing capture oligonucleotide probes for use on a support to which

PT complementary oligonucleotides hybridize with little mismatch.

XX Example 5; Fig 29; 300pp; English.

XX The present invention describes a method (M1) for designing capture

CC oligonucleotide probes (I) for use on a support to which complementary

CC oligonucleotide probes (II) will hybridise with little mismatch, where

CC (I) have melting temperatures within a narrow range. The method is useful

CC for detecting infectious diseases caused by bacterial infectious agents

CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal

CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and

CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,

CC Epstein-Barr virus and polio virus, and parasitic infectious agents

CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus

CC medinensis. The method is also useful for detecting genetic defects.

CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes

CC involved in DNA amplification, replication, recombination or repair, the

CC cancer is specifically associated with a gene selected from BRCA1 gene,

CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The

CC method is also used for environmental monitoring, forensics and the food

CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention

SQ Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 74.4%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGGCGA 17
|||||
Db 20 TGAGGCTGTGGCGA 6

RESULT 4
AAF49930/c
ID AAF49930 standard; DNA; 15 BP.
XX AC
XX AAF49930;
XX AC
XX 30-MAR-2001 (first entry)
XX DE
XX IGF-I oligonucleotide #890.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.

XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX PN
XX 28-DEC-2000.
XX PD
XX 21-JUN-2000; 2000WO-AU000693.
XX PF
XX 21-JUN-1999; 99US-0140345P.
XX PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX PA
XX Wright CJ, Werther GA, Edmondson SR;
XX PI
XX WPI; 2001-041421/05.
XX DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 68.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 34;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGGCG 16
|||||
Db 15 TGAGGCTGTGGCG 2

RESULT 5
AAF49931/c
ID AAF49931 standard; DNA; 15 BP.
XX AC
XX AAF49931;
XX AC
XX 30-MAR-2001 (first entry)
XX DT
XX DE
XX IGF-I oligonucleotide #891.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.

XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX PN
XX 28-DEC-2000.
XX PD
XX 21-JUN-2000; 2000WO-AU000693.
XX PF
XX 21-JUN-1999; 99US-0140345P.
XX PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX PA
XX Wright CJ, Werther GA, Edmondson SR;
XX PI
XX WPI; 2001-041421/05.
XX DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia

SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 68.9%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 34;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGGCG 16
 Db 14 TGAGGATGTGGCG 1

RESULT 6
 AAT09992/c
 ID AAT09992 standard; cDNA; 17 BP.
 XX
 AC AAT09992;
 XX
 DT 14-OCT-1996 (first entry)
 XX
 DE Degenerate primer for amplifying glucan elicitor receptor.
 XX
 KW Glucan elicitor receptor protein; binding; resistance; fungi;
 KW fungal infection; signal transmission; ss.
 XX
 OS Synthetic.
 XX
 PN WO9535371-A1.
 XX
 PD 28-DEC-1995.
 XX
 PF 16-JUN-1995; 95WO-JP001206.
 XX
 PR 17-JUN-1994; 94JP-00136100.
 XX
 PA (KIRI) KIRIN BEER KK.
 PA (YOSH/) YOSHIKAWA K.
 XX
 PI Yoshikawa M, Kakitani M, Umemoto N, Ishida I, Iwamatsu A;
 XX
 DR WPI; 1996-059408/06.
 XX
 PT DNA encoding soya bean glucan elicitor receptor - for conferring fungal
 PT resistance on plants such as tobacco.
 XX
 PS Example 1; Page 15; 53pp; Japanese.
 CC Insertion of DNA encoding the glucan elicitor receptor protein confers
 CC fungal resistance on plants e.g. tobacco. The DNA and encoded protein are
 CC also useful in the investigation of elicitor binding and signal
 CC transmission. Two primers (AAT09991, AAT09992) were used to amplify the
 CC elicitor receptor coding sequence
 XX
 SQ Sequence 17 BP; 6 A; 7 C; 1 G; 1 T; 0 U; 2 Other;
 Query Match 66.7%; Score 12; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCGA 17
 Db 17 TTGGKGTGTGTGGCGA 2

RESULT 7
 AAT74646/c
 ID AAT74646 standard; DNA; 17 BP.
 XX
 AC AAT74646;
 XX
 DT 03-MAR-1998 (first entry)
 XX
 DE Primer U19 SEQ ID NO:14 from WO9722242 Example 2.
 XX

KW Glucan elicitor receptor; plant; resistance; pathogenic mould;
 KW Phytophthora; primer; ss.
 OS Synthetic.
 XX
 PN WO9722242-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 13-DEC-1996; 96WO-JP003653.
 XX
 PR 15-DEC-1995; 95JP-00347823.
 XX
 PA (KIRI) KIRIN BEER KK.
 XX
 PI Kakitani M, Umemoto N, Ishida I, Yamaoka N;
 XX
 DR WPI; 1997-341345/31.
 XX
 PT Production of plants resistant to pathogenic mold(s) such as Phytophthora
 PT - by incorporation into the genome of DNA encoding glucan elicitor
 PT receptor.
 XX
 PS Example 2; Page 18; 90pp; Japanese.
 CC The present sequence represents a primer used in example 2 of the present
 CC invention for producing plants resistant to pathogenic moulds such as
 CC phytophthora. By incorporating DNA encoding a glucan elicitor receptor
 CC into plant chromosomes, resistance to pathogenic moulds is conferred. The
 CC method may be used to produce plants (in particular those of commercial
 CC importance) which are resistant to pathogenic moulds. These include
 CC tobacco, rice, soybean, chrysanthemum and carnation
 XX
 SQ Sequence 17 BP; 6 A; 7 C; 1 G; 1 T; 0 U; 2 Other;
 Query Match 66.7%; Score 12; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCGA 17
 Db 17 TTGGKGTGTGTGGCGA 2

RESULT 8
 AAA08469
 ID AAA08469 standard; DNA; 18 BP.
 XX
 AC AAA08469;
 XX
 DT 17-JUL-2000 (first entry)
 XX
 DE Human Akt-2 phosphorothioate antisense oligonucleotide SEQ ID NO:22.
 XX
 KW Human, Akt-2, antisense oligonucleotide; phosphorothioate; inhibition;
 KW serine/threonine kinase; antiinflammatory; cytostatic; antifetitious;
 KW gene therapy; infection; inflammation; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /*tag= a
 FT /note= "phosphorothioate linkages"
 XX
 PN US6043090-A.
 XX
 PD 28-MAR-2000.
 XX
 PF 23-FEB-1999; 99US-00256465.
 XX
 PR 23-FEB-1999; 99US-00256465.
 XX

PA (ISIS-) ISIS PHARM INC.
XX Monia BP, Cowsert LM;
XX WPI; 2000-270345/23.
XX Antisense compound for diagnosis and treatment of infection, inflammation
PT and tumor formation is targeted towards the nucleic acid encoding a
PT member of serine/threonine family of kinases.
XX Claim 3; Col 38; 30pp; English.
XX The present invention describes antisense compounds of about 8-30
CC nucleotides in length targeted to the 5' UTR (untranslated region), 3'
CC UTR or coding region of the nucleic acid encoding human Akt-2, which
CC inhibits the expression of human Akt-2. Human Akt-2 is a member of the
CC Akt/PKB family of serine/threonine kinases. The antisense compounds have
CC antiinflammatory, cytostatic and antifection activities, and can be
CC used in gene therapy. They are useful in inhibiting the expression of
CC human Akt-2 by contacting the cells or the tissues in vitro. They can
CC also be used for diagnosis and treatment of infection, inflammation and
CC tumour formation, and for prophylaxis. The present sequence represents a
CC human Akt-2 phosphorothioate antisense oligonucleotide used in the
CC exemplification of the present invention
XX Sequence 18 BP; 1 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGGCTGTT 12
Db 7 CTTGAGGCTGTT 18
RESULT 9
ADB97992
ID ADB97992 standard; DNA; 17 BP.
XX
XX ADB97992;
AC
DT 04-DEC-2003 (first entry)
XX Human K-Ras sense microarray probe SEQ ID NO:76.
DE Kinetic detection; nucleic acid; hybridisation; high speed detection;
XX microarray; human; K-Ras; probe; ss.
XX Homo sapiens.
XX WO2003062418-A1.
PN 31-JUL-2003.
PD
XX 24-JAN-2003; 2003WO-JP000668.
PF
XX 25-JAN-2002; 2002JP-00017272.
PR 27-AUG-2002; 2002JP-00247023.
XX (OLYU) OLYMPUS OPTICAL CO LTD.
XX Koike H, Nagaoka T, Satoh T, Kaneko Y, Hatanaka M, Fukuoka M;
PI Sakamoto H, Yonekawa H;
XX WPI; 2003-608193/57.
XX Detecting nucleic acid data for rapid analysis.
XX Example 6; Page 61; 67pp; Japanese.
XX The invention relates to a method for kinetically detecting nucleic acid
CC data. The method comprises allowing a target nucleic acid and a probe to
CC bind and form a hybrid, and then detecting for it by kinetic collection
CC of the signal data. The method of the invention provides for the high
CC speed detection of nucleic acid data, and is capable of detecting a
CC single base difference between nucleic acid sequences. The present
CC sequence represents a human K-Ras microarray probe used in an example of
CC the invention.
XX Sequence 17 BP; 2 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
SQ Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTTGGCG 16
Db 1 TTGAGGCTGTTGGCG 15
RESULT 10
ADB97999/C
ID ADB97999 standard; DNA; 17 BP.
XX
XX ADB97999;
AC
DT 04-DEC-2003 (first entry)
XX Human K-Ras antisense microarray probe SEQ ID NO:83.
DE Kinetic detection; nucleic acid; hybridisation; high speed detection;
XX microarray; human; K-Ras; probe; ss.
XX Homo sapiens.
XX WO2003062418-A1.
PN 31-JUL-2003.
PD
XX 24-JAN-2003; 2003WO-JP000668.
PF
XX 25-JAN-2002; 2002JP-00017272.
PR 27-AUG-2002; 2002JP-00247023.
XX (OLYU) OLYMPUS OPTICAL CO LTD.
XX Koike H, Nagaoka T, Satoh T, Kaneko Y, Hatanaka M, Fukuoka M;
PI Sakamoto H, Yonekawa H;
XX WPI; 2003-608193/57.
XX Detecting nucleic acid data for rapid analysis.
XX Example 6; Page 63; 67pp; Japanese.
XX The invention relates to a method for kinetically detecting nucleic acid
CC data. The method comprises allowing a target nucleic acid and a probe to
CC bind and form a hybrid, and then detecting for it by kinetic collection
CC of the signal data. The method of the invention provides for the high
CC speed detection of nucleic acid data, and is capable of detecting a
CC single base difference between nucleic acid sequences. The present
CC sequence represents a human K-Ras microarray probe used in an example of
CC the invention.
XX Sequence 17 BP; 6 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
SQ Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTTGGCG 16
Db 17 TTGAGGCTGTTGGCG 3

```

RESULT 11
AAV11174
ID AAV11174 standard; DNA; 18 BP.
XX
XX AC AAV11174;
XX
XX DT 14-JUL-1998 (first entry)
XX
XX DE Human Ki-ras oncogene primer #6.
XX
XX KW Oncogene; Ki-ras; detection; diagnosis; tumour; pancreas; colon; primer;
XX ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FN DE19737917-A1.
XX
XX PD 05-MAR-1998.
XX
XX PF 26-AUG-1997; 97DE-01037917.
XX
XX PR 26-AUG-1996; 96DE-01035609.
XX
XX PA (INVI-) INVITEK GMBH.
XX
XX PI Hillebrand T, Berndt H, Bendzko P;
XX
XX DR WPI; 1998-160660/15.
XX
XX PT Detection of Ki-ras oncogene alterations - useful for cancer diagnosis
XX especially of colon and pancreas.
XX
XX PS Claim 7; Col 10; 7pp; German.
XX
XX CC AAV11169-Vill174 are primers involved in a method which detects
XX alterations in the human Ki-ras oncogene. This method involves extracting
XX genomic DNA from a sample through multiple purification steps to
XX eliminate inhibitors, and performing a hybridisation assay using six
XX oligonucleotide probes with defined complementarity to altered Ki-ras
XX gene sequences. The method is useful for the early diagnosis of tumours,
XX especially of pancreatic and colonic tumours using stool samples
XX
XX SQ Sequence 18 BP; 2 A; 2 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 47;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCG 16
Db 2 TTGAGGCTGTGGCG 16

RESULT 12
AAF49932/c
ID AAF49932 standard; DNA; 15 BP.
XX
XX AC AAF49932;
XX
XX DT 30-MAR-2001 (first entry)
XX
XX DE IGF-I oligonucleotide #892.
XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX
XX KW Homo sapiens.
XX

```

```

KW neovascular condition of the retina; ss.
XX
XX OS Homo sapiens.
XX
XX DN WO200078341-A1.
XX
XX PD 28-DEC-2000.
XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX
XX PR 21-JUN-1999; 99US-0140345P.
XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX
XX DR WPI; 2001-041421/05.
XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX PS Example 8; Page 66; 201pp; English.
XX
XX CC The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGGC 15
Db 13 TGAGGATGTGGC 1

RESULT 13
AAF49929/c
ID AAF49929 standard; DNA; 15 BP.
XX
XX AC AAF49929;
XX
XX DT 30-MAR-2001 (first entry)
XX
XX DE IGF-I oligonucleotide #889.
XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX
XX KW Homo sapiens.
XX

```

```
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
PR
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 66; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GAGCGCTGTCGCG 16
Db |||||
15 GAGCATGTCGCG 3
RESULT 14
ABN09845/c
ID ABN09845 standard; DNA; 17 BP.
XX
XX AC ABN09845;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9837.
DE
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 9837; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 5 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 55;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGCGCTGTTGG 14
Db |||||
13 TTGAGCGCTGTTGG 1
RESULT 15
ABN09843/c
ID ABN09843 standard; DNA; 17 BP.
XX
XX AC ABN09843;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9835.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
```



```
OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 9835; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 63.3%; Score 11.4; DB 1; Length 17;
XX Best Local Similarity 92.3%; Pred. No. 55;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 2 TTGAGGCTGTGG 14
XX |||||
XX Db 15 TTGAGGCTGTGG 3
XX
XX RESULT 16
XX ABN09842/c
XX ID ABN09842 standard; DNA; 17 BP.
```

```
XX
XX AEN09842;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9834.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 9834; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 63.3%; Score 11.4; DB 1; Length 17;
```

Best Local Similarity 92.3%; Pred. No. 55;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
|||||
Db 16 TTGAGGCTGTGG 4

RESULT 17
ABN09841/c
ID ABN09841 standard; DNA; 17 BP.
XX AC ABN09841;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9833.
DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 9833; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 55;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
|||||
Db 17 TTGAGGCTGTGG 5

RESULT 18
ABN09844/c
ID ABN09844 standard; DNA; 17 BP.
XX AC ABN09844;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9836.
DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 9836; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequence
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 63.3%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 55;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
 Db 14 TTGAGGCTGTGG 2

RESULT 19
 AAX69183/c
 ID AAX69183 standard; RNA; 17 BP.

XX AAX69183;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #478.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.

XX Homo sapiens.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 61; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 6 A; 7 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 62.2%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 61;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTGGCG 16

Db 16 CTTGAGGCTGTGGAG 1

RESULT 20

ABZ65365

ID ABZ65365 standard; RNA; 17 BP.

XX ABZ65365;

XX 21-MAR-2003 (first entry)

XX Human HER2 DNAzyme substrate #822.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2001; 2001US-0294140P.

XX 06-JUN-2001; 2001US-0296249P.

XX 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 4; Page 148; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 62.2%; Score 11.2; DB 1; Length 17;

Best Local Similarity 62.5%; Pred. No. 61;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGGGAC 18
:||||:|||||
Db 1 UGAGACTUGAGGCUAC 16

RESULT 21
ABK11208/c
ID ABK11208 standard; DNA; 14 BP.
XX AC ABK11208;
XX XX
XX DT 21-MAY-2002 (first entry)
XX DE
XX DE Molecular bar code #5.
XX KW Molecular bar code; MBC; ss; genetic material tracking;
XX KW vector identification.
XX OS Synthetic.
XX XX
XX PN WO200214553-A2.
XX XX
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US025106.
XX XX
XX PR 11-AUG-2000; 2000US-0224618P.
XX XX
XX PA (FAVR-) FAVRILLE INC.
XX PI Gold DP, Shopes RJ;
XX XX
XX DR WPI; 2002-241912/29.
XX XX
XX PT Tracking genetic material, involves attaching a molecular bar code to the
XX PT genetic material, detecting the presence of molecular bar code in the
XX PT sample and thus tracking the genetic material.
XX PS
XX PS Example 2; Page 21; 30pp; English.
XX CC
XX CC The invention relates to tracking (M1) genetic material, involves
XX CC attaching a molecular bar code (MBC) to the genetic material to associate
XX CC MBC with the genetic material uniquely, detecting the presence of MBC in
XX CC a sample, and thus tracking the genetic material. The MBC consists of
XX CC essentially of a random series of nucleotides. Also included are
XX CC distinguishing (M2) a unique pairing of a gene of interest with a vector
XX CC from a number of vectors comprising genes, by inserting MBC into a
XX CC molecular bar code insertion site in the vector that comprises the gene
XX CC of interest, thus uniquely associating MBC with the gene of interest in
XX CC the vector, and detecting the presence of MBC in a sample, and thus
XX CC tracking the gene of interest and the vector in the sample, a means for
XX CC specifically identifying a vector comprising genetic information from a
XX CC patient, by inserting a means for identifying the vector that comprises
XX CC the genetic material from the patient, detecting the presence of MBC in a
XX CC sample, and thus identifying the vector containing the genetic material
XX CC from the patient in the sample and, a vector comprising a gene of
XX CC interest and MBC, prepared (M3) by preparing a vector comprising the gene
XX CC of interest to accept MBC by digesting the vector with appropriate
XX CC restriction endonucleases, preparing MBC by synthesising an
XX CC oligonucleotide chain which involves synthesising one strand of a
XX CC restriction endonuclease target site, randomly synthesising 10-100
XX CC nucleotides, and synthesising one strand of a restriction endonuclease
XX CC target site at the other end of the oligonucleotide, preparing a
XX CC complementary strand and annealing it to the synthesised
XX CC oligonucleotides, preparing the double stranded oligonucleotide by
XX CC digesting it with the appropriate restriction endonuclease, and ligating
XX CC the vector with MBC. M1 is useful for tracking the genetic material. M2
XX CC is useful for distinguishing a unique pairing of gene of interest with a
XX CC vector from a number of vectors comprising genes. An MBC is useful for
XX CC monitoring vectors that are subjected to multiple generations of growth.

CC The present sequence is a molecular bar code of the invention
XX
XX SQ Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 61.1%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGTGGC 15
|||||
Db 14 AGGCTGTGGC 4

RESULT 22
AAK57835
ID AAK57835 standard; DNA; 16 BP.
XX AC AAK57835;
XX XX
XX DT 15-JUL-1999 (first entry)
XX DE
XX DE PCR primer for G. oxydans autonomous replication domain.
XX KW Autonomous replication domain; plasmid pF4; L-sorbose dehydrogenase;
XX KW L-sorbose dehydrogenase production; 2-keto-L-gulonic acid; PCR primer;
XX KW ss.
XX OS Synthetic.
XX OS Gluconobacter oxydans.
XX PN WO9920772-A1.
XX PD
XX PD 29-APR-1999.
XX PF 13-OCT-1998; 98WO-JF004611.
XX PR 16-OCT-1997; 97JP-00303395.
XX XX
XX XX (FUJI) FUJISAWA PHARM CO LTD.
XX PI Saito Y, Noguchi Y, Yoshikawa K, Soeda S;
XX XX
XX XX WPI; 1999-302744/25.
XX PT Gluconobacter-originated plasmid pF4 DNAs, useful for producing
XX PT biologically active substance e.g. L-sorbose dehydrogenase and 2-keto-L-
XX PT gulonic acid.
XX PS
XX PS Example; Page 15; 57pp; Japanese.
XX CC
XX CC This sequence represents a PCR primer for the autonomous replication
XX CC domain of Gluconobacter oxydans. The invention relates to a DNA
XX CC originating in plasmid pF4 with a domain controlling the autonomous
XX CC replication in Gluconobacter and a domain from which polynucleotides in
XX CC the region unnecessary in the autonomous replication have been wholly or
XX CC partly deleted, with exception of the pF4 body. Transformants transformed
XX CC with the vector can be used to produce physiologically active substances,
XX CC particularly L-sorbose dehydrogenase and/or L-sorbose dehydrogenase and
XX CC 2-keto-L-gulonic acid. The DNAs contain the domain controlling the
XX CC autonomous replication in a bacterium and a domain with polynucleotides
XX CC in the region unnecessary for this function completely or partially
XX CC removed to cut down the size, while other domains of the vector can be
XX CC enlarged by integrating a greater variety of structural genes to impart
XX CC more functions
XX SQ Sequence 16 BP; 3 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 60.0%; Score 10.6; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGCTGTGGC 15
|||||

Db 3 TGGAGGCTGTAGGC 16

RESULT 24

AA54337

ID AAX54337 standard; DNA; 16 BP.

XX AC AAX54337;

XX DT 05-JUL-1999 (first entry)

XX DE Inducible nitric oxide synthase antisense oligonucleotide.

XX Antisense oligonucleotide; multiple target; antisense treatment;

KW impaired respiration; inflammation; lung disease;

KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

KW acute asthma; allergy; asthma; impaired respiration;

KW respiratory distress syndrome; pain; cystic fibrosis;

KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;

KW colon cancer; breast cancer; lung cancer; pancreatic cancer;

KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.

XX OS Synthetic.

XX WO9913886-A1.

XX PD 25-MAR-1999.

XX PF 17-SEP-1998; 98WO-US019419.

XX PR 17-SEP-1997; 97US-0059160P.

XX PR 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX NYce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.

XX Disclosure; Page 62; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX5272-74. These multiple target oligonucleotides (specifically AAX5180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer

SQ Sequence 16 BP; 0 A; 1 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 10.8; DB 1; Length 16;

Best Local Similarity 85.7%; Pred. No. 72;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGAGGCTGTGGCG 16

Db 3 TGGGCTGTGGTG 16

RESULT 24

AAA33781

ID AAA33781 standard; DNA; 16 BP.

XX AC AAA33781;

XX DT 28-JUL-2000 (first entry)

XX DE Low adenosine antisense oligonucleotide SEQ ID NO:1470.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX WO200009525-A2.

XX PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US017712.

XX PR 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX NYce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

XX Claim 18; Page 448; 1343pp; English.

XX The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

SQ Sequence 16 BP; 0 A; 1 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 60.0%; Score 10.8; DB 1; Length 16;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGGCG 16
 || || || || || || || ||
 Db 3 TGGGGCTGTGGTG 16
 || || || || || || || ||
 RESULT 25
 AAF19903
 ID AAF19903 standard; DNA; 16 BP.
 XX AAF19903;
 AC AAF19903;
 XX AAF19903;
 DT 14-MAR-2001 (first entry)
 DE Human inducible nitric oxide synthase polynucleotide fragment #1470.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 XX
 XX 06-APR-1999; 99US-0127958P.
 PA
 PA (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 256; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders

CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC anti-inflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 16 BP; 0 A; 1 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGGCG 16
Db 3 TGGGCTGTGGTG 16
||| ||||| |||||

RESULT 27

AB102022/c
ID AB102022 standard; DNA; 12 BP.

XX AC AB102022;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 301995 for detecting SNP TSC0019737.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 301995; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 12 TTGAGGCTGTG 1
||||| |||||

RESULT 28

AB112176/c

ID AB112176 standard; DNA; 12 BP.

XX AC AB112176;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 312149 for detecting SNP TSC0024874.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 312149; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 12 TTGAGGCTGTG 1
||||| |||||

RESULT 29

ABF36582

ID ABF36582 standard; DNA; 13 BP.

```

XX ABF36582;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 136579 for detecting SNP TSC0034131.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 136579; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 57.8%; Score 10.4; DB 1; Length 13;
XX Best Local Similarity 91.7%; Pred. No. 83;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3 TGAGGCGTGTGG 14
XX ||||| |||||
XX 2 TGAGGCGTGTGG 13
XX
XX RESULT 30
XX ABC72612
XX ID ABC72612 standard; DNA; 13 BP.
XX
XX AC ABC72612;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 72629 for detecting SNP TSC0018766.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX

```

```

PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 72629; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 57.8%; Score 10.4; DB 1; Length 13;
XX Best Local Similarity 91.7%; Pred. No. 83;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2 TTGAGGCTGTGG 13
XX ||||| |||||
XX 1 TTGAGGCTGTGG 12
XX
XX RESULT 31
XX ABC21120
XX ID ABC21120 standard; DNA; 13 BP.
XX
XX AC ABC21120;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 21137 for detecting SNP TSC0004268.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

```


XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 21137; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 1 TTGAGGCTGTG 12
|||||
|||||

RESULT 32
ABC21119/c
ID ABC21119 standard; DNA; 13 BP.
XX
AC ABC21119;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 21136 for detecting SNP TSC0004269.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 21136; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 13 TTGAGGCTGTG 2
|||||
|||||

RESULT 33
ABC72614
ID ABC72614 standard; DNA; 13 BP.
XX
AC ABC72614;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 72631 for detecting SNP TSC0018766.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 72631; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      2 TTGAGGCTGTTG 13
Db      1 TTGAGGATGTTG 12
||||| |||||

RESULT 34
ABC21118
ID ABC21118 standard; DNA; 13 BP.
XX
AC ABC21118;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 21135 for detecting SNP TSC0004268.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (SPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 21135; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTGAGGCTGTTG 13
Db      1 TTGAGGATGTTG 12
||||| |||||

RESULT 35
ABC72613/c
ID ABC72613 standard; DNA; 13 BP.
XX
AC ABC72613;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 72632 for detecting SNP TSC0018766.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PS Claim 1; SEQ ID NO 72630; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTGAGGCTGTTG 13
Db      1 TTGAGGATGTTG 12
||||| |||||

RESULT 36
ABC72615/c
ID ABC72615 standard; DNA; 13 BP.
XX
AC ABC72615;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 72632 for detecting SNP TSC0018766.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

```

XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 72632; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 83;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTTG 13
 Db 13 TTGAGGATGTTG 2
 RESULT 37
 ABC21121/C
 ID ABC21121 standard; DNA; 13 BP.
 AC ABC21121;
 XX AC
 XX DT 20-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 21138 for detecting SNP TSC0004269.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 72632; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 83;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTTG 13
 Db 13 TTGAGGATGTTG 2

PS Claim 1; SEQ ID NO 21138; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 83;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTTG 13
 Db 13 TTGAGGATGTTG 2
 RESULT 38
 ABF36583/C
 ID ABF36583 standard; DNA; 13 BP.
 XX AC
 XX AC ABF36583;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 136580 for detecting SNP TSC0034131.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 136580; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at

```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 83;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTGG 14
Db 12 TGAGGCGGTTGG 1

RESULT 39
ACD56122
ID ACD56122 standard; RNA; 13 BP.
XX
AC ACD56122;
DT
DT 23-SEP-2003 (first entry)
XX
DE HBV enzymatic nucleic acid substrate sequence #45.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW anberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PACV/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 213; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
CC inozymes, zinzymes, anberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

```

```

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC enzymatic nucleic acid sequences disclosed in the present invention
XX
XX Sequence 13 BP; 2 A; 2 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTGGC 15
Db 2 GAGGCGUAGGC 13

RESULT 40
AAV92057
ID AAV92057 standard; RNA; 14 BP.
XX
AC AAV92057;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human C-raf target sequence nucleotide position 2390.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 23-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kiseich K, Bellon L;
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
XX
PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer.
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
PS Claim 179; Page 156; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method

```

CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, resenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene

XX SQ Sequence 14 BP; 2 A; 4 C; 4 G; 0 T; 4 U; 0 Other;
 Query Match 57.8%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 85;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTCTTGGCGAC 18
 ||:|||||
 Db 3 GCUGUGGCUAC 14

RESULT 41
 AAF49933/c
 ID AAF49933 standard; DNA; 15 BP.

XX AC AAF49933;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #893.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wraight CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 8; Page 66; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 57.8%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 86;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGG 14
 |||||
 Db 12 TGAGGATGTGG 1

RESULT 42
 AAF49928/c
 ID AAF49928 standard; DNA; 15 BP.

XX AC AAF49928;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #888.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wraight CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 8; Page 66; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an

```
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
CC P45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
  Query Match 57.8%; Score 10.4; DB 1; Length 15;
  Best Local Similarity 91.7%; Pred. No. 86;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGCG 16
  ||| |||||
Db 15 AGGATGTTGGCG 4

RESULT 43
AAD26142/c
ID AAD26142 standard; DNA; 15 BP.
XX
AC AAD26142;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human endothelin 2 (EDN2) gene polymorphism detecting ASO primer #15.
XX
KW Human; endothelin 2; EDN2; polymorphic site; PS; therapy; hypertension;
KW drug screening; cardiovascular disorder; renal insufficiency; ASO;
KW allele specific oligonucleotide; cerebroprotective; polymorphism;
KW hypotensive; cerebrovascular condition; primer; ss.
XX
OS Homo sapiens.
XX
PN W0200190118-A2.
XX
PD 29-NOV-2001.
XX
PF 21-MAY-2001; 2001WO-US016433.
XX
PR 19-MAY-2000; 2000US-0205761P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Koshy B, Tanguay DA;
XX
DR WPI; 2002-083075/11.
XX
PT New human endothelin 2 (EDN2) polymorphic variants and encoding genes,
PT useful in expressing EDN2 protein for screening candidate drugs to treat
PT diseases related to EDN2 activity.
XX
PS Claim 16; Page 14; 91pp; English.
XX
CC The invention relates to genetic variants of human endothelin 2 (EDN2)
CC gene. EDN2 gene contains 17 polymorphic sites PSI-PS17. The polymorphic
CC variants are useful in studying the expression and function of EDN2, in
CC expressing EDN2 protein for use in screening for candidate drugs to treat
CC diseases related to EDN2 activity, in studying the effect of the
CC variation on the biological activity of EDN2, and the binding affinity of
CC candidate drugs targeting EDN2 for the treatment of hypertension,
CC cardiovascular disorders, renal insufficiency and cerebrovascular
CC conditions. The haplotyping methods are useful in validating EDN2 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with EDN2 activity, or in the design of clinical trials
CC of candidate drugs for treating a specific condition or disease
CC associated with EDN2 activity. Allele specific oligonucleotides (ASO) are
CC used as probes and primers, and for detecting polymorphism in EDN2 gene.
CC The present sequence is an ASO primer used to detect polymorphism in

CC human EDN2 gene
XX
SQ Sequence 15 BP; 3 A; 7 C; 1 G; 3 T; 0 U; 1 Other;
  Query Match 57.8%; Score 10.4; DB 1; Length 15;
  Best Local Similarity 78.6%; Pred. No. 86;
  Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTTGGC 15
  |:||||| |||||
Db 15 TYGAGGGAGTTGGC 2

RESULT 44
ACD82315
ID ACD82315 standard; DNA; 15 BP.
XX
AC ACD82315;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #16.
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
PN US2003044791-A1.
XX
PD 06-MAR-2003.
XX
PF 13-JUN-2001; 2001US-00880313.
XX
PR 13-JUN-2001; 2001US-00880313.
XX
PA (FLEM/) FLEMINGTON E K.
XX
PI Flemington EK;
XX
DR WPI; 2003-521745/49.
XX
PT New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.
XX
PS Claim 12; Fig 1; 100pp; English.
XX
CC The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
SQ Sequence 15 BP; 2 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
  Query Match 56.7%; Score 10.2; DB 1; Length 15;
  Best Local Similarity 80.0%; Pred. No. 94;
  Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTTGGC 16
  | ||||| |||||
Db 1 TCAGAGGCTGAGGCG 15
```

```
RESULT 45
ACD82329
ID ACD82329 standard; DNA; 15 BP.
XX
AC ACD82329;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #30.
XX
DE Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
XX KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
FN US2003044791-A1.
XX
PD 06-MAR-2003.
XX
PF 13-JUN-2001; 2001US-00880313.
XX
PR 13-JUN-2001; 2001US-00880313.
XX
PA (FLEM/) FLEMINGTON E K.
XX
PI Flemington EX;
XX
DR WPI; 2003-521745/49.
XX
FT New adaptor molecules, useful for cloning nucleic acid molecules that
FT does not require the design and synthesis of oligonucleotides or PCR
FT primers.
XX
PS Claim 12; Fig 1; 100pp; English.
XX
CC The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
SQ Sequence 15 BP; 2 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 56.7%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCG 16
| | | | | | | |
Db 1 TCGAGGCTGCAGCG 15

RESULT 46
AAA72649/C
ID AAA72649 standard; DNA; 11 BP.
XX
AC AAA72649;
XX
DT 01-DEC-2000 (first entry)
XX
DE K-ras SW480 UDG-digest fragment SEQ ID #6.
XX
KW Uracil DNA glycosylase; UDG; infectious disease detection; cancer;
KW sickle cell anaemia; cystic fibrosis; thalassaemia; muscular dystrophy;
KW Tay-Sachs disease; K-ras; ss.

XX
OS Synthetic.
XX
FN US6090553-A.
XX
PD 18-JUL-2000.
XX
PF 29-OCT-1997; 97US-00959853.
XX
PR 29-OCT-1997; 97US-00959853.
XX
PA (BECI ) BECKMAN COULTER INC.
XX
PI Matson RS;
XX
DR WPI; 2000-531416/48.
XX
PT Detecting specific nucleic acid sequence in sample containing nucleic
PT acids involves amplifying nucleic acid, cleaving amplified products with
PT uracil-DNA glycosylase to obtain DNA segments and detecting segments.
XX
PS Example 2; Col 17; 21pp; English.
XX
CC A new method for detecting specific nucleic acid sequences in a sample
CC involves amplifying the nucleic acid sample by PCR and then cleaving the
CC amplified products with uracil DNA glycosylase (UDG), the resulting DNA
CC fragments are detected using reverse blot hybridisation techniques. The
CC method can be used to distinguish between two different sequences, for
CC example for the detection of a DNA fragment carrying a mutation. The
CC method is useful for detecting the presence or absence of a nucleic acid
CC sequence containing a polymorphic restriction site associated with a
CC diseases such as cystic fibrosis disease, and may be used for detecting
CC infectious diseases. Genetic disorders such as sickle cell anaemia,
CC cystic fibrosis, alpha or beta thalassaemia, muscular dystrophy, and Tay-
CC Sachs disease may also be detected using the method. Oncogenes such as
CC RAS may also be detected using the method, for the diagnosis of certain
CC cancers. The present sequence represents a fragment of the K-ras gene
CC created by UDG cleavage. This sequence is used in an example of the
CC invention and contains the position of a mutation site in K-ras SW480.
CC This fragment and the corresponding wild type fragment (AAA72648) can be
CC used to produce probes specifically to identify the mutation, which can
CC then be used in the method of the invention
XX
SQ Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
| | | | | | | |
Db 11 GCTGTTGGCG 2

RESULT 47
ABV66396/C
ID ABV66396 standard; cDNA; 11 BP.
XX
AC ABV66396;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4182.
XX
KW Human; skin; dermatological; vulvular; antipsoriatic; antineoplastic;
KW immunosuppressive; antiinflammatory; cytotoxic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
FN WO200253774-A2.
XX
PD 11-JUL-2002.
```

```
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX CC In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 141; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AGGCTGTTGG 14
Db 11 AGGCTGTTGG 2
RESULT 48
AAV06832
ID AAV06832 standard; DNA; 13 BP.
XX AC AAV06832;
XX DT 01-JUL-1998 (first entry)
XX DE Amino derivatised K-ras mutant oligonucleotide.
XX KW H-ras; wild-type; immobilising; diagnosis; ethylene acrylic acid;
XX KW ethylene methacrylic acid; polypropylene; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /note= "H2N-Guanine"
XX PN WO9746597-A1.
XX PD 11-DEC-1997.
XX PF 22-MAY-1997; 97WO-US008880.
XX PR 05-JUN-1996; 96US-00658664.
XX PA (BECI ) BECKMAN INSTR INC.
XX PI Milton RC;
XX DR WPI; 1998-051910/05.
XX CC Polymeric reagents for immobilising biopolymers - are stable under
XX PT synthesis conditions.
XX XX Example 3; Page 26; 66pp; English.
XX CC This sequence is shown in the specification. The invention relates to a
XX CC new reagent for immobilising a biopolymer. It comprises a solid support
XX CC fabricated from a polymeric material having at least one surface
XX CC comprising pendant acyl fluoride functionalities. The reagent is stable
XX CC under conditions for synthesising and immobilising biopolymers and is
XX CC stable under conditions used to analyse the biopolymers. The reagents can
XX CC be formed into devices which are physically rugged and inexpensive which
XX CC can be used in analytical and diagnostic procedures
XX SQ Sequence 13 BP; 1 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 18+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTGGCG 16
Db 3 GCTGTTGGCG 12
RESULT 49
ABA99743
ID ABA99743 standard; DNA; 13 BP.
XX AC ABA99743;
XX DT 07-JUN-2002 (first entry)
XX DE Human K-ras codon 12 capture probe SEQ ID NO 9.
XX KW K-ras; detection; hybridisation; cancer cell; mutation; diagnosis; probe;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200210447-A2.
XX XX WO200210447-A2.
XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-EP008895.
XX PR 01-AUG-2000; 2000DE-01037506.
XX PA (GIES/) GIESING M.
XX PI Grill H, Schuetz A, Prix L;
XX DR WPI; 2002-195968/25.
XX CC Detecting nucleic acid by hybridization, useful e.g. for diagnosis of
XX PT cancer associated with K-ras gene mutations, in presence of competitor
XX PT oligonucleotide to increase discrimination.
XX PS Claim 12; Page 37; 39pp; German.
XX CC This invention describes a novel method for detecting at least one
XX CC nucleic acid having a specific sequence in a sample. The method comprises
XX CC hybridisation to at least one immobilised probe in the presence of at
XX CC least one oligonucleotide having a sequence similar to the specific
XX CC sequence being investigated. The method of the invention is used for
XX CC genetic analysis, especially for identifying and characterising cancer
XX CC cells, particularly detecting mutations in codons 12, 13 and/or 61 of the
XX CC K-ras gene, e.g. for cancer diagnosis or for monitoring/selection of
XX CC treatment. It can also be used to detect viruses and bacteria,
XX CC particularly for differentiating between genotypes. The use of the second
```


CC oligonucleotide as a competitor improves discrimination between a perfect
CC match and a mismatch in very similar sequences, particularly to
CC discrimination level better than 3:1. The sensitivity, after mutation-
CC enriching amplification and competitive hybridization, is over 1:10,
CC preferably 1:100. This sequence represents a probe used to illustrate the
CC method of the invention

XX SQ Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 55.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTGTTGGCG 16
Db 2 GCTGTTGGCG 11

RESULT 50
ABL41213
ID ABL41213 standard; DNA; 13 BP.

XX AC ABL41213;

XX DT 07-MAY-2002 (first entry)

XX DE Ki-ras codon 12 mutation detection probe 4.

XX KW Bio-chips; immobilisation; detection; hapten; pesticide; hormone;
XX KW antibiotic; pharmaceutical; dye; Ki-ras; mutation; probe; ss.

XX OS Synthetic.

XX PN DE10038080-A1.

XX PD 21-FEB-2002.

XX PF 04-AUG-2000; 2000DE-01038080.

XX PR 04-AUG-2000; 2000DE-01038080.

XX PA (GIES/) GIESING M.

XX PA (MICR-) SL MICROTTEST WISS GERAETE GMBH.

XX PI Leclerc N, Grill H, Schuetz A, Prix L;

XX DR WPI; 2002-218030/28.

XX PT Registering the presence of immobilized substances on a bio-chip carrier,
PT comprises using a fluorescence scanner, where a pulsed laser excites
PT fluorescent markings to be detected between the pulses with local
PT resolution.

XX PS Example 3; Col 14; 16pp; German.

XX CC The invention relates a method to show the presence of immobilised
CC substances on a carrier, comprising a series of light pulses directed at
CC the defined surface under study as an excitation light beam, fluorescent
CC light is detected between successive light pulses, shown by the carrier
CC substances in the measurement field and the light beams and the carrier
CC are moved in relation to each other until a sufficient surface area has
CC been scanned. The method and system is used for the evaluation of bio-
CC chips, where immobilised substances are held on a flat carrier as fixed
CC biological probes and/or samples bonded in the probes. The probes are
CC nucleic acids and especially oligonucleotides e.g. single- and/or twin-
CC strand DNA, RNA, PNA, LNA in pure or combination forms, antibodies,
CC enzymes, haptens, pesticides, hormones, antibiotics, pharmaceuticals,
CC dyes, synthetic receptors or receptor ligands and the like. The
CC system gives a high local resolution and the non-specific background
CC illumination is eliminated, especially in the evaluation of bio-chips.
CC The present sequence is that of an oligonucleotide probe for detecting
CC mutations in codon 12 of the Ki-ras gene, useful in examples of the
CC invention

XX SQ Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTGTTGGCG 16
Db 2 GCTGTTGGCG 11

RESULT 51
AAQ62037/c
ID AAQ62037 standard; DNA; 15 BP.

XX AC AAQ62037;

XX DT 25-MAR-2003 (revised)

XX DT 17-NOV-1994 (first entry)

XX DE Mutant Ki-ras codon 12 antisense phosphorothioate oligo ref. 7453.

XX KW Antisense; phosphorothioate; H-ras; translation initiation codon;
XX KW codon-12 point mutation; activated; inhibition; ras-luciferase; activity;
XX KW detection; modulation; inhibition; expression; oncogene; proliferation;
XX KW Ki-ras; cancer cell; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc_difference 1. .15

XX FT /*tag= a

XX FT /note= "Phosphorothioate linkages"

XX PN W09408003-A1.

XX PD 14-APR-1994.

XX PF 01-OCT-1993; 93WO-US009346.

XX PR 05-OCT-1992; 92US-00958134.

XX PR 21-JAN-1993; 93US-00007996.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Ecker DJ;

XX DR WPI; 1994-135570/16.

XX CC New oligo:nucleotides hybridisable with H-ras or Ki-ras gene nucleic acid
XX - in normal or mutated form, for detecting or modulating gene expression,
XX specifically inhibiting proliferation of cancer cells.

XX PS Claim 105 and 115; Page 37; 104pp; English.

XX CC The sequences given in AAQ62025-38 are antisense phosphorothioate
CC oligonucleotides which are targeted to various regions of Ki-ras
CC oncogene. These oligonucleotides gave significant and reproducible
CC inhibition of the level of Ki-ras mRNA. These oligonucleotides may be
CC used for detecting and modulating, esp. inhibiting, expression of the Ki-
CC ras gene, esp. for inhibiting proliferation of cancer cells, and other
CC conditions associated with Ki-ras oncogene activation. Activated (mutant)
CC Ki-ras can be detected from its differential affinity for particular
CC oligos. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTGTTGGCG 16

XX 06-JUL-1998; 98WO-US013966.
XX 08-JUL-1997; 97US-00889296.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Cowsett LM, Manoharan M;
XX WPI; 1999-120932/10.
XX New oligonucleotide targetting human N-ras nucleic acid - is capable of
XX inhibiting human N-ras expression, useful for preventing or treating
XX conditions arising from the activation of a human N-ras oncogene.
XX Disclosure; Page 35; 97pp; English.
XX The invention relates to oligonucleotides, which target a nucleic acid
XX encoding human N-ras, and are capable of inhibiting human N-ras
XX expression. The antisense oligonucleotides form a pharmaceutical
XX composition, which is useful for modulating the expression of human N-
XX ras, inhibiting the proliferation of cancer cells, and preventing or
XX treating conditions arising from the activation of a human N-ras
XX oncogene. The oligonucleotides are also useful in diagnostics,
XX therapeutics, and as research reagents and kits. The oligonucleotides
XX enable the specific modulation of activated human N-ras expression, which
XX is associated with tumour formation. Sequences AAX21620-633 represent
XX antisense oligonucleotides complementary to human Ki-ras
XX Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 GCTGTTGGCG 16
XX |||||
XX 12 GCTGTTGGCG 3
XX
XX RESULT 55
XX AAX56996/C
XX ID AAX56996 standard; DNA; 15 BP.
XX AC AAX56996;
XX 16-JUL-1999 (first entry)
XX DE Ras gene modulating liposomal entrapped oligonucleotide primer 40.
XX KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
XX cell growth inhibitor; treatment; cancer; ras protein; ss.
XX OS Synthetic.
XX WO9922772-A1.
XX 14-MAY-1999.
XX 28-OCT-1998; 98WO-US022821.
XX 31-OCT-1997; 97US-00961469.
XX (ISIS-) ISIS PHARM INC.
XX Hardee GE, Geary RS, Levin A, Templin MV, Howard R, Mehta RC;
XX WPI; 1999-313181/26.
XX Liposome-encapsulated oligonucleotides useful for treating or preventing
XX cancers associated with ras gene activation.
XX Example 1; Page 114; 120pp; English.

XX This invention describes novel compositions comprising oligonucleotides
XX (AAX56957-X57017), entrapped within liposomes, that hybridize
XX specifically to a target DNA or mRNA which encodes a mutant or wild-type
XX ras protein. The products of the invention have anticancer activity and
XX specifically bring about the antisense inhibition of ras genes or mRNA.
XX The products of the invention are used to modulate expression of a ras
XX gene in cells, tissue, organs or organisms, particularly to inhibit cell
XX growth and especially to treat or prevent cancers associated with
XX activation of a ras gene. Encapsulating the oligonucleotide reduces the
XX rate at which it is cleared from the blood when compared with non-
XX encapsulated material, and the oligonucleotides become distributed to
XX practically all parts of the body
XX Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 GCTGTTGGCG 16
XX |||||
XX 12 GCTGTTGGCG 3
XX
XX RESULT 56
XX AAA95870/C
XX ID AAA95870 standard; DNA; 15 BP.
XX AC AAA95870;
XX 18-JAN-2001 (first entry)
XX DE Human Ki-ras antisense oligonucleotide ISIS #7453.
XX KW Human; antisense oligonucleotide; ras; H-ras; Ki-ras; N-ras; cytostatic;
XX phosphorothioate; cancer; ss.
XX OS Homo sapiens.
XX US6117848-A.
XX 12-SEP-2000.
XX 03-AUG-1998; 98US-00128494.
XX 05-OCT-1992; 92US-00958134.
XX 21-JAN-1993; 93US-00007996.
XX 01-OCT-1993; 93WO-US009346.
XX 03-APR-1995; 95US-00411734.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cowsett LM, Monia BP;
XX WPI; 2000-610851/58.
XX Oligonucleotides targeted to human H-ras or human Ki-ras coding
XX sequences, useful for treating and preventing cancer.
XX Claim 9; Col 20; 41pp; English.
XX The present sequence was used in methods for the modulation of ras
XX expression. Antisense oligonucleotides were designed to specifically
XX target mRNA encoding human H-ras, Ki-ras and N-ras. The oligonucleotides
XX can be used to inhibit the proliferation of cancer cells and to prevent
XX or treat a condition arising from the activation of a ras oncogene. They
XX may also be used to modulate the expression of human H-ras or human Ki-
XX ras. The antisense oligonucleotides may contain modified backbones,
XX substituted sugar moieties and modified bases. The sequences preferably
XX have a phosphorothioate backbone. They are preferably
XX oligodeoxynucleotides or chimeric oligonucleotides containing 2'-O-methyl
XX ends and a central deoxy gap

```
XX SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 57
AAS18673/C
ID AAS18673 standard; DNA; 15 BP.
XX AC AAS18673;
XX DT 12-MAR-2002 (first entry)
XX DE ASO probe #6 to detect human SCYA3 gene polymorphisms.
XX KW Human; single nucleotide polymorphism; SNP; SCYA3; chromosome 17q11-q21;
XX KW small inducible cytokine A3; haplotyping; genotyping; ASO; probe; ss;
XX KW inflammatory disorder; allele-specific oligonucleotide.
XX OS Homo sapiens.
XX PN WO200179217-A2.
XX PD 25-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US010595.
XX PR 14-APR-2000; 2000US-0197830P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2002-055247/07.
XX New polymorphic variants comprising small inducible cytokine A3 (SCYA3)
PT isogene, useful in expressing SCYA3 protein for use in screening for
PT candidate drugs to treat diseases related to SCYA3 activity, e.g.
PT inflammatory disorders.
XX Claim 15; Page 14; 67pp; English.
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on
CC chromosome 17q11-q21, and methods for haplotyping and/or genotyping the
CC SCYA3 gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA3 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for (developing)
CC treatment of diseases associated with SCYA3 activity, such as
CC inflammatory disorders e.g. atopic dermatitis, rheumatoid arthritis,
CC multiple sclerosis, pulmonary fibrosis and sarcoidosis. AAS18668-AAS18682
CC represent ASO probes for detecting human SCYA3 gene polymorphisms
XX SQ Sequence 15 BP; 3 A; 8 C; 2 G; 1 T; 0 U; 1 Other;
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGCG 16
Db 15 AGGCGGTGGCG 4

RESULT 58
ABA96471
ID ABA96471 standard; DNA; 15 BP.
XX AC ABA96471;
XX DT 03-APR-2002 (first entry)
XX DE Human IL-4 probe SEQ ID NO 15.
XX KW Human; IL-2; IL-4; probe; ss.
XX OS Homo sapiens.
XX PN JP2001286285-A.
XX PD 16-OCT-2001.
XX PF 28-APR-2000; 2000JP-00130793.
XX PR 04-FEB-2000; 2000JP-00028117.
XX PA (BUNS-) BUNSHI BIOHOTOINICS KENKYUSHO KK.
XX WPI; 2002-134187/18.
XX Selective separation of live cells expressing a specific gene.
XX Example; Page 9; 65pp; Japanese.
XX The invention relates to selectively separating live cells expressing a
CC specific gene and involves introducing a labelling agent which can label
CC a specific mRNA in the cells of a live cell group expressing the mRNA.
CC The method is used for selectively separating live cells expressing a
CC specific gene. The present sequence is that of a human IL-4 probe
XX SQ Sequence 15 BP; 2 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 4 TGAGGCTGTT 13

RESULT 59
ACA92593/C
ID ACA92593 standard; DNA; 15 BP.
XX AC ACA92593;
XX DT 11-AUG-2003 (first entry)
XX DE Human Ki-ras antisense oligonucleotide ISIS 7453.
XX KW Human; ras; cancer; cancer cell proliferation; ras oncogene; oncogene;
XX KW colorectal cancer; melanoma; liposarcoma; ss; mesothelioma; sarcoma;
XX KW colon cancer; pancreatic cancer; antisense.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2003013670-A1.
XX PD 16-JAN-2003.
XX PF 30-MAY-2001; 2001US-00870002.
XX PR 05-OCT-1992; 92US-00958134.
XX PR 21-JAN-1993; 93US-00007996.
XX PR 01-OCT-1993; 93WO-US009346.
XX PR 03-APR-1995; 95US-00411734.
```

```
PR 08-JUL-1997; 97US-00889296.
PR 03-AUG-1998; 98US-00128494.
PR 22-MAY-2000; 2000US-00575554.
XX
PA (MONI/) MONIA B P.
PA (COMS/) COMSERT L M.
PA (MANO/) MANOHARAN M.
PA (DORR/) DORR F A.
PA (HOLM/) HOLMLUND J.
XX
PI Monia BP, Cowseert LM, Manoharan M, Dorr FA, Holmlund J;
XX
DR WPI; 2003-438917/41.
XX
PT Composition comprising an antisense oligonucleotide targeted to nucleic
PT acids encoding human ras, and capable of inhibiting ras expression,
PT useful for treating or preventing colorectal cancer, melanoma, or
PT sarcoma.
XX
PS Disclosure; Page 13; 46pp; English.
XX
CC The invention relates to a composition comprising an oligonucleotide
CC which is targeted to a nucleic acid encoding human ras, which is capable
CC of inhibiting ras expression, and at least one chemotherapeutic agent.
CC The composition is useful for modulating the expression of human ras in
CC tissues or cells containing a ras gene. The composition is also useful for
CC inhibiting the proliferation of cancer cells, where the cancer cells are
CC blood cells, preferably peripheral blood mononuclear cells. The
CC composition is useful for treating or preventing a condition arising from
CC the activation of ras oncogene which involves contacting an animal
CC suspected of having a condition (e.g. hyperproliferative condition such
CC as cancer preferably colorectal cancer, melanoma, liposarcoma,
CC mesothelioma, sarcoma, colon cancer or pancreatic cancer) arising from
CC the activation of ras oncogene such as abnormal expression of the ras
CC oncogene. The present sequence represents a human ras antisense
CC oligonucleotide
XX
SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3
RESULT 60
ABCL14108
XX ABC14108 standard; DNA; 13 BP.
XX
AC ABC14108;
XX
XX 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 14115 for detecting SNP TSC0003223.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14115; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTGG 14
Db 1 TTGAGGCGGATGG 13
RESULT 61
ABFL14528
XX ID ABFL14528 standard; DNA; 13 BP.
XX
XX AC ABFL14528;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 114525 for detecting SNP TSC0028668.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 114525; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
Db 1 TTGAGGATGTTG 13
||||| |||

RESULT 62

ABH07515/c
ID ABH07515 standard; DNA; 13 BP.

XX AC ABH07515;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 207492 for detecting SNP TSC0005639.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 207492; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
Db 13 TTGAGGCTGTGG 1
||||| |||

RESULT 63

ABF14529/c
ID ABF14529 standard; DNA; 13 BP.

XX AC ABF14529;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 114526 for detecting SNP TSC0028668.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 114526; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
Db 13 TTGAGGATGTTG 1
||||| |||

RESULT 64

ABH07516
ID ABH07516 standard; DNA; 13 BP.

XX

```
AC ABH07516;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 207493 for detecting SNP TSC0005639.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 207493; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 1.le+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 TTGAGGCTGTGG 14
XX 1 TTAGGAGTGTGG 13
XX
XX RESULT 65
XX ABC43490
XX ID ABC43490 standard; DNA; 13 BP.
XX
XX AC ABC43490;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 43507 for detecting SNP TSC0012866.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
```

```
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 43507; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 1.le+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 TTGAGGCTGTGG 14
XX 1 TTGAGGCGGTGG 13
XX
XX RESULT 66
XX ABF14531/C
XX ID ABF14531 standard; DNA; 13 BP.
XX
XX AC ABF14531;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 114528 for detecting SNP TSC0028668.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX
 PS Claim 1; SEQ ID NO 114528; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14

Db 13 TTGAGGCTGTGG 1

RESULT 67

ABF14530
 ID ABF14530 standard; DNA; 13 BP.

XX
 AC ABF14530;

XX
 DT 21-FEB-2002 (first entry)

XX
 DE Oligonucleotide SEQ ID NO 114527 for detecting SNP TSC0028668.

XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX
 OS Homo sapiens.

XX
 PN WO200177384-A2.

XX
 PD 18-OCT-2001.

XX
 PF 06-APR-2001; 2001WO-IB000713.

XX
 PR 07-APR-2000; 2000DE-01019173.

XX
 PA (EPIG-) EPIGENOMICS AG.

XX
 PI Olek A, Piepenbrock C, Berlin K;

XX
 WPI; 2001-657177/75.

XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX
 PS Claim 1; SEQ ID NO 114527; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 13 BP; 1 A; 0 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14

Db 1 TTGAGGCTGTGG 13

RESULT 68

ABH07517/C

ID ABH07517 standard; DNA; 13 BP.

XX
 AC ABH07517;

XX
 DT 22-FEB-2002 (first entry)

XX
 DE Oligonucleotide SEQ ID NO 207494 for detecting SNP TSC0005639.

XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX
 OS Homo sapiens.

XX
 PN WO200177384-A2.

XX
 PD 18-OCT-2001.

XX
 PF 06-APR-2001; 2001WO-IB000713.

XX
 PR 07-APR-2000; 2000DE-01019173.

XX
 PA (EPIG-) EPIGENOMICS AG.

XX
 PI Olek A, Piepenbrock C, Berlin K;

XX
 WPI; 2001-657177/75.

XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX
 PS Claim 1; SEQ ID NO 207494; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14


```
XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGGCG 16
    |||||
Db 1 GAGGATGTTGGTG 13

RESULT 74
ID AAV92813/c
AAV92813 standard; RNA; 14 BP.
XX AC AAV92813;
XX DT 18-FEB-1999 (first entry)
XX DE Human A-raf target sequence nucleotide position 1806.
XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX OS Homo sapiens.
XX PN W09850530-A2.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US009249.
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman C, Beaudry A, Sweedler D;
XX PD WPI; 1999-009494/01.
XX PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX PS Claim 179; Page 164; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs

CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX SQ Sequence 14 BP; 4 A; 6 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTTG 13
    |||||
Db 13 CTTGGGGCAGTTG 1

RESULT 75
ID AAX66654 standard; RNA; 15 BP.
XX AC AAX66654;
XX DT 20-JUL-1999 (first entry)
XX DE Human CD40 hammerhead ribozyme target SEQ ID NO:3286.
XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX OS Homo sapiens.
XX PN W09618736-A2.
XX PD 20-JUN-1996.
XX PF 22-NOV-1995; 95WO-US015516.
XX PR 13-DEC-1994; 94US-00354920.
XX PR 23-DEC-1994; 94US-00363253.
XX PR 23-DEC-1994; 94US-00363254.
XX PR 17-FEB-1995; 95US-00390850.
XX PR 20-APR-1995; 95US-00426124.
XX PR 02-MAY-1995; 95US-00432874.
XX PR 04-MAY-1995; 95US-00434509.
XX PR 07-JUL-1995; 95US-0000951P.
XX PR 07-JUL-1995; 95US-0000974P.
XX PR 07-AUG-1995; 95US-00512861.
XX PR 05-OCT-1995; 95US-00541365.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
XX PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
XX PI Karpeisky A, Thompson JD, Modak A, Burgin A;
XX PD WPI; 1996-300653/30.
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX PS Claim 10; Page 205; 307pp; English.
XX CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
```

CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX
SQ Sequence 15 BP; 4 A; 3 C; 6 G; 0 T; 2 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 AGGCTGTTGGCA 17
Db 1 AGGAGUUGGCCA 13
RESULT 76
AAT49719
ID AAT49719 standard; RNA; 15 BP.
AC AAT49719;
XX
DT 02-MAR-1997 (first entry)
XX
DE Human CERP HH ribozyme target sequence #1114.
XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; athrectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN W09620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US016000.
XX
PR 23-DEC-1994; 94US-00363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN) WARNER LAMBERT CO.
XX
PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX
DR WPI; 1996-321852/32.
XX
PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
PS Claim 4; Page 30; 72pp; English.
XX
CC AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CERP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence
CC is immediately upstream. The ribozymes are able to cleave mRNA from the

CC gene encoding CERP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CERP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypoalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, athrectomy and
CC angioplastic restenosis. By inhibiting CERP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CERP mRNA. As the HH
CC ribozymes target specific regions of the CERP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 3 A; 2 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTTGGCG 16
Db 3 GAGGUGUGCGCG 15
RESULT 77
AAX31027
ID AAX31027 standard; DNA; 15 BP.
XX
AC AAX31027;
XX
DT 21-MAY-1999 (first entry)
XX
DE Tag sequence of a transcript increased in colorectal cancer.
XX
KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW diagnosis; prognosis; treatment; ss.
XX
OS Homo sapiens.
XX
PN W09853319-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010277.
XX
PR 21-MAY-1997; 97US-0047352P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1999-070161/06.
XX
PT Use of isolated gene transcripts - useful for developing products for the
PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX
PS Claim 2; Page 27; 120pp; English.
XX
CC AAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic cancer, or
CC in both. The tag sequences can be used to identify genes by matching the
CC tag to a gen data base member, or by using the tag sequences as probes to
CC isolate unidentified genes from cDNA libraries. The tag sequences can
CC also be used in a method for diagnosing colon or pancreatic cancer in a
CC sample suspected of being neoplastic. The method comprises comparing the
CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.

CC The transcript is identified by a tag selected from AAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer

XX Sequence 15 BP; 2 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGCGA 17
Db 2 ATGCTGTGGTGA 14

RESULT 78

AAX31715

ID AAX31715 standard; DNA; 15 BP.

AC AAX31715;

XX 21-MAY-1999 (first entry)

XX Transcript tag sequence increased in pancreatic and colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;

KW diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010277.

XX 21-MAY-1997; 97US-0047352P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Vogelstein B, Kinzler KW;

XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the
PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.

XX Disclosure; Page 72; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic cancer, or
CC in both. The tag sequences can be used to identify genes by matching the
CC tag to a gen data base member, or by using the tag sequences as probes to
CC isolate unidentified genes from cDNA libraries. The tag sequences can
CC also be used in a method for diagnosing colon or pancreatic cancer in a
CC sample suspected of being neoplastic. The method comprises comparing the
CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.
CC The transcript is identified by a tag selected from AAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer

XX Sequence 15 BP; 2 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGCGA 17
Db 2 ATGCTGTGGTGA 14

RESULT 79

AAH18881

ID AAH18881 standard; DNA; 15 BP.

XX AAH18881;

XX 21-JUN-2001 (first entry)

XX UCP3 polymorphism detection allele specific probe #32.

XX UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.

XX Homo sapiens.

XX WO200118232-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US024784.

XX 08-SEP-1999; 99US-0152789P.

XX (GENA-) GENAISSANCE PHARM INC.

XX (STEP/) STEPHENS J C.

XX Chew A, Choi JY, Denton RR, Nandabalan K;

XX WPI; 2001-218562/22.

XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
PT useful for the design of drugs for treating obesity.

XX Claim 15; Page 22; 94pp; English.

XX The present invention relates to the human uncoupling protein 3
CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
CC polymorphisms are associated with obesity, especially diabetes mellitus
CC associated obesity. They polymorphisms may be identified and analysed to
CC determine whether an individual is susceptible to obesity and may be used
CC as the basis for targeted design of drugs to treat obesity. The present
CC sequence was used in the identification and amplification of UCP3
CC polymorphisms

XX Sequence 15 BP; 1 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGGC 15
Db 2 TGAGGCTTGGC 14

RESULT 80

ABK31980

ID ABK31980 standard; DNA; 15 BP.

XX ABK31980;

XX 23-APR-2002 (first entry)

XX Human colon cancer SAGE tag #81.

XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.

XX Homo sapiens.

XX

```

PN US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 17; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 15;
XX Best Local Similarity 84.6%; Pred. No. 1.1e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5 AGGCTGTGGCGA 17
XX | ||||| ||
XX 2 ATGCTGTGTGGA 14
XX
XX RESULT 82
XX ABL94755
XX ID ABL94755 standard; DNA; 15 BP.
XX
XX AC ABL94755;
XX
XX 12-JUN-2002 (first entry)
XX
XX Human VR1 antisense oligonucleotide #95.
XX
XX Analgesic; antisense; VR1; antiinflammatory; uropathic; pain; cancer;
XX vanilloid receptor; antipruritic; cytostatic; antiasthmatic; pruritis;
XX gene therapy; tactile allodynia; urinary incontinence; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200218407-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP010081.
XX
XX 02-SEP-2000; 2000DE-01043674.
XX
XX 04-SEP-2000; 2000DE-01043702.
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX Kurreck J, Erdmann VA;
XX
XX WPI; 2002-281058/32.
XX
XX New antisense oligonucleotides and ribozymes, useful for treating e.g.
XX pain and for diagnosis, are directed against mRNA for vanilloid-family
XX receptors.
XX
XX Claim 1; Fig 16; 76pp; German.
XX
XX The present invention provides antisense sequences directed against the
XX VR1 mRNA. These can be used in the treatment of pain, especially chronic,
XX heat-induced or inflammatory pain, tactile allodynia, urinary and
XX incontinence, neurogenic bladder symptoms, pruritis, tumours and
XX inflammation (particularly where associated with the VR1 vanilloid
XX receptor such as asthma). They are also useful for identifying analgesic
XX agents. The present sequence is a VR1 antisense sequence identified in
XX the invention
XX
XX Sequence 15 BP; 0 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 15;
XX Best Local Similarity 84.6%; Pred. No. 1.1e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 TGAGGCTGTGGC 15
XX || ||||| |||||

```

```

PN US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 17; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 15;
XX Best Local Similarity 84.6%; Pred. No. 1.1e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5 AGGCTGTGGCGA 17
XX | ||||| ||
XX 2 ATGCTGTGTGGA 14
XX
XX RESULT 81
XX ABK32669
XX ID ABK32669 standard; DNA; 15 BP.
XX
XX AC ABK32669;
XX
XX 23-APR-2002 (first entry)
XX
XX Human colorectal and pancreatic cancer SAGE tag #36.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
XX Homo sapiens.
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 85; 161pp; English.
XX

```



```

PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Claim 24; Page 289; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGC 15
Db 11 ATGCTGTTGGC 1
| | | | | | | |
Human skin EST 8323.
Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
Homo sapiens.
WO200253774-A2.
11-JUL-2002.
20-DEC-2001; 2001WO-EP015179.
03-JAN-2001; 2001DE-01000127.
(HENK ) HENKEL KGAA.
Petersohn D, Conradt M, Hofmann K;
WPI; 2002-590638/63.
In vitro identification of skin-expressed genes, useful for determining
homeostasis and identifying cosmetic or pharmaceutical agents against
e.g. skin cancer.
Claim 24; Page 266; 1345pp; German.
The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGC 15
Db 11 ATGCTGTTGGC 1
| | | | | | | |
Human skin EST 902.
Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
Homo sapiens.
WO200253774-A2.
11-JUL-2002.
20-DEC-2001; 2001WO-EP015179.
03-JAN-2001; 2001DE-01000127.
(HENK ) HENKEL KGAA.
Petersohn D, Conradt M, Hofmann K;
WPI; 2002-590638/63.
In vitro identification of skin-expressed genes, useful for determining
homeostasis and identifying cosmetic or pharmaceutical agents against
e.g. skin cancer.
Disclosure; Page 50; 1345pp; German.
The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
Sequence 11 BP; 4 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTG 13
Db 11 TGGGGCTGTTG 1
| | | | | | | |
Human skin EST 902.
Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
Homo sapiens.
WO200253774-A2.
11-JUL-2002.
20-DEC-2001; 2001WO-EP015179.
03-JAN-2001; 2001DE-01000127.
(HENK ) HENKEL KGAA.
Petersohn D, Conradt M, Hofmann K;
WPI; 2002-590638/63.
In vitro identification of skin-expressed genes, useful for determining
homeostasis and identifying cosmetic or pharmaceutical agents against
e.g. skin cancer.
Disclosure; Page 50; 1345pp; German.
The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
Sequence 11 BP; 4 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 11;

```



```

PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286588; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGAGGCTGTGG 13
Db 12 TGAGGTTGTG 2
RESULT 91
ABI48684/c
ID ABI48684 standard; DNA; 12 BP.
XX
XX AC ABI48684;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 348657 for detecting SNP TSC0001217.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286588; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGAGGCTGTGG 13
Db 12 TGAGGTTGTG 2
RESULT 91
ABI48684/c
ID ABI48684 standard; DNA; 12 BP.
XX
XX AC ABI48684;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 348657 for detecting SNP TSC0001217.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 286573; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GAGGCTGTGG 14
Db 11 GAGGTTGTGG 1
RESULT 92
ABH80580
ID ABH80580 standard; DNA; 12 BP.
XX
XX AC ABH80580;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 280573 for detecting SNP TSC0008780.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 280573; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GAGGCTGTGG 14
Db 11 GAGGTTGTGG 1

```

CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGG 13
|||||
Db 2 TGAGGATGTGG 12

RESULT 93
ABI07308
ID ABI07308 standard; DNA; 12 BP.
XX
AC ABI07308;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 307281 for detecting SNP TSC0022417.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 307281; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
|||||

Db 1 TTGAGGTTGTT 11

RESULT 94
ABI23645/c
ID ABI23645 standard; DNA; 12 BP.
XX
AC ABI23645;
XX
DT 22-FEB-2002 (first entry)
XX

DE Oligonucleotide primer SEQ ID NO 323618 for detecting SNP TSC0031499.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 323618; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 12 GAGGATGTGG 2

RESULT 95
ABI51206/c
ID ABI51206 standard; DNA; 12 BP.
XX
AC ABI51206;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 351179 for detecting SNP TSC0009652.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 2 GAGGATGTGG 12

RESULT 98
ABH82809/c
ID ABH82809 standard; DNA; 12 BP.
XX AC ABH82809;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 282802 for detecting SNP TSC0011004.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 282802; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
|||||
Db 11 TTGAGGTTGTT 1

RESULT 99
ABI55301
ID ABI55301 standard; DNA; 12 BP.
XX AC ABI55301;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 35274 for detecting SNP TSC0049563.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 35274; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
|||||
Db 2 TTGAGGCTGTT 12

RESULT 100
ABC81894

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 214690; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 1 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGGC 15
Db 13 TGTGGTGTGGY 1
RESULT 103
ABF31455/c
ID ABF31455 standard; DNA; 13 BP.
XX
AC ABF31455;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 131452 for detecting SNP TSC0032808.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 131452 for detecting SNP TSC0032808.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 131452; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 8 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGGC 15
Db 13 TGAGGCTGTGGY 1
RESULT 104
ABF30191/c
ID ABF30191 standard; DNA; 13 BP.
XX
AC ABF30191;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 130188 for detecting SNP TSC0032553.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 130188; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 8 C; 2 G; 0 T; 0 U; 1 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      6 GGCTGTTGGC 16
DB      12 GCGCGTTGGC 2
      ||| |||||
RESULT 105
ABH14712
ID ABH14712 standard; DNA; 13 BP.
XX AC ABH14712;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 214689 for detecting SNP TSC0052243.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 214689; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 1 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      3 TGAGGCTGTGGC 15
DB      1 TGTGGTGTGGY 13
      ||| |||||
RESULT 106
ABC44423/C
ID ABC44423 standard; DNA; 13 BP.
XX AC ABC44423;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 81912 for detecting SNP TSC0020702.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 214689; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      3 TGAGGCTGTGGC 15
DB      1 TGTGGTGTGGY 13
      ||| |||||

```

```

XX DE 6 GGCTGTTGGC 16
XX ||| |||||
KW KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 44440; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      3 TGAGGCTGTGGC 15
DB      13 TGAAGGTGTGGY 1
      ||| |||||
RESULT 107
ABC81895/C
ID ABC81895 standard; DNA; 13 BP.
XX AC ABC81895;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 81912 for detecting SNP TSC0020702.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.

```



```

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 81912; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 4 GAGCGCTTGG 14
Db 12 GAGCGGTTGG 2
|||||
|||||

RESULT 108
ABC70901/c
ID ABC70901 standard; DNA; 13 BP.
XX
AC ABC70901;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 70918 for detecting SNP TSC0018403.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 70917; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 6 GGCTGTGGCG 16
Db 13 GGATGTGGCG 3
|||||
|||||

RESULT 109
ABC70900
ID ABC70900 standard; DNA; 13 BP.
XX
XX AC ABC70900;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 70917 for detecting SNP TSC0018403.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 70917; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 6 GGCTGTGGCG 16
Db 13 GGATGTGGCG 3
|||||
|||||

```

```
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGATGTTGGCG 11

RESULT 110
ABF30190
ID ABF30190 standard; DNA; 13 BP.
XX
AC ABF30190;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 130187 for detecting SNP TSC0032533.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 130187; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 2 C; 8 G; 2 T; 0 U; 1 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 2 GGCGTTGGCG 12

RESULT 111
ABC44422
ID ABC44422 standard; DNA; 13 BP.
XX
AC ABC44422;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 44439 for detecting SNP TSC0013039.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 44439; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTGGC 15
Db 1 TGAAGGTGTTGGY 13

RESULT 112
ABQ84081
ID ABQ84081 standard; DNA; 13 BP.
XX
AC ABQ84081;
XX
DT 18-FEB-2003 (first entry)
XX
DE Tubercle bacillus diagnosis probe M35E.
XX
KW Tubercle bacillus; diagnosis; probe; rpoB; DNA chip; drug tolerance;
KW deoxyribonucleic acid chip; ss.
```

XX Bacillus sp.
 XX CN1351176-A.
 XX 29-MAY-2002.
 XX 31-OCT-2000; 2000CN-00133796.
 XX 31-OCT-2000; 2000CN-00133796.
 XX (MENG/) MENGUS Y.
 XX WPI; 2002-644410/70.
 XX DNA chip for diagnosing tubercle bacillus and its drug tolerance.
 XX Claim 1; Page 2 (Claims); 15pp; Chinese.
 XX ABQ84043 to ABQ84083 represent specifically claimed DNA probes which can
 CC be used in a deoxyribonucleic acid (DNA) chip (I) comprising 12-100 DNA
 CC probes fixed to a glass plate, silicon chip, membrane or high-molecular
 CC material. (II) is useful for diagnosing tubercle bacillus and its drug
 CC tolerance. (I) has a high diagnosing efficiency and accuracy, low cost
 CC and short detection time
 XX
 SQ Sequence 13 BP; 1 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCTGTTGGCG 16
 DB 1 GACTGTTGGCG 11
 RESULT 113
 ADC33633
 ID ADC33633 standard; DNA; 13 BP.
 AC ADC33633;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE M. tuberculosis oligonucleotide probe #41.
 XX
 KW ss; probe; rifampin resistance; rpoB; tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US2003104387-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 07-SEP-2001; 2001US-00949041.
 XX
 PR 07-SEP-2001; 2001US-00949041.
 XX
 PA (YANG/) YANG M.
 PA (WOOH/) WOO H S.
 XX
 PI Yang M, Woo HS;
 XX
 DR WPI; 2003-787043/74.
 XX
 XX Detecting tendency to rifampin resistance caused by mutation in RNA
 PT polymerase beta-subunit gene of Mycobacterium tuberculosis.
 XX
 PS Claim 20; SEQ ID NO 44; 27pp; English.
 XX
 XX The invention relates to a method of detecting a tendency to rifampin
 CC resistance caused by mutations in rpoB gene of Mycobacterium tuberculosis

CC comprising extracting DNA from M. tuberculosis cells, amplifying rpoB
 CC gene to produce fluorescently labelled product, contacting the labelled
 CC product with first and second array of oligonucleotide probes, detecting
 CC fluorescent hybridisation signal and correlating with tendency to
 CC rifampin resistance. The method is useful for detecting a tendency to
 CC rifampin resistance caused by mutations in a rpoB gene of M.
 CC tuberculosis. The method is easy to perform and is cost effective to be
 CC performed on a large-scale basis. The results produced is reliable and
 CC readily detectable. The method is easily adaptable to automation. The
 CC present sequence represents a M. tuberculosis probe.
 XX
 SQ Sequence 13 BP; 1 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCTGTTGGCG 16
 DB 1 GACTGTTGGCG 11
 RESULT 114
 AAQ83339
 ID AAQ83339 standard; DNA; 14 BP.
 AC AAQ83339;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE jub-B antisense oligonucleotide.
 XX
 KW c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO9502051-A2.
 XX
 PD 19-JAN-1995.
 XX
 PF 06-JUL-1994; 94WO-EP002218.
 XX
 PR 10-JUL-1993; 93EP-00111059.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
 XX
 DR WPI; 1995-066896/09.
 XX
 PT Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
 PT treating neuronal injury, degeneration, cell death and/or neoplasms.
 XX
 PS Claim 2; Page 40; 86pp; English.
 XX
 CC Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
 CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a
 CC causal role in neuronal injury, degeneration, cell death and/or
 CC neoplasms, can be used to prevent and treat such conditions. c-jun
 CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
 CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
 CC fos antisense sequences are described in AAQ83364-439 and AAQ83446-51.
 CC Preferably the antisense sequences are phosphorothioate oligonucleotides
 CC since these are not destroyed as fast by endogenous factors as naturally
 CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGGCGAC 18
 DB 1 CTGTTGGCGAC 11
 SQ Sequence 14 BP; 4 A; 6 C; 2 G; 0 T; 2 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.3%; Pred. NO. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 115
 AAA17677/C
 ID AAA17677 standard; RNA; 14 BP.
 AC AAA17677;
 XX
 XX 19-JUN-2000 (first entry)
 DE Aryl hydrocarbon nuclear transport target site SEQ ID NO:903.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammarhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US0006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 53; Page 91; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 14 BP; 4 A; 6 C; 2 G; 0 T; 2 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.3%; Pred. NO. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TGAGGCTGCTG 13
 DB 11 TGAGGCTGCTG 1
 RESULT 116
 AAA17649
 ID AAA17649 standard; RNA; 14 BP.
 XX
 XX AAA17649;
 AC
 XX
 XX 19-JUN-2000 (first entry)
 DE Aryl hydrocarbon nuclear transport target site SEQ ID NO:875.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammarhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US0006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 53; Page 89; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3

CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 14 BP; 2 A; 4 C; 3 G; 0 T; 5 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 63.6%; Pred. No. 1.3e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 CTGTGGCGAC 18
 Db 4 CUGUUGGCUAC 14
 RESULT 117
 AAV92817/C
 ID AAV92817 standard; RNA; 14 BP.
 XX
 AC AAV92817;
 XX
 DT 18-FEB-1999 (first entry)
 XX
 DE Human A-raf target sequence nucleotide position 1839.
 XX
 KW Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 KW WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Belgelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 DR WPI; 1999-009494/01.
 XX
 PT Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 PS Claim 179; Page 164; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to

CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 14 BP; 3 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CTTGAGGCTGT 11
 Db 13 CTTGAGGCACT 3
 RESULT 118
 AAF95192
 ID AAF95192 standard; DNA; 14 BP.
 XX
 AC AAF95192;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Oligonucleotide: SEQ ID 186.
 XX
 KW Tubercle bacillus; drug sensitivity; drug resistance; rifampicin;
 KW streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene;
 KW rpsL gene; inhA gene; katG gene; embB gene; probe; PCR primer; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN EPI076099-A2.
 XX
 PD 14-FEB-2001.
 XX
 PF 02-AUG-2000; 2000EP-00306563.
 XX
 PR 03-AUG-1999; 99JP-00220357.
 XX
 PA (NISN) NISSHINEO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX
 PI Suzuki Y, Nishida M, Takenishi S;
 XX
 DR WPI; 2001-246696/26.
 XX
 PT New oligonucleotides, nucleic acid probes and primers are useful for
 PT differentiating drug-resistance and determining infection with tubercle
 PT bacilli.
 XX
 PS Example 1; Page 70; 114pp; English.
 XX
 CC The present invention relates to oligonucleotides based on nucleotide
 CC sequences obtained from both wild-type tubercle bacilli (wtTB) that are
 CC susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are
 CC resistant to a drug. The drugs used in the present invention are
 CC rifampicin (RFP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and
 CC ethambutol (EB). The rpoB gene is responsible for resistance to RFP; the
 CC rrs gene is responsible for resistance to SM and KM; the rpsL gene is
 CC responsible for resistance to SM; the inhA gene is responsible for
 CC resistance to INH; the katG gene is responsible for resistance to INH;
 CC and the embB gene is responsible for resistance to EB. The present
 CC invention also relates to nucleic acid probes having part of a nucleotide
 CC sequence of tubercle bacilli (TB) responsible for drug resistance and
 CC primers used to generate the probes. The present sequence is an
 CC oligonucleotide of the present invention. The oligonucleotides of the

CC present invention can be used to enable the differentiation of drug
 CC resistance and the determination of infection with tubercle bacilli
 CC simultaneously
 XX .
 SQ Sequence 14 BP; 1 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCTGTGGCG 16
 | |||||
 Db 2 GACTGTGGCG 12
 RESULT 119
 ABX0551/c
 ID ABX0551 standard; DNA; 14 BP.
 AC ABX0551;
 XX
 XX 17-JAN-2003 (first entry)
 DT
 XX Secondary PENTamers adapter A3 strand 2.
 DE
 XX Adapter; ss; primer extension/nick translation; PENT; PENTamer;
 KW positional amplification by nick translation; PANT; genomic library;
 KW DNA sequencing; ordered positional library; genomic sequencing;
 KW gene mapping; chromosomal rearrangement diagnosis;
 KW organism identification.
 XX
 OS Synthetic.
 XX
 XX WO200190415-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-US016264.
 PF
 XX 20-MAY-2000; 2000US-0206095P.
 PR
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX Langmore JP, Makarov V;
 XX
 XX WPI; 2002-114290/15.
 DR
 XX Preparing a DNA molecule comprising an amplifiable region, useful for
 XX producing a genomic library, comprises subjecting the DNA molecules to
 PT primer extension/nick translation.
 PT
 XX Example 24; Page 193; 373pp; English.
 PS
 XX The invention relates to a method (M1) of preparing a DNA molecule having
 CC an amplifiable region comprises: (a) obtaining a DNA sample comprising
 CC DNA molecules having regions to be amplified; (b) attaching upstream
 CC adapter molecules to ends of DNA molecules of the sample to provide a
 CC nick translation initiation site; (c) subjecting the DNA molecules to
 CC nick translation comprising DNA polymerisation and 5'-3' exonuclease
 CC activity to produce nick translate molecules; and (d) attaching
 CC downstream adapter molecules to the nick translate molecules to produce
 CC creating hybridisation probes comprising preparing a labelled, amplified
 CC adapter attached nick translate molecules. Also included are: (1)
 CC DNA; (2) shotgun sequencing of DNA; (3) constructing a genomic library;
 CC (4) preparing an unordered DNA library; (5) sequencing a BAC clone; (6)
 CC kits comprising amplifiable DNA; (7) an adapter construct comprising: (a)
 CC a first domain comprising nucleotides that facilitate ligation of the
 CC construct to a nucleic acid; and (b) a second domain proximal to the
 CC first domain, comprising a site which facilitates the initiation of a
 CC nick translation reaction and a site that facilitates recombination,
 CC where ligation of the adapter construct to a polynucleotide results in
 CC the only free 3' OH group capable of initiating a nick translation
 CC reaction within the second domain; (8) an adapter construct comprising:

CC (a) a first oligonucleotide comprising a phosphate group at the 5' end
 CC and a blocking nucleotide at the 3' end; (b) a second oligonucleotide
 CC comprising a blocked 3' end, a non-phosphorylated 5' end, and a
 CC nucleotide sequence complementary to the 5' element of the first
 CC oligonucleotide; and (c) a third oligonucleotide comprising a 3' hydroxyl
 CC group, a non-phosphorylated 5' end, and a nucleotide sequence
 CC complementary to the 3' element of the first oligonucleotide; (9) kits
 CC comprising a DNA polymerase, nucleotide triphosphates, and an adapter
 CC construct; (10) methods of recombining DNA molecules comprising
 CC recombining ends of adapter attached template molecules in a dilute
 CC solution; and (11) a method of detecting a specific DNA sequence. The
 CC method (primer extension/nick translation or PENT also known as
 CC positional amplification by nick translation, PANT) is useful in
 CC producing DNA to be sequenced or amplified with specific regions for
 CC which the sequence is not known, and in producing a genomic library. The
 CC method is useful for sequencing internal regions of short templates using
 CC primary and secondary PENTamers, and complement PENTamers; sequencing
 CC large insert clones using ordered positional libraries of PENTamers;
 CC genomic sequencing; determining gene positions; sequencing and re-
 CC sequencing; cDNA sequencing; diagnosing chromosomal rearrangements;
 CC detecting and identifying organisms and variants of organisms; and
 CC amplifying specific subsets of genomes. The present sequence is a adapter
 CC used to demonstrate the method of the invention
 XX
 SQ Sequence 14 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTG 13
 | |||||
 Db 14 TGAGGTTGTG 4
 RESULT 120
 ABX0593/c
 ID ABX0593 standard; DNA; 14 BP.
 XX
 XX AC ABX0593;
 XX
 XX 17-JAN-2003 (first entry)
 DT
 XX
 DE Simplified recombinant adapter Sra1 component oligonucleotide B.
 XX
 KW adapter; ss; primer extension/nick translation; PENT; PENTamer;
 KW positional amplification by nick translation; PANT; genomic library;
 KW DNA sequencing; ordered positional library; genomic sequencing;
 KW gene mapping; chromosomal rearrangement diagnosis;
 KW organism identification; simplified recombinant adapter; Sra.
 XX
 OS Synthetic.
 XX
 XX WO200190415-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-US016264.
 PF
 XX 20-MAY-2000; 2000US-0206095P.
 PR
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX Langmore JP, Makarov V;
 XX
 XX WPI; 2002-114290/15.
 DR
 XX Preparing a DNA molecule comprising an amplifiable region, useful for
 XX producing a genomic library, comprises subjecting the DNA molecules to
 PT primer extension/nick translation.
 PT
 XX Example 25; Fig 69; 373pp; English.
 PS
 XX

CC The invention relates to a method (M1) of preparing a DNA molecule having
 CC an amplifiable region comprising: (a) obtaining a DNA sample comprising
 CC DNA molecules having regions to be amplified; (b) attaching upstream
 CC adapter molecules to ends of DNA molecules of the sample to provide a
 CC nick translation initiation site; (c) subjecting the DNA molecules to
 CC nick translation comprising DNA polymerisation and 5'-3' exonuclease
 CC activity to produce nick translate molecules; and (d) attaching
 CC downstream adapter molecules to the nick translate molecules to produce
 CC adapter attached nick translate molecules. Also included are: (1)
 CC creating hybridisation probes comprising preparing a labelled, amplified
 CC DNA; (2) shotgun sequencing of DNA; (3) constructing a genomic library;
 CC kits comprising amplifiable DNA; (5) sequencing a genomic library;
 CC a first domain comprising nucleotides that facilitate ligation of the
 CC construct to a nucleic acid; and (b) a second domain proximal to the
 CC first domain, comprising a site which facilitates the initiation of a
 CC nick translation reaction and a site that facilitates recombination,
 CC where ligation of the adapter construct to a polynucleotide results in
 CC the only free 3' OH group capable of initiating a nick translation
 CC reaction within the second domain; (8) an adapter construct comprising:
 CC (a) a first oligonucleotide comprising a phosphate group at the 5' end
 CC and a blocking nucleotide at the 3' end; (b) a second oligonucleotide
 CC comprising a blocked 3' end, a non-phosphorylated 5' end, and a
 CC nucleotide sequence complementary to the 5' element of the first
 CC oligonucleotide; and (c) a third oligonucleotide comprising a 3' hydroxyl
 CC group, a non-phosphorylated 5' end, and a nucleotide sequence
 CC complementary to the 3' element of the first oligonucleotide; (6)
 CC comprising a DNA polymerase, nucleotide triphosphates, and an adapter
 CC construct; (10) methods of recombining DNA molecules comprising
 CC recombining ends of adapter attached template molecules in a dilute
 CC solution; and (11) a method of detecting a specific DNA sequence. The
 CC method (primer extension/nick translation, PANT) is useful in
 CC positional amplification by nick translation or PENT also known as
 CC producing DNA to be sequenced or amplified with specific regions for
 CC which the sequence is not known, and in producing a genomic library. The
 CC method is useful for sequencing internal regions of short templates using
 CC primary and secondary PENTamers, and complement PENTamers; sequencing
 CC large insert clones using ordered positional libraries of PENTamers;
 CC genomic sequencing; determining gene positions; sequencing and re-
 CC sequencing; cDNA sequencing; diagnosing chromosomal rearrangements;
 CC detecting and identifying organisms and variants of organisms; and
 CC amplifying specific subsets of genomes. The present sequence is a
 CC component part of a simplified recombinant adapter (Sra) used in an
 CC example to demonstrate the method of the invention

SQ Sequence 14 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTG 13
 |||||
 Db 14 TGAGGTTGTTG 4

RESULT 121

ABX05569/c
 ID ABX05569 standard; DNA; 14 BP.

AC ABX05569;

XX 17-JAN-2003 (first entry)

DE Secondary PENTamers adapter A3 blocking primer.

XX Primer; ss; primer extension/nick translation; PENT; PENTamer;
 KW positional amplification by nick translation; PANT; genomic library;
 KW DNA sequencing; ordered positional library; genomic sequencing;
 KW gene mapping; chromosomal rearrangement diagnosis;
 KW organism identification; blocking primer.

OS Synthetic.

XX WO200190415-A2.
 PN 29-NOV-2001.
 PD 18-MAY-2001; 2001WO-US016264.
 XX 20-MAY-2000; 2000US-0206095P.
 PF (UNMI) UNIV MICHIGAN.
 PR Langmore JP, Makarov V;
 FI WPI; 2002-114290/15.
 DR Preparing a DNA molecule comprising an amplifiable region, useful for
 PT producing a genomic library, comprises subjecting the DNA molecules to
 PT primer extension/nick translation.
 XX Example 24; Page 195; 373pp; English.
 PS The invention relates to a method (M1) of preparing a DNA molecule having
 CC an amplifiable region comprising: (a) obtaining a DNA sample comprising
 CC DNA molecules having regions to be amplified; (b) attaching upstream
 CC adapter molecules to ends of DNA molecules of the sample to provide a
 CC nick translation initiation site; (c) subjecting the DNA molecules to
 CC nick translation comprising DNA polymerisation and 5'-3' exonuclease
 CC activity to produce nick translate molecules; and (d) attaching
 CC downstream adapter molecules to the nick translate molecules to produce
 CC adapter attached nick translate molecules. Also included are: (1)
 CC creating hybridisation probes comprising preparing a labelled, amplified
 CC DNA; (2) shotgun sequencing of DNA; (3) constructing a genomic library;
 CC kits comprising amplifiable DNA; (5) sequencing a genomic library;
 CC a first domain comprising nucleotides that facilitate ligation of the
 CC construct to a nucleic acid; and (b) a second domain proximal to the
 CC first domain, comprising a site which facilitates the initiation of a
 CC nick translation reaction and a site that facilitates recombination,
 CC where ligation of the adapter construct to a polynucleotide results in
 CC the only free 3' OH group capable of initiating a nick translation
 CC reaction within the second domain; (8) an adapter construct comprising:
 CC (a) a first oligonucleotide comprising a phosphate group at the 5' end
 CC and a blocking nucleotide at the 3' end; (b) a second oligonucleotide
 CC nucleotide sequence complementary to the 5' element of the first
 CC oligonucleotide; and (c) a third oligonucleotide comprising a 3' hydroxyl
 CC group, a non-phosphorylated 5' end, and a nucleotide sequence
 CC complementary to the 3' element of the first oligonucleotide; (9) kits
 CC comprising a DNA polymerase, nucleotide triphosphates, and an adapter
 CC construct; (10) methods of recombining DNA molecules comprising
 CC recombining ends of adapter attached template molecules in a dilute
 CC solution; and (11) a method of detecting a specific DNA sequence. The
 CC method (primer extension/nick translation, PANT) is useful in
 CC positional amplification by nick translation or PENT also known as
 CC producing DNA to be sequenced or amplified with specific regions for
 CC which the sequence is not known, and in producing a genomic library. The
 CC method is useful for sequencing internal regions of short templates using
 CC primary and secondary PENTamers, and complement PENTamers; sequencing
 CC large insert clones using ordered positional libraries of PENTamers;
 CC genomic sequencing; determining gene positions; sequencing and re-
 CC sequencing; cDNA sequencing; diagnosing chromosomal rearrangements;
 CC detecting and identifying organisms and variants of organisms; and
 CC amplifying specific subsets of genomes. The present sequence is a
 CC component part of a simplified recombinant adapter (Sra) used in an
 CC example to demonstrate the method of the invention

SQ Sequence 14 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTG 13

```
Db      14 TGAGGTGTG 4
RESULT 122
ABX05603/c
ID      ABX05603 standard; DNA; 14 BP.
XX
AC      ABX05603;
XX
XX      17-JAN-2003 (first entry)
XX
DE      Simplified recombinant adapter, Sra, oligonucleotide Sra 1B.
XX
XX      adapter; ss; primer extension/nick translation; PENT; PENTamer;
XX      positional amplification by nick translation; PANT; genomic library;
XX      DNA sequencing; ordered positional library; genomic sequencing;
XX      gene mapping; chromosomal rearrangement diagnosis;
XX      organism identification; simplified recombinant adapter; Sra.
XX
OS      Synthetic.
XX
XX      WO200190415-A2.
XX
XX      29-NOV-2001.
XX
XX      18-MAY-2001; 2001WO-US016264.
XX
XX      20-MAY-2000; 2000US-0206095P.
XX
XX      (UNMI ) UNIV MICHIGAN.
XX
XX      Langmore JP, Makarov V;
XX
XX      WPI; 2002-114290/15.
XX
XX      Preparing a DNA molecule comprising an amplifiable region, useful for
XX      producing a genomic library, comprises subjecting the DNA molecules to
XX      primer extension/nick translation.
XX
XX      Example 25; Fig 70; 373pp; English.
XX
XX      The invention relates to a method (M1) of preparing a DNA molecule having
XX      an amplifiable region comprises: (a) obtaining a DNA sample comprising
XX      DNA molecules having regions to be amplified; (b) attaching upstream
XX      adapter molecules to ends of DNA molecules of the sample to provide a
XX      nick translation initiation site; (c) subjecting the DNA molecules to
XX      nick translation comprising DNA polymerisation and 5'-3' exonuclease
XX      activity to produce nick translate molecules; and (d) attaching
XX      downstream adapter molecules to the nick translate molecules to produce
XX      adapter attached nick translate molecules. Also included are: (1)
XX      creating hybridisation probes comprising preparing a labelled, amplified
XX      DNA; (2) shotgun sequencing of DNA; (3) constructing a genomic library;
XX      (4) preparing an unordered DNA library; (5) sequencing a BAC clone; (6)
XX      kits comprising amplifiable DNA; (7) an adapter construct comprising: (a)
XX      a first domain comprising nucleotides that facilitate ligation of the
XX      construct to a nucleic acid; and (b) a second domain proximal to the
XX      first domain, comprising a site which facilitates the initiation of a
XX      nick translation reaction and a site that facilitates recombination,
XX      where ligation of the adapter construct to a polynucleotide results in
XX      the only free 3' OH group capable of initiating a nick translation
XX      reaction within the second domain; (8) an adapter construct comprising:
XX      (a) a first oligonucleotide comprising a phosphate group at the 5' end
XX      and a blocking nucleotide at the 3' end; (b) a second oligonucleotide
XX      comprising a blocked 3' end, a non-phosphorylated 5' end, and a
XX      nucleotide sequence complementary to the 5' element of the first
XX      oligonucleotide; and (c) a third oligonucleotide comprising a 3' hydroxyl
XX      group, a non-phosphorylated 5' end, and a nucleotide sequence
XX      complementary to the 3' element of the first oligonucleotide; (9) kits
XX      comprising a DNA polymerase, nucleotide triphosphates, and an adapter
XX      construct; (10) methods of recombining DNA molecules comprising
XX      recombining ends of adapter attached template molecules in a dilute
XX      solution; and (11) a method of detecting a specific DNA sequence. The
```

```
CC      method (primer extension/nick translation or PENT also known as
CC      positional amplification by nick translation, PANT) is useful in
CC      producing DNA to be sequenced or amplified with specific regions for
CC      which the sequence is not known, and in producing a genomic library. The
CC      method is useful for sequencing internal regions of short templates using
CC      primary and secondary PENTamers, and complementary PENTamers; sequencing
CC      large insert clones using ordered positional libraries of PENTamers;
CC      genomic sequencing; determining gene positions; sequencing and re-
CC      sequencing; cDNA sequencing; diagnosing chromosomal rearrangements;
CC      detecting and identifying organisms and variants of organisms; and
CC      amplifying specific subsets of genomes. The present sequence is a
CC      component part of a simplified recombinant adapter (Sra) used in an
CC      example to demonstrate the method of the invention
XX
SQ      Sequence 14 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
Query Match      52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      3 TGAGGCTGTG 13
Db      14 TGAGGTGTG 4
RESULT 123
ABZ58027/c
ID      ABZ58027 standard; DNA; 14 BP.
XX
AC      ABZ58027;
XX
XX      22-APR-2003 (first entry)
XX
DE      Adaptor A3 blocking primer.
XX
XX      PENTamer; DNA library; nick translation; chromosome walking;
XX      genome walking; primer; ss.
XX
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 14
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "3' C7 amino blocked"
XX
XX      WO2002103054-A1.
XX
XX      27-DEC-2002.
XX
XX      15-NOV-2001; 2001WO-US044970.
XX
XX      02-MAY-2001; 2001US-0288205P.
XX
XX      (RUBI-) RUBICON GENOMICS INC.
XX
XX      Makarov VL, Kamzerov E, Sleptsova I;
XX
XX      WPI; 2003-167543/16.
XX
XX      Producing a library of consecutive overlapping series of nucleic acid
XX      sequences, useful in chromosome walking, comprises generating a first
XX      amplifiable nick translation product, and sequencing a part of the
XX      translation product.
XX
XX      Example 1; Page 84; 160pp; English.
XX
XX      The present invention is directed to chromosome walking through the
XX      generation of adaptor-attached nick translate molecules (designated a
XX      PENTamer). In the simplest implementation, a primary PENTamer is
XX      generated by: ligating a nick-translation first adaptor to the proximal
XX      end of the source DNA (template); initiating a nick translation reaction
XX      at the nick site of the adaptor using a DNA polymerase with 5' to 3'
```


CC exonuclease activity; elongating the PENT product a specific time; and
 CC appending a nick-ligation second adaptor to the distal, 3' end of the
 CC PENT product to form a PENTamer-template hybrid (nascent PENTamer). The
 CC method is useful for: filling gaps in genomic sequencing projects, 1-2
 CC time redundancy genomic sequencing, sequencing unculturable
 CC microorganisms and sequencing mixtures of microorganisms. The present
 CC sequence is that of an adaptor A3 blocking primer. Adaptor A3 (see
 CC AB258041) was used in examples of the invention for the preparation of
 CC primary PENTamer libraries of *Escherichia coli* and human genomic DNA
 XX
 SQ Sequence 14 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
 Db 14 TGAGGTTGTTG 4

RESULT 124
 AAX31459
 ID AAX31459 standard; DNA; 14 BP.
 XX
 AC AAX31459;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Tag sequence of a transcript decreased in colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UWJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.
 XX
 PT Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX
 PS Claim 1; Page 51; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer
 XX
 SQ Sequence 14 BP; 3 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 51.1%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 1.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTTGG 14
 Db 1 CATGAGGATGTTGG 14

RESULT 125
 AAA26152
 ID AAA26152 standard; DNA; 14 BP.
 XX
 AC AAA26152;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2650.
 XX
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 XX
 PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX
 PS Claim 79; Page 100; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(dithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium), or
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 51.1%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 1.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
OS Synthetic.
XX WO200242459-A2.
PN
XX
XX
PD 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US043438.
XX PF
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI
XX PI Liu Q;
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 63; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsequence. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (W) (i) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsequence, selecting the F2 zinc finger such that it
CC binds to the S2 target subsequence, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsequence, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsequence
CC having the nucleotide G in the 5'-most position of the subsequence. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
XX Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
Db |||||
1 GAGGCTGTT 9

RESULT 128
ADA64507
ID ADA64507 standard; DNA; 9 BP.
XX
XX ADA64507;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX DE Zinc finger target sequence DNA #965.
XX
XX de; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.
XX
XX Synthetic.
XX
XX US2003069675-A1.
```

```
QY 5 AGGCTGTGGCAG 18
Db |||||
1 ATGCTGTGGCTAC 14

RESULT 126
ABK32413
ID ABK32413 standard; DNA; 14 BP.
XX
XX AC ABK32413;
XX
XX 23-APR-2002 (first entry)
XX DT
XX DE Human colon cancer SAGE tag #514.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
XX Homo sapiens.
XX
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 57; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 14 BP; 3 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTGAGGCTGTGG 14
Db |||||
1 CATGAGGATGTGG 14

RESULT 127
ABQ72180
ID ABQ72180 standard; DNA; 9 BP.
XX
XX AC ABQ72180;
XX
XX 28-AUG-2002 (first entry)
XX DT
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:2478.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
XX
```

XX 10-APR-2003.
XX 20-NOV-2001; 2001US-00990186.
XX 24-MAR-1999; 99US-0126238P.
XX 24-MAR-1999; 99US-0126239P.
XX 30-JUL-1999; 99US-0146595P.
XX 30-JUL-1999; 99US-0146615P.
XX 23-MAR-2000; 2000US-00535008.
XX 20-NOV-2000; 2000US-00716637.
XX (LIUQ/) LIU Q.
XX Liu Q;
XX WPI; 2003-567233/53.
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX Disclosure; Page 27; 34pp; English.
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTGTT 12
Db 1 GAGGCTGTT 9
RESULT 129
ID AAF40252 standard; DNA; 10 BP.
AC AAF40252;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6991.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO20007214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 249; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGCGA 17
Db 2 TGTGGCGA 10
RESULT 130
ID AAF56191 standard; DNA; 12 BP.
XX AAF56191;
XX 19-APR-2001 (first entry)
XX Microarray capture probe k7.
XX Array-based nucleic acid hybridisation; hybridisation probe;
KW microarray capture probe; ss.
XX Unidentified.
XX WO200106011-A2.
XX 25-JAN-2001.
XX 12-JUL-2000; 2000WO-US019045.
XX 14-JUL-1999; 99US-0143926P.
XX (GENO-) GENOMETRIX GENOMICS INC.
XX Belosludtsev Y;
XX WPI; 2001-147356/15.
XX

PT Producing nucleic acid array for use in hybridization reactions, by
PT employing adsorptive, non-covalent attachment of nucleic acids and
PT oligonucleotide probes to positively charged solid surfaces.
XX
XX Example 1; Page 29; 46pp; English.
XX
XX The present sequence is a probe used to demonstrate array-based nucleic
CC acid hybridisation. This was an example in a specification relating to a
CC method for producing an array of discrete biosites comprising non-
CC covalently attached nucleic acids. The nucleic acids are useful as probes
CC in hybridisation reactions. The affinity and selectivity of the non-
CC covalently immobilised probe to sample target duplex formation is
CC excellent and compact compared to conventional methods and unlabelled
CC probes are applied at a concentration which is at least five times lower
CC than required for conventional methods
XX
XX Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGGCG 16
Db |||||
4 CTGTTGGCG 12
RESULT 131
AAI65972
ID AAI65972 standard; DNA; 12 BP.
XX
XX AAI65972;
AC
XX
DT 15-JAN-2002 (first entry)
XX
DE Synthetic k-ras codon 12 point mutant capture probe K7.
XX
XX Hybridisation device; single base pair difference; diagnostic test;
KW protein purification; nucleic acid purification; secondary structure;
KW probe; ss; k-ras; codon 12.
XX
XX Synthetic.
OS
XX
XX WO200166687-A1.
PN
XX
XX 13-SEP-2001.
PD
XX 24-AUG-2000; 2000WO-US023438.
XX
XX 09-MAR-2000; 2000US-00522240.
PR
PR 10-AUG-2000; 2000US-00636268.
XX
XX (GENO-) GENOMETRIX GENOMIX INC.
PA
XX
XX Hogan M, Powderill T, Iverson B, Belosludtsev YY, Belosludtsev IY;
PI
XX
XX WPI; 2001-611328/70.
DR
XX
XX Association device for nucleic acid-based diagnostic test, isolation of
PT nucleic acids, comprises oligonucleotide probe and solid substrate having
PT support surface comprising association surface for linking probe to
PT substrate.
XX
XX
XX Example 13; Page 63; 101pp; English.
PS
XX The invention relates to an association/hybridisation device comprising
CC nucleic acid and polypeptide probes, or combinations of these, linked to
CC a porous solid substrate, comprising an external substrate surface and
CC several internal pores. The pore surfaces comprise an association surface
CC which is charged with net positive or negative charge density where the
CC pH is lower or higher than the pI of association surface. The device is
CC useful for associating a nucleic acid or a polypeptide in a sample to a
CC nucleic acid or a polypeptide probe. The device is also useful for

CC detecting a single base pair difference between a nucleic acid in a test
CC sample and an oligonucleotide probe. The device finds application in
CC nucleic acid-based diagnostic tests, isolation and purification of
CC nucleic acids or polypeptides from a sample. The device can be used at
CC any temperature and the kinetics of association between the
CC oligonucleotide probe and the nucleic acid in the test sample are 10 fold
CC more rapid than the kinetics of association under conditions when the
CC substrate surface or association surface has a neutral or net negative
CC charge density. The device and the method can be used for hybridisation
CC of probes to target DNA or RNA at low bulk ion concentrations. The
CC present sequence is that of a k-ras capture probe. As a representative
CC DNA hybridisation model a 157bp PCR fragment of the human k-ras oncogene
CC was used to examine hybridisation rate enhancement under low ionic
CC strength and low pH conditions. The capture probes (AAI65966-AAI65972)
CC comprise biologically significant codon 12 point mutations
XX
XX Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGGCG 16
Db |||||
4 CTGTTGGCG 12
RESULT 132
ABF62110
ID ABF62110 standard; DNA; 13 BP.
XX
XX ABF62110;
AC
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 162107 for detecting SNP TSC0040792.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
XX Claim 1; SEQ ID NO 162107; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: the sequence
CC data for this patent did not form part of the printed specification, but

```
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 1 Other;

  Query Match      50.0%; Score 9; DB 1; Length 13;
  Best Local Similarity 81.8%; Pred. No. 1.6e+02;
  Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 3 TTGAGGATGTY 13
   ||||| |||

RESULT 133
ABCF47060
ID ABC47060 standard; DNA; 13 BP.
XX
AC ABC47060;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 47077 for detecting SNP TSC0013546.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 47077; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 1 Other;

  Query Match      50.0%; Score 9; DB 1; Length 13;
  Best Local Similarity 81.8%; Pred. No. 1.6e+02;
  Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
   ||| |||||
Db 3 AGGATGTGGY 13
   ||| |||||

RESULT 134
ABCF67043/C
ID ABF67043 standard; DNA; 13 BP.
XX
AC ABF67043;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 167040 for detecting SNP TSC0010735.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 167040; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match      50.0%; Score 9; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.6e+02;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGCGCA 17
   ||||| |||||
Db 11 TGTGGCGCA 3
   ||||| |||||

RESULT 135
ABCF62114
ID ABF62114 standard; DNA; 13 BP.
XX
AC ABF62114;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 162111 for detecting SNP TSC0040792.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```


CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGC 15
Db 11 AGGATGTGGY 1
|||||

RESULT 138
ABF62111/C
ID ABF62111 standard; DNA; 13 BP.
XX AC ABF62111;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 162108 for detecting SNP TSC0040792.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 162108; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 11 TTGAGGATGTY 1
|||||

RESULT 139
ABH49553/C
ID ABH49553 standard; DNA; 13 BP.
XX AC ABH49553;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 249530 for detecting SNP TSC0060952.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.

Claim 1; SEQ ID NO 249530; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTTGGCGA 17
Db 13 TGTTGGCGA 5
|||||

RESULT 140
ABF67042
ID ABF67042 standard; DNA; 13 BP.
XX

```
AC ABF67042;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 167039 for detecting SNP TSC0010735.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 167039; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred.No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 9 TGTTCGCGA 17
XX
XX 3 TGTTCGCGA 11
XX
XX RESULT 141
XX ABF62115/c
XX ID ABF62115 standard; DNA; 13 BP.
XX
XX AC ABF62115;
XX
XX AC ABF62115;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 162112 for detecting SNP TSC0040792.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 162112; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred.No. 1.6e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2 TTGAGGCTGTT 12
XX
XX 11 TTGAGGATGTY 1
XX
XX RESULT 142
XX ABH49552
XX ID ABH49552 standard; DNA; 13 BP.
XX
XX AC ABH49552;
XX
XX AC ABH49552;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 249529 for detecting SNP TSC0060952.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX
```


PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 249529; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 TGTGGCGA 17
 Db 1 TGTGGCGA 9
 RESULT 143
 ABF87322
 ID ABF87322 standard; DNA; 13 BP.
 XX
 AC ABF87322;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 187319 for detecting SNP TSC0046172.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A; Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 187319; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 1 C; 6 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 TGTGGCGA 17
 Db 1 TGTGGCGA 9
 RESULT 144
 AAT03074
 ID AAT03074 standard; DNA; 12 BP.
 XX
 AC AAT03074;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAY-1996 (first entry)
 XX
 DE E. coli small ribosomal subunit 16S rRNA antisense oligo (528-517).
 XX
 KW E. coli; small ribosomal subunit; 16S; rRNA; antisense; retrovirus; HIV;
 KW HTLV type 1; pol gene; ribosomal frameshifting; human; 18S; ss.
 XX
 OS Synthetic.
 XX
 PN WO9527054-A1.
 XX
 PD 12-OCT-1995.
 XX
 PF 28-MAR-1995; 95WO-CA000169.
 XX
 PR 30-MAR-1994; 94US-00220604.
 PR 23-MAR-1995; 95US-00409852.
 XX
 PA (UYMO-) UNIV MONTREAL.
 XX
 PI Brakier-Gingras L, Melancon P, Cote M, Payant C;
 XX
 DR WPI; 1995-366159/47.
 XX
 PT New anti-sense DNA oligomers - which decrease ribosomal frame-shifting
 PT and inhibit the expression of viral enzymatic proteins.
 XX
 PS Claim 2; Page 25; 34pp; English.
 XX
 CC The antisense oligonucleotides AAT03073-80 are targeted against specific
 CC regions in the 16S and 18S rRNA of the E. coli and human small ribosomal
 CC subunit, respectively. They can be used to inhibit enzymatic protein
 CC expression by a retrovirus in a host, and are therefore useful in the
 CC treatment of retroviral infections, e.g. HIV, HTLV type 1 or human
 CC retroviruses requiring ribosomal frameshifting for the expression of the
 CC pol gene. The antisense sequences are shown 3' to 5' in the
 CC specification. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GAGCTCTTGGC 15
 Db 1 CGGCTCTTGGC 12

```

RESULT 145
AAV04827
ID AAV04827 standard; cDNA; 12 BP.
XX
AC AAV04827;
XX
DT 27-APR-1998 (first entry)
XX
DE Antisense DNA oligomer targeted against the 16S RNA of E. coli.
XX
KW Antisense oligomer; 16S RNA; small ribosomal subunit; human; 18S rRNA;
KW ribosomal frameshifting; expression; HIV enzymatic protein;
KW HIV infection; ss.
XX
OS Synthetic.
XX
PN US5707866-A.
XX
PD 13-JAN-1998.
XX
PF 21-MAY-1996; 96US-00651835.
XX
PR 30-MAR-1994; 94US-00220604.
PR 23-MAR-1995; 95US-00409852.
XX
PA (UWMO-) UNIV MONTREAL.
XX
PI Cote M, Payant C, Brakier-Gingras L, Melancon P;
XX
DR WPI; 1998-100350/09.
XX
PT Antisense oligonucleotide(s) complementary to human 18S rRNA - for
PT inhibiting HIV ribosomal frameshifting and enzyme expression.
XX
PS Claim 2; Col 5; 14pp; English.
XX
CC Antisense oligomers AAV04822-29 are targeted against specific regions in
CC the 16S RNA of Escherichia coli small ribosomal subunit. These regions
CC correspond to the human 18S rRNA nucleotides 595-641. The present
CC oligomer is targeted toward positions 528-517. The oligonucleotides
CC decrease the occurrence of ribosomal frameshifting and inhibits the
CC expression of HIV enzymatic proteins. The antisense oligonucleotides are
CC used for treating HIV infections
XX
SQ Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGGC 15
Db 1 GCGGCTGCTGGC 12

RESULT 146
ABI66024/c
ID ABI66024 standard; DNA; 12 BP.
XX
AC ABI66024;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 365997 for detecting SNP TSC0055481.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX

RESULT 147
ABI46177
ID ABI46177 standard; DNA; 12 BP.
XX
AC ABI46177;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 346150 for detecting SNP TSC0044401.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is

```

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 346150; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTGG 13
 Db 1 TTGAGGATGATG 12
 ||||| ||||
 RESULT 148
 ABI19567/c
 ID ABI19567 standard; DNA; 12 BP.
 XX
 AC ABI19567;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 319540 for detecting SNP TSC0029288.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 319540; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 5 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 TGAGGCTGTGG 14
 Db 12 TGGGGTGTGG 1
 ||||| |||||
 RESULT 149
 ABH71852
 ID ABH71852 standard; DNA; 12 BP.
 XX
 AC ABH71852;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 271829 for detecting SNP TSC0002627.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 271829; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 TGAGGCTGTGG 14
 ||||| |||||

XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 295739; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 3 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGG 14
 Db 12 TGAGGGGTGG 1
 ||||| |||||
 RESULT 153
 ABH79948
 ID ABH79948 standard; DNA; 12 BP.
 XX AC ABH79948;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 279941 for detecting SNP TSC0007963.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 279941; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGAGGCTGTG 13
 Db 1 TTGAGGTTGTAG 12
 ||||| |||||
 RESULT 154
 ABH86298/C
 ID ABH86298 standard; DNA; 12 BP.
 XX AC ABH86298;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 286291 for detecting SNP TSC0012660.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 286291; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

```
SQ Sequence 12 BP; 3 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTTG 13
Db 12 TTGAGGCGGTG 1

RESULT 155
ABI22194/c
ID ABI22194 standard; DNA; 12 BP.
XX AC
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 322167 for detecting SNP TSC0030707.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 322167; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGCGA 17
Db 12 GGTTTGGCGA 1

RESULT 156
ABI48872
ID ABI48872 standard; DNA; 12 BP.
XX AC
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 348845 for detecting SNP TSC0045785.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 348845; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTGG 14
Db 1 TGAGGCTGTTAG 12

RESULT 157
ABI52064/c
ID ABI52064 standard; DNA; 12 BP.
XX AC
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 352037 for detecting SNP TSC0047644.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 352037; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGG 14
 Db 12 TGAGTTGTGG 1
 RESULT 158
 ABH75412/c
 ID ABH75412 standard; DNA; 12 BP.
 XX AC ABH75412;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 275403 for detecting SNP TSC0003884.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 352037; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGG 14
 Db 12 TGAGTTGTGG 1

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 275403; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGG 14
 Db 12 TGCGAGTTGG 1
 RESULT 159
 ABI32027
 ID ABI32027 standard; DNA; 12 BP.
 XX AC ABI32027;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 332000 for detecting SNP TSC0036634.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 332000; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTG 13
 DB 1 TTGAAGGTGTG 12
 |||||
 |||||

RESULT 160
 ABI53770
 ID ABI53770 standard; DNA; 12 BP.
 XX
 AC ABI53770;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 353743 for detecting SNP TSC0004574.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 353743; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTG 13
 DB 1 TTGAAGGTGTG 12
 |||||
 |||||

RESULT 160
 ABI53770
 ID ABI53770 standard; DNA; 12 BP.
 XX
 AC ABI53770;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 353743 for detecting SNP TSC0004574.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 353743; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCGA 17
 DB 1 GGTGTGGTGA 12
 |||||
 |||||

RESULT 161
 ABH75018
 ID ABH75018 standard; DNA; 12 BP.
 XX
 AC ABH75018;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 275005 for detecting SNP TSC0003761.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 275005; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGG 14
 DB 1 TGAGGCTGTGG 12
 |||||
 |||||

RESULT 162
 ABI32026/C
 ID ABI32026 standard; DNA; 12 BP.
 XX
 AC ABI32026;
 XX
 DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 331999 for detecting SNP TSC0036634.
XX XX
XX XX SNP; single nucleotide polymorphism; human; diagnosis; DNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX XX WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIC-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 331999; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTTGGCGA 17
Db 12 GGGAGTTGGCGA 1
RESULT 163
AAD55093
ID AAD55093 standard; DNA; 12 BP.
XX AC
XX AD55093;
XX XX
XX DT 07-AUG-2003 (first entry)
XX XX
XX DE ShDN256 primer #2 used in the synthesis of DNA molecules.
XX XX
XX KW Gene expression; DNA microchip; gene therapy; primer; ss.
XX OS Unidentified.
XX XX
XX PN WO2003020979-A1.
XX XX
XX PD 13-MAR-2003.
XX XX
XX PF 17-JUL-2002; 2002WO-US022787.
XX XX

PR 31-AUG-2001; 2001US-0316648P.
XX XX
XX PA (ROSE-) ROSETTA INPHARMATICS INC.
XX XX
XX PI Shoemaker DD, Armour CD, Garrett-Englele P;
XX XX
XX DR WPI; 2003-300903/29.
XX XX
XX XX Synthesizing DNA molecules useful for generating gene expression
PT profiles, comprises utilizing RNA molecules as templates to prime the
PT enzymatic synthesis of DNA molecules complementary to the template RNA
PT molecules.
XX XX
XX PS Disclosure; Page 56; 58pp; English.
XX XX
XX CC The invention relates to a method of synthesizing DNA molecules useful
CC for generating gene expression profiles. The method involves utilizing
CC RNA molecules as templates to prime the enzymatic synthesis of DNA
CC molecules complementary to the template RNA molecules. The method is
CC useful in preparing nucleic acid samples that are useful for screening
CC populations of immobilised nucleic acid molecules such as DNA molecules
CC immobilised on a DNA microchip. The method may also be used in generating
CC gene expression profiles for purposes of screening, diagnosing or staging
CC a disease, monitoring a response to therapy, or identifying genetic
CC targets of drugs and of pathogens. The processed DNA samples may be
CC utilised in any experiment, process or therapeutic treatment that
CC requires DNA. The invention is useful in gene therapy. The present
CC sequence is a primer used in the synthesis of DNA molecules
XX XX
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTTG 13
Db 1 TAGATGCTGTTG 12
RESULT 164
AAQ53394/c
ID AAQ53394 standard; RNA; 13 BP.
XX XX
XX AC AAQ53394;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-JUN-1994 (first entry)
XX XX
XX DE Liver RNA fingerprint band 16 P36 primer target sequence.
XX XX
XX KW mRNA; analysis; poly(A)+ RNA; prepn; cDNA; pattern; myoma; uterus;
KW neoplastic human tumours; ss.
XX OS Synthetic.
XX XX
XX PN WO9324655-A1.
XX XX
XX PD 09-DEC-1993.
XX XX
XX PF 27-MAY-1993; 93WO-GB001102.
XX XX
XX PR 27-MAY-1992; 92EP-00304790.
XX XX
XX PA (AMSH) AMERSHAM INT PLC.
XX XX
XX PI Chenchik AA, Diachenko LB, Beabashvili RS, Carter CJ;
XX DR WPI; 1993-405843/50.
XX XX
XX XX Prodn. of RNA fingerprint from poly(A) plus RNA or single-stranded cDNA
PT derived from it - using oligo-nucleotide primers, nucleotide(s) and a
PT terminator nucleotide.

XX Example; Page 25; 43pp; English.

XX This is the target sequence of the band 16 P36 primer which was used as

CC part of the prodn. of an RNA fingerprint of a poly(A)+ RNA prepn. . It has

CC been identified in cytochrome p450 and cysteine proteinase inhibitor RNA

CC (Genbank references HUMCYP219 (1088) and HUMINCP (1280)). The method is

CC useful for analysing and comparing the relative amts. of several hundred

CC of the more abundant individual mRNAs present in different poly(A)+ RNA

CC prepn. . It produces data that can be used to reveal poly(A)+ RNA/cDNA

CC pattern differences for a number of human tissues from several

CC individuals, and identifies changes in RNA patterns between normal

CC tissues and neoplastic human tumours (e.g. myoma of the uterus) and

CC during differentiation of F9 foetal carcinoma cells. Sequencing of the

CC isolated bands is sufficient to provide information for the

CC identification of differentially expressed genes in the GenBank database.

CC This information can be used to allow direct primer extension sequencing

CC of poly(A)+ RNA, PCR amplification/cloning, and identification of

CC differentially expressed genes from a cDNA library using hybridisation.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

XX

Query Match 48.9%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCGA 17

DB 13 GGCTGTGGCGA 2

RESULT 165

AAV11064

ID AAV11064 standard; RNA; 13 BP.

XX

AC AAV11064;

XX

DT 25-MAR-2003 (revised)

DT 14-JUL-1998 (first entry)

XX

XX Human ribozyme target sequence from HLA-DQB 10DQB.

XX

XX Ribozyme; target; human lymphocyte antigen; HLA-DQB; MHC allele;

XX major histocompatibility complex; cleavage; suppression; transplant;

XX incompatibility; autoimmune disease; juvenile diabetes;

XX rheumatoid arthritis; ss.

XX

OS Homo sapiens.

XX

XX WO9704087-A1.

XX

PD 06-FEB-1997.

XX

XX 18-JUL-1996; 96WO-EP003173.

XX

XX 18-JUL-1995; 95EP-00111256.

XX

XX (KRUP/) KRUPP G.

XX (MARG/) MARGET M.

XX (WEST/) WESTPHAL E.

XX (MUEL/) MUELLER-RUCHHOLTZ W.

XX

XX Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;

XX

XX WPI; 1997-132628/12.

XX

XX Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft

XX versus host reactions, to overcome blood incompatibility and to treat

XX auto:immune disease.

XX

XX Claim 5; Fig 1; 76pp; German.

XX

CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves

CC specific alleles from the major histocompatibility complex (MHC). This

CC ribozyme contains a catalytic region and a hybridisation region which is

CC complementary to all mRNA transcribed from vertebrate genes of a specific

CC family of closely related MHC alleles or to mRNA from a single MHC

CC allele, and is able to cleave such mRNA. The mRNA has a target region

CC which in case is essentially conserved in all genes of the family but

CC differs from genes of all other MHC alleles to such a degree that no

CC cleavage of mRNA transcribed from these other alleles occurs. This allows

CC the selective reduction or inhibition of expression of all genes of a

CC family or of a single gene. This ribozyme can be used for permanent or

CC transient suppression of expression of MHC alleles, in vivo or in vitro.

CC Specific applications are to prevent guest vs. host or host vs. guest

CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus

CC and Kell systems) and to treat autoimmune diseases such as juvenile

CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the

CC need for immunosuppressants in transplant patients. It provides very

CC specific reduction of particular HLA molecules that cause incompatibility

CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA

CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

XX Sequence 13 BP; 1 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

XX

Query Match 48.9%; Score 8.8; DB 1; Length 13;

Best Local Similarity 58.3%; Pred. No. 1.7e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCGA 17

DB 2 GCCUGUUGCGA 13

RESULT 166

AAV11109

ID AAV11109 standard; RNA; 13 BP.

XX

AC AAV11109;

XX

DT 25-MAR-2003 (revised)

DT 14-JUL-1998 (first entry)

XX

XX Human ribozyme target sequence from HLA-DRB 16DRB #3.

XX

XX Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;

XX major histocompatibility complex; cleavage; suppression; transplant;

XX incompatibility; autoimmune disease; juvenile diabetes;

XX rheumatoid arthritis; ss.

XX

OS Homo sapiens.

XX

XX WO9704087-A1.

XX

PD 06-FEB-1997.

XX

XX 18-JUL-1996; 96WO-EP003173.

XX

XX 18-JUL-1995; 95EP-00111256.

XX

XX (KRUP/) KRUPP G.

XX (MARG/) MARGET M.

XX (WEST/) WESTPHAL E.

XX (MUEL/) MUELLER-RUCHHOLTZ W.

XX

XX Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;

XX

XX WPI; 1997-132628/12.

XX

XX Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft

XX versus host reactions, to overcome blood incompatibility and to treat

XX auto:immune disease.

XX

XX Claim 5; Fig 1; 76pp; German.

XX

CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
 CC specific alleles from the major histocompatibility complex (MHC). This
 CC ribozyme contains a catalytic region and a hybridisation region which is
 CC complementary to all mRNA transcribed from vertebrate genes of a specific
 CC family of closely related MHC alleles or to mRNA from a single MHC
 CC allele, and is able to cleave such mRNA. The mRNA has a target region
 CC which in case is essentially conserved in all genes of the family but
 CC cleavage of mRNA transcribed from these other alleles occurs. This allows
 CC the selective reduction or inhibition of expression of all genes of a
 CC family or of a single gene. This ribozyme can be used for permanent or
 CC transient suppression of expression of MHC alleles, in vivo or in vitro.
 CC Specific applications are to prevent guest vs. host or host vs. guest
 CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
 CC and Kell systems) and to treat autoimmune diseases such as juvenile
 CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
 CC need for immunosuppressants in transplant patients. It provides very
 CC specific reduction of particular HLA molecules that cause incompatibility
 CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 13 BP; 1 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 58.3%; Pred. No. 1.7e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCGA 17

Db 2 GCGUUGCCGA 13

RESULT 167

ABF37605/C
 ID ABF37605 standard; DNA; 13 BP.

XX AC ABF37605;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 137602 for detecting SNP TSC0034395.

XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 137602; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGCGCTGTGG 14

Db 13 TTAGGATGTGG 2

RESULT 168

ABC59513/C
 ID ABC59513 standard; DNA; 13 BP.

XX AC ABC59513;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 59530 for detecting SNP TSC0015945.

XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 59530; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 30186; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTCG 14
Db 12 TGAGGGTTTGG 1
|||||

RESULT 172
ABF44123/C
ID ABF44123 standard; DNA; 13 BP.
XX
AC ABF44123;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144120 for detecting SNP TSC0036202.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 144120; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTCG 13
Db 12 TTGRTGTGTTCG 1
|||||

RESULT 173
ABC19815/C
ID ABC19815 standard; DNA; 13 BP.
XX
AC ABC19815;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 19832 for detecting SNP TSC0004095.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 19832; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

```
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 4 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 13
Db 13 TTGAGGCGGTGG 2

RESULT 174
ABC20130
ID ABC20130 standard; DNA; 13 BP.
XX
AC ABC20130;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 20147 for detecting SNP TSC0004134.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 20147; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 13
Db 2 TTGAGGCTGTGG 13

RESULT 175
ABC21255/c
ID ABC21255 standard; DNA; 13 BP.
XX
AC ABC21255;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 21272 for detecting SNP TSC0004284.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 21272; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGG 14
Db 13 TGAGGCGGTGG 2

RESULT 176
ABC03600
ID ABC03600 standard; DNA; 13 BP.
XX
AC ABC03600;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 3591 for detecting SNP TSC0001380.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 3591; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGG 14
Db 1 TAAGGTTGTGG 12
RESULT 177
ABC89242
ID ABC89242 standard; DNA; 13 BP.
XX AC ABC89242;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 89259 for detecting SNP TSC0022389.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.

central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
SEQ ID NO 89259; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGG 14
Db 1 TAAGGTTGTGG 12
RESULT 177
ABC89242
ID ABC89242 standard; DNA; 13 BP.
XX AC ABC89242;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 89259 for detecting SNP TSC0022389.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 89259; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTGG 13
Db 2 TTGAGGTTATTG 13
RESULT 178
ABC52204
ID ABC52204 standard; DNA; 13 BP.
XX AC ABC52204;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 52221 for detecting SNP TSC0014517.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 52221; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGCGA 17
 Db 1 GGTGTTGGTGA 12
 |||||

RESULT 179
 ABC30168
 ID ABC30168 standard; DNA; 13 BP.
 XX
 AC ABC30168;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 30185 for detecting SNP TSC0009149.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 30185; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTGG 14
 Db 2 TGAGGCTTTGG 13
 |||||

RESULT 180
 ABH32317/c
 ID ABH32317 standard; DNA; 13 BP.
 XX
 AC ABH32317;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 232294 for detecting SNP TSC0004542.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 232294; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTG 13
 Db 12 TTGAGGAGGTG 1
 |||||

RESULT 181
 ABC30166
 ID ABC30166 standard; DNA; 13 BP.
 XX


```
AC ABC30166;
XX
XX
DT 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 30183 for detecting SNP TSC0009149.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 30183; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 3 TGAGGCTGTGG 14
Db 2 TGAGATTTTGG 13
|||||
RESULT 182
ABF27833/C
ID ABF27833 standard; DNA; 13 BP.
XX
XX ABF27833;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 127830 for detecting SNP TSC0032007.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 127830; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 3 TGAGGCTGTGG 14
Db 2 TGAGATTTTGG 13
|||||
RESULT 182
ABF27833/C
ID ABF27833 standard; DNA; 13 BP.
XX
XX ABF27833;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 127830 for detecting SNP TSC0032007.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 127830; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 TTGAGGCTGTGG 13
Db 13 TTGAGTTTGTG 2
|||||
RESULT 183
ABF36581/C
ID ABF36581 standard; DNA; 13 BP.
XX
XX ABF36581;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 136578 for detecting SNP TSC0034131.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX
```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 136578; 29pp + Sequence Listing; German.

PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTGAGGCTGTGG 14

Db 12 TTGAGGCTGTGG 1

RESULT 184

ABH11623/C

ID ABH11623 standard; DNA; 13 BP.

XX AC ABH11623;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 211600 for detecting SNP TSC0051606.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 211600; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 13

Db 13 TTGAGGCTGTAG 2

RESULT 185

ABF29703/C

ID ABF29703 standard; DNA; 13 BP.

XX AC ABF29703;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 129700 for detecting SNP TSC0032456.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 129700; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 13


```

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 102119; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGAGGCTGTG 13
Db 2 TTGAGGATGTG 13
XX
XX RESULT 189
XX ABF09481/C
XX ID ABF09481 standard; DNA; 13 BP.
XX AC ABF09481;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 109478 for detecting SNP TSC0027391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 109478; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGAGGCTGTG 13
Db 2 TTGAGGATGTG 13
XX
XX RESULT 189
XX ABF09481/C
XX ID ABF09481 standard; DNA; 13 BP.
XX AC ABF09481;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 109478 for detecting SNP TSC0027391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 109478; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3 TGAGGCTGTGG 14
Db 13 TGAGGTTGTAGG 2
XX
XX RESULT 190
XX ABF27831/C
XX ID ABF27831 standard; DNA; 13 BP.
XX AC ABF27831;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 127828 for detecting SNP TSC0032007.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 127828; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

```

```
XX SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 13
Db 13 TTGAGTATGTGG 2

RESULT 191
ABF37604
ID ABF37604 standard; DNA; 13 BP.
XX AC ABF37604;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 137601 for detecting SNP TSC0034395.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX AC ABF37604;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 137601 for detecting SNP TSC0034395.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX Claim 1; SEQ ID NO 137601; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTGAGGCTGTGG 14
Db 1 TTGAGTATGTGG 12

RESULT 192
ABF09480
ID ABF09480 standard; DNA; 13 BP.
XX AC ABF09480;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 109477 for detecting SNP TSC0027391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX Claim 1; SEQ ID NO 21271; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTGG 14
Db 1 TGAGCGCGGTGG 12

RESULT 193
ABF09480
ID ABF09480 standard; DNA; 13 BP.
XX AC ABF09480;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 109477 for detecting SNP TSC0027391.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX Claim 1; SEQ ID NO 21271; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 109477; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGG 14
Db 1 TGAGGTTGTAGG 12
|||||
RESULT 194
ABF23512
ID ABF23512 standard; DNA; 13 BP.
XX
AC ABF23512;
XX
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 123509 for detecting SNP TSC0030884.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 123509; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGCG 16
Db 2 AGGTAGTGGCG 13
|||||
RESULT 195
ABF27832
ID ABF27832 standard; DNA; 13 BP.
XX
AC ABF27832;
XX
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 127829 for detecting SNP TSC0032007.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 127829; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 13
Db 1 TTGAGTTGTG 12

RESULT 196

ABF36580
ID ABF36580 standard; DNA; 13 BP.

AC ABF36580;

XX
XX
DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 136577 for detecting SNP TSC0034131.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.

XX WO200177384-A2.

FN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 136577; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 1 A; 0 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGG 14
Db 2 TGAGGCTGTGG 13

RESULT 197

ABF44122
ID ABF44122 standard; DNA; 13 BP.

XX
AC ABF44122;

XX
DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 144119 for detecting SNP TSC0036202.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.

XX WO200177384-A2.

FN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 144119; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 13
Db 2 TTGAGTTGTG 13

RESULT 198

ABC17883/C
ID ABC17883 standard; DNA; 13 BP.

XX
AC ABC17883;

XX

```

DT 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 17890 for detecting SNP TSC0003824.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 17890; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTG 13
DB 12 TTAAGGTATTG 1
RESULT 199
ABC89243/C
ID ABC89243 standard; DNA; 13 BP.
XX
XX ABC89243;
AC
XX
XX 21-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 89260 for detecting SNP TSC0022389.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 17890; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTG 13
DB 12 TTAAGGTATTG 1
RESULT 200
ABF23513/C
ID ABF23513 standard; DNA; 13 BP.
XX
XX ABF23513;
AC
XX
XX 21-FEB-2002 (first entry)
DT
DE Oligonucleotide SEQ ID NO 123510 for detecting SNP TSC0030884.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 89260; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTG 13
DB 12 TTAAGGTATTG 1

```


PT methylation status.
PS Claim 1; SEQ ID NO 123510; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGG 16
Db 12 AGGTAGTGGG 1
|||||
|
RESULT 201
ABF48775/c
ID ABF48775 standard; DNA; 13 BP.
XX AC ABF48775;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 148772 for detecting SNP TSC0037553.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 148772; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGG 16
Db 12 AGGTAGTGGG 1
|||||
|
RESULT 202
ABF02123/c
ID ABF02123 standard; DNA; 13 BP.
XX AC ABF02123;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 102120 for detecting SNP TSC0025437.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 102120; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 12 TTGAGGCTGTG 1
|||||
|
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTG 13
Db 12 TTGAGGCTGTG 1
|||||
|

```
RESULT 203
ABC52205/c
ID ABC52205 standard; DNA; 13 BP.
XX AC ABC52205;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 52222 for detecting SNP TSC0014517.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 52222; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GGCTGTGGCGCA 17
DB 13 GGTGTGGTGA 2
RESULT 204
ABC03601/c
ID ABC03601 standard; DNA; 13 BP.
XX AC ABC03601;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 3592 for detecting SNP TSC0001380.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 52222; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TGAGGCTGTGG 14
DB 13 TAAGGTGTGG 2
RESULT 205
ABC59512
ID ABC59512 standard; DNA; 13 BP.
XX AC ABC59512;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 59529 for detecting SNP TSC0015945.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX DR
```

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 59529; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 TGAGGCTGTTGG 14
 Db 1 TGAGATGTTGG 12
 ||||| |||||
 ||||| |||||

RESULT 206
 ABF27830
 ID ABF27830 standard; DNA; 13 BP.
 XX AC ABF27830;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 127827 for detecting SNP TSC0032007.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 127827; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TTGAGGCTGTTG 13
 Db 1 TTGAGTATGTTG 12
 ||||| |||||
 ||||| |||||

RESULT 207
 ABF29702
 ID ABF29702 standard; DNA; 13 BP.
 XX AC ABF29702;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 129699 for detecting SNP TSC0032456.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 129699; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 1 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
 SQ

```
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTGAGGCTGTG 13
Db 1 TTGATGCGGTG 12
|||||
|

RESULT 208
ABC20131/c
ID ABC20131 standard; DNA; 13 BP.
XX
AC ABC20131;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 20148 for detecting SNP TSC0004134.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 20148; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTGAGGCTGTG 13
Db 12 TTTAGGTGTG 1
|||||
|

RESULT 209
ABC17882
ID ABC17882 standard; DNA; 13 BP.
XX
AC ABC17882;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 148771 for detecting SNP TSC0037553.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
```

```
XX
AC ABC17882;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 17889 for detecting SNP TSC0003824.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 17889; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTGAGGCTGTG 13
Db 2 TTAAGGTGTG 13
|||||
|

RESULT 210
ABF48774
ID ABF48774 standard; DNA; 13 BP.
XX
AC ABF48774;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 148771 for detecting SNP TSC0037553.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
```

```

PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (SPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 148771; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTG 13
Db 2 TTGAGGTTGTAG 13
RESULT 211
ABS60659
ID ABS60659 standard; DNA; 13 BP.
AC
AC ABS60659;
DT
DT 05-NOV-2002 (first entry)
DE
DE Human DNA representing a single nucleotide polymorphism #210.
XX
XX Aminopeptidase P; XPNEP2; bradykinin receptor B1; ds; SNP; BDKRB1;
XX tachykinin receptor B1; TACR1; C1 esterase inhibitor (CINH); kallikrein 1;
XX KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
XX autoimmune disease; inflammatory arthritis; cancer; wound;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis;
XX single-nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX

```

```

XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX
XX 23-JAN-2001; 2001US-0263678P.
XX
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUIL/) HUI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX Swanson EN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Disclosure; Page 859; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (CINH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX polymorphic position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX obtaining the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX; (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasoconstrictor inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX and compositions are useful for detecting, diagnosing, treating,
XX preventing various disorders such as angioedema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hyperaerisativity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polymorphisms are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence represents or contains the
XX region surrounding a single-nucleotide polymorphism in one of the genes
XX encoding one of the proteins listed above
XX
XX Sequence 13 BP; 2 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTGGC 15
Db 1 GAAGCTGTGGC 12

```

```

AAZ79478
ID AAZ79478 standard; DNA; 10 BP.
AC AAZ79478;
XX
XX 10-APR-2000 (first entry)
XX Human dendritic cell SAGE tag, SEQ ID NO:1906.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-008991P.
XX 19-JUN-1998; 98US-0089922P.
XX 19-JUN-1998; 98US-0089933P.
XX 19-JUN-1998; 98US-0089944P.
XX 19-JUN-1998; 98US-008997P.
XX 19-JUN-1998; 98US-008999P.
XX 19-JUN-1998; 98US-009000P.
XX 19-JUN-1998; 98US-0090035P.
XX 19-JUN-1998; 98US-0090036P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX 19-JUN-1998; 98US-0090042P.
XX 19-JUN-1998; 98US-0090043P.
XX 19-JUN-1998; 98US-0090044P.
XX 19-JUN-1998; 98US-0090045P.
XX 19-JUN-1998; 98US-0090047P.
XX 19-JUN-1998; 98US-0090048P.
XX 19-JUN-1998; 98US-0090072P.
XX 19-JUN-1998; 98US-0090076P.
XX 19-JUN-1998; 98US-0090077P.
XX 19-JUN-1998; 98US-0090078P.
XX 19-JUN-1998; 98US-0090079P.
XX 19-JUN-1998; 98US-0090080P.
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 119; 130pp; English.
XX
XX Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell

```

```

CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TCAGGCTGTT 12
DB 1 TCAGGCTGTT 10
RESULT 213
AAZ82953
ID AAZ82953 standard; DNA; 10 BP.
XX
XX AAZ82953;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #2187.
DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-008997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and

```

```

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 118; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunosays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX immunotherapy
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14
Db 1 AGGCTATGG 10

RESULT 214
AAZ84008
ID AAZ84008 standard; DNA; 10 BP.
XX
AC AAZ84008;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3242.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 145; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunosays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX immunotherapy
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 17
Db 1 CTGATGGCGA 10

RESULT 215
AAZ82804
ID AAZ82804 standard; DNA; 10 BP.
XX
AC AAZ82804;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2038.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.

```

```

XX WPI; 2000-106079/09.
DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 114; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in the primary or non-metastatic breast tumour
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGAGGCTGTT 12
DB 1 TCAGGCTGTT 10
RESULT 216
AAZ82395
ID AAZ82395 standard; DNA; 10 BP.
AC
AC AAZ82395;
XX
DT 07-APR-2000 (first entry)
DE
DE Metastatic breast tumour cell upregulated transcript tag #1629.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.

```

```

XX Roberts BL, Shankara S;
PI
XX WPI; 2000-106079/09.
DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 102; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in the primary or non-metastatic breast tumour
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCTGTGGCG 16
DB 1 GCTGTGGTG 10
RESULT 217
AAC74125
ID AAC74125 standard; cDNA; 10 BP.
AC
AC AAC74125;
XX
XX 02-FEB-2001 (first entry)
DE
DE Human monocyte and dendritic cell expressed gene oligonucleotide #212.
XX
XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
XX
XX Homo sapiens.
XX
XX WO200060074-A1.
XX
XX 12-OCT-2000.
XX
XX 30-MAR-2000; 2000WO-JP002019.
XX
XX 01-APR-1999; 99JP-00095481.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Hashimoto S, Matsushima K, Suzuki T;
XX WPI; 2000-619172/59.
XX

```


PT Groups of genes expressed in human dendritic cells at a greater or lesser
 PT extent than in monocytes for investigation and diagnosis of autoimmune
 PT disease and tumors.

XX Claim 19; Page 15; 95pp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterized in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGGCGA 17

DB 1 CTGATGGCGA 10

RESULT 218

AAA56499

ID AAA56499 standard; DNA; 10 BP.

AC AAA56499;

XX 07-SEP-2000 (first entry)

XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:393.

XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.

XX Homo sapiens.

XX WO200024892-A1.

XX 04-MAY-2000.

XX 28-OCT-1999; 99WO-JP005982.

XX 28-OCT-1998; 98JP-00307532.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Hashimoto S, Matsushima K, Suzuki T;

XX WPI; 2000-350734/30.

XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.

XX Claim 37; Page 117; 138pp; Japanese.

XX The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody

CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
 CC specifically claimed oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGGCGA 17

DB 1 CTGATGGCGA 10

RESULT 219

AAA56172

ID AAA56172 standard; DNA; 10 BP.

AC AAA56172;

XX 07-SEP-2000 (first entry)

XX Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:66.

XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.

XX Homo sapiens.

XX WO200024892-A1.

XX 04-MAY-2000.

XX 28-OCT-1999; 99WO-JP005982.

XX 28-OCT-1998; 98JP-00307532.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Hashimoto S, Matsushima K, Suzuki T;

XX WPI; 2000-350734/30.

XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.

XX Claim 1; Page 52; 138pp; Japanese.

XX The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody
 CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by

CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
XX
QY 8 CTGTTGGCGA 17
DB 1 CTGTTGGTGA 10
RESULT 220
AAA56442
ID AAA56442 standard; DNA; 10 BP.
XX
AC AAA56442;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:336.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1998; 98JP-00307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.
XX
PT Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
PS Claim 25; Page 106; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 CTGTTGGCGA 17
DB 1 CTGATGCGA 10
RESULT 221
AAA56393
ID AAA56393 standard; DNA; 10 BP.
XX
AC AAA56393;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:287.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1998; 98JP-00307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.
XX
PT Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
PS Claim 13; Page 96; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 CTGTTGGCGA 17

```
Db      ||||| ||
        1 CTGTGGTGA 10

RESULT 222
AAH99860
ID   AAA99860 standard; DNA; 10 BP.
XX
AC   AAA99860;
XX
DT   06-AUG-2003 (revised)
DT   26-JAN-2001 (first entry)
XX
XX   Prokaryote RT-PCR primer PCR2.
DE
XX   Prokaryote; gene identification; environmental stimulus; gene regulation;
KW   bioprocess fermentation; PCR primer; ss.
XX   Bacteria.
XX
XX   WO200056936-A1.
XX
XX   28-SEP-2000.
XX
XX   24-MAR-2000; 2000WO-US007912.
XX
XX   25-MAR-1999; 99US-0126038P.
XX
XX   (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
XX   Bentley WE, Gill RT;
XX
XX   WPI; 2000-587669/55.
XX
XX   Performing differential display of prokaryotic mRNA by a RT (reverse
PT   transcriptase)/RAP (random arbitrary-primed) PCR based technique comprises
PT   using a unique combination of random primers in a single amplification
PT   step.
XX
XX   Claim 1; Page 19; 63pp; English.
XX
XX   The present invention is concerned with a method of differential display
CC   of prokaryotic mRNA by RT-PCR. This involves the amplification of the
CC   mRNA once, and the further amplification of the cDNA, rather than the
CC   repeated amplification of the mRNA sample. It also eliminates the need
CC   for sequencing gels using Northern and total RNA dot blots to confirm
CC   differentially displayed transcript levels. The primers AAA99849-A99868
CC   were used in a reverse transcription PCR amplification, and primers
CC   AAA99869-A99876 were used to prepare probes for a Northern blot analysis.
CC   The method can be used to rapidly identify genes with increased or
CC   decreased transcription following environmental stimuli, in bioprocess
CC   fermentations, and to analyse gene regulation. (Updated on 06-AUG-2003 to
CC   correct OS field.)
XX
XX   Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCTGTGGCG 16
Db      ||||| ||
        1 GCTGTGGCG 10

RESULT 223
AAH63507
ID   AAH63507 standard; cDNA; 10 BP.
XX
AC   AAH63507;
XX
XX   20-SEP-2001 (first entry)
DT
XX
```

```
DE
XX   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 347.
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
XX   Homo sapiens.
XX
XX   WO200138577-A2.
XX
XX   31-MAY-2001.
XX
XX   21-NOV-2000; 2000WO-US031922.
XX
XX   24-NOV-1999; 99US-00448480.
XX
XX   (UYJO ) UNIV JOHNS HOPKINS.
XX
XX   Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX   WPI; 2001-367706/38.
XX
XX   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
XX   Claim 13; Page 46; 94pp; English.
XX
XX   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
XX   Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CTGTGGCGA 17
Db      ||||| ||
        1 CTGTGGTGA 10

RESULT 224
AAH32809
ID   AAH32809 standard; cDNA; 10 BP.
XX
AC   AAH32809;
XX
XX   13-AUG-2001 (first entry)
DT
XX
XX   LPS activated human monocyte expression gene cDNA tag SEQ:182.
DE
XX   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX   Homo sapiens.
XX
XX   JP2001069993-A.
XX
XX   21-MAR-2001.
XX
XX   28-APR-2000; 2000JP-00131079.
XX
XX   08-JUL-1999; 99JP-00195103.
XX
XX   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX   WPI; 2001-304369/32.
```

```
XX LPS activated human monocyte expression gene group.
PT
XX
PS Claim 19; Page 34; 52pp; Japanese.
XX
XX The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGCCGA 17
DB 1 CTGATGCCGA 10

RESULT 225
ABA06207
ID ABA06207 standard; cDNA; 10 BP.
XX
AC ABA06207;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 184.
XX
XX Human; hepatocyte; gene expression; hepatopathy; ss.
XX
XX Homo sapiens.
XX
XX JP2001211883-A.
XX
PD 07-AUG-2001.
XX
XX 31-JAN-2000; 2000JP-00023170.
XX
PR 31-JAN-2000; 2000JP-00023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2001-629566/73.
XX
XX Human normal hepatocyte expression gene group.
PT
PS Claim 1; Page 9; 26pp; Japanese.
XX
XX The invention relates to a human normal hepatocyte expression gene group
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
CC gene comprises one of 200 fully defined nucleotide sequences as given in
CC the specification. The gene group and the cDNAs corresponding to each of
CC the genes in the group are useful in the diagnosis and treatment of human
CC hepatopathy. The present sequence is a cDNA corresponding to a gene
CC expressed by normal human hepatocytes
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGCCGA 17
DB 1 CTGTTGGTGA 10

RESULT 226
AAF38690/c
ID AAF38690 standard; DNA; 10 BP.
XX
AC AAF38690;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5429.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO2000077214-A2.
PN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
PI
XX WPI; 2001-061874/07.
DR
XX
XX Yeast Gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 193; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
```

Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
| | | | |
Db 10 TGAGGCTGTT 1

RESULT 227
AAF37013/c
ID AAF37013 standard; DNA; 10 BP.

AC AAF37013;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3752.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 134; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
| | | | |
Db 10 TGAGGCTATT 1

RESULT 228

AAF39203/c

ID AAF39203 standard; DNA; 10 BP.

XX AAF39203;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5942.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 212; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.

```
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
    Query Match      46.7%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 2e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGT 11
    ||||| |||
Db 10 TTGAGGATGT 1

RESULT 229
AAF36787
ID AAF36787 standard; DNA; 10 BP.
XX
AC AAF36787;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3526.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 125; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
```

```
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
    Query Match      46.7%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 2e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
    ||||| |||
Db 1 TGAGGCAGTT 10

RESULT 230
AAH42233
ID AAH42233 standard; DNA; 10 BP.
XX
AC AAH42233;
XX
DT 17-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a SAGE tag.
XX
KW Serial analysis of gene expression tag; SAGE tag; gene identification;
KW GLGI; gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200148247-A2.
XX
XX 05-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US035579.
XX
XX 29-DEC-1999; 99US-0173617P.
XX
XX 03-JAN-2000; 2000US-0174391P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Wang SM, Chen J, Rowley JD;
XX
XX WPI; 2001-441722/47.
XX
XX Generating longer cDNA fragments from serial analysis of gene expression,
XX SAGE tags for gene identification, using SAGE tag sequence as sense
XX primer, single-base anchored oligo-dT as antisense primer for
XX amplification.
XX
XX Example 2; Page 38; 62pp; English.
XX
XX AAF42227-44 represent SAGE (serial analysis of gene expression) tags,
XX isolated from human colon tissue. The specification describes a method
XX for characterizing SAGE tag fragments. The method comprises obtaining RNA
XX from the tissue used in generating the SAGE tag, generating cDNA
XX fragments that correspond to the SAGE tag from the RNA by amplifying
XX using primers comprising a SAGE tag sequence as a sense primer and a
XX single-base anchored oligonucleotide primer as an antisense primer and a
XX analysing the cDNA fragments. The method is useful for converting a SAGE
XX tag sequence into a longer cDNA fragment containing up to several 100
XX bases from the SAGE tag to the 3' end of the corresponding cDNA, for gene
XX identification. The high-throughput generation of longer SAGE tags for
XX gene identification (GLGI) procedure has several applications, including
XX wider application of SAGE technique for quantitative analysis of global
XX gene expression and to identify the 3' DNA sequence from any exon within
XX a gene. The combined application of SAGE/GLGI can be applied to define
XX the 3' boundary of expressed genes in the genomic sequences in humans and
XX in other eukaryotic genomes
XX
XX Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
```

```
Query Match      46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTTGGCGA 17
DB      1 CTGTTGGTGA 10

RESULT 231
ABQ71507
ID ABQ71507 standard; DNA; 10 BP.
XX AC
XX AC
XX ABQ71507;
DT 28-AUG-2002 (first entry)
DE Zinc finger protein related oligonucleotide target SEQ ID NO:626.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX WO200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 45; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subsite. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subsite, selecting the F2 zinc finger such that it
XX binds to the S2 target subsite, and selecting the F3 zinc finger such
XX that it binds to the S3 target subsite, thus designing (I) that binds to
XX a target site. (I) is useful for recognition of triplet target subsites
XX having the nucleotide G in the 5'-most position of the subsite. (I) is
XX useful in studying gene function, and for human therapeutics and plant
XX engineering. (I), (II) or (III) is useful in therapeutic methods to
XX modulate the expression of a target region within a subject, in
XX diagnostic methods for sequence specific detection of target nucleic acid
XX in a sample, and in assays to determine the phenotype and function of
XX gene expression. (I) has improved affinity and specificity for their
XX target sequences, as well as enhanced biological activity. ABQ71213 to
XX ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX finger peptides which are given in the exemplification of the present
XX invention
XX
XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTTGGCGA 17
DB      1 CTGTTGGTGA 10

RESULT 233
ADA26780
ID ADA26780 standard; cDNA; 10 BP.
XX AC
XX AC
XX ADA26780;
DT 20-NOV-2003 (first entry)
XX
```

```
QY      4 GAGGCTGTG 13
DB      1 GAGGCTGTG 10

RESULT 232
ABK23412
ID ABK23412 standard; DNA; 10 BP.
XX AC
XX AC
XX ABK23412;
DT 09-APR-2002 (first entry)
DE Transcript tag DNA sequence #1 induced or suppressed by N-myc.
XX
XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;
XX myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
XX Homo sapiens.
XX OS
XX WO200185941-A2.
XX
XX 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-NL000361.
XX
XX 11-MAY-2000; 2000EP-00201698.
XX
XX 29-JUN-2000; 2000EP-00202284.
XX
XX (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
XX Versteeg R, Caron HN;
XX WPI; 2002-066603/09.
XX
XX A new nucleic acid library of myc-dependent downstream genes capable of
XX supporting a neoplastic characteristic of cancer is useful to find new
XX therapies and diagnoses for cancer.
XX
XX Disclosure; Page 49; 69pp; English.
XX
XX The present invention relates to a nucleic acid library comprising myc-
XX dependent downstream genes or their functional fragments essentially
XX capable of supporting a neoplastic character of cancer such as growth,
XX invasion or spread. These myc target or tag sequences are identified by
XX SAGE (serial analysis of gene expression). The library is useful to find
XX new diagnoses and treatments for cancer. The invention is also useful to
XX enhance production of recombinant proteins in a production system with
XX high expression of endogenous or transfected myc oncogenes. ABK23412-
XX ABK23828 represent transcript tag DNA sequences that are activated or
XX repressed by N-myc in human neuroblastoma
XX
XX Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match      46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTTGGCGA 17
DB      1 CTGTTGGTGA 10

RESULT 233
ADA26780
ID ADA26780 standard; cDNA; 10 BP.
XX AC
XX AC
XX ADA26780;
DT 20-NOV-2003 (first entry)
XX
```

DE Human rhophilin-like SAGE tag #26.
XX Metastasis; neoplastic growth; detection; prediction;
KW neoplastic growth marker; drug screening; cancer; tumour;
KW gastrointestinal; prostate; breast; colorectal; diagnostic imaging;
KW drug targeting; human; cytostatic; serial analysis of gene expression;
XX SAGE tag; ss.
XX Homo sapiens.
XX WO2003031930-A2.
XX 17-APR-2003.
XX 02-OCT-2002; 2002WO-US031247.
XX 09-OCT-2001; 2001US-0327332P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW, Saha S, Bardelli A;
XX WPI; 2003-393457/37.
XX Identifying regions of neoplastic growth in a human body, useful for
XX detecting or predicting metastasis, comprises administering to the human
XX body an antibody or peptide that specifically binds to a protein marker
XX of neoplastic growth.
XX Example 2; Page 21; 42pp; English.
XX The invention relates to methods for identifying regions of neoplastic
XX growth in a human patient, especially for detecting or predicting
XX metastasis. The methods involve determining whether a neoplastic growth
XX marker protein is overexpressed, either by the use of an antibody
XX specific for the protein, or by the use of PCR or hybridisation to detect
XX nucleic acids encoding the marker proteins. A set of neoplastic growth
XX markers are disclosed (SAGE (serial analysis of gene expression) tags for
XX these are given in ADA26759-ADA26796), with protein tyrosine phosphatase
XX type IVA member 3 (also known as PRL-3) being a preferred neoplastic
XX growth marker. The neoplastic growth markers are specifically expressed
XX at a higher level in metastatic cancers, compared with advanced and early
XX stage cancers and normal cells from which the cancer is derived.
XX Overexpression of the neoplastic growth markers is taken as an indication
XX that the tissue has a propensity to metastasise. The invention also
XX encompasses methods for treating a patient with an advanced or metastatic
XX cancer, and for identifying candidate drugs for treating advanced or
XX metastatic cancers. The methods of the invention are useful for
XX identifying regions of neoplastic growth, for detecting or predicting
XX metastasis, or identifying candidate drugs for treating advanced or
XX metastatic cancers. The invention is particularly applicable to
XX gastrointestinal, prostate, breast or colorectal cancers. Antibodies
XX which bind to the neoplastic growth marker proteins are additionally
XX useful for diagnostic imaging and for targeting cytotoxic or
XX chemotherapeutic drugs. The present sequence represents a human
XX neoplastic growth marker SAGE tag identified in an example of the
XX invention.
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTTGAGGCTG 10
|| |||||
Db 1 CTGAGGCTG 10
RESULT 234
ACA94457
ID ACA94457 standard; DNA; 10 BP.
XX

AC ACA94457;
XX 18-JUL-2003 (first entry)
XX DNA tag from human transcript elevated in adenomas/cancers #38.
DE Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
XX macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
KW kidney proximal tubule.
XX Homo sapiens.
OS WO2003022863-A1.
XX 20-MAR-2003.
XX 09-SEP-2002; 2002WO-US028518.
XX 07-SEP-2001; 2001US-0317494P.
XX 30-MAY-2002; 2002US-0383805P.
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA Buckhaults P, Kinzler KW, Vogelstein B;
XX WPI; 2003-313220/30.
XX Detecting colorectal cancer in a subject, involves detecting macrophage
XX inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
XX of the subject.
XX Disclosure; Page 25; 59pp; English.
XX The invention relates to detecting CC (colorectal cancer e.g. colorectal
XX adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
XX or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
XX amount of MIC or RDP detected to that in normal subjects, where an
XX elevated amount of MIC or RDP in the subject is an indicator of CC in
XX subject; (b) isolating mRNA sample from faeces of a subject, detecting
XX MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
XX mRNA detected to that in normal subjects, where an elevated amount of MIC
XX or RDP mRNA in the subject is an indicator of CC in subject; (c)
XX isolating epithelial cells from blood of a subject, isolating an mRNA
XX sample from faeces of a subject or epithelial cells, detecting MIC or RDP
XX mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
XX the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
XX an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
XX of CC in the subject; (d) contacting blood or faeces of a subject, with
XX an RDP substrate, detecting activity of RDP in the blood or faeces by
XX detection of increased reaction product or decreased RDP substrate, and
XX comparing the amount of activity of RDP in blood or faeces of the subject
XX to that in normal subjects, where an elevated amount of activity of RDP
XX in the blood or faeces of the subject is an indicator of CC in the
XX subject; (e) administering to a subject an antibody which specifically
XX binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
XX labeled with a moiety which is detectable from outside of the subject and
XX detecting the moiety in the subject from outside of the subject, where an
XX area of localisation of the moiety within the subject but outside the
XX proximal tubules of the kidney identifies CC; or (f) administering to a
XX subject a substrate for RDP, the substrate being labeled with a
XX detectable moiety, isolating faeces or blood from the subject, and
XX detecting in the faeces or blood RDP reaction product or RDP substrate
XX with the detectable moiety, where increased product or decreased
XX substrate in the faeces or blood indicates CC in the subject. The methods
XX are useful for detecting colorectal cancer in a subject. The present
XX sequence is a DNA tag derived from a human transcript whose expression is
XX elevated in colorectal cancer or colorectal adenoma
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
FT /note= "labelled with a Fluorescent dye leading to
FT fluorescent resonance energy transfer"
FT 11
FT /*tag= a
FT /note= "labelled with a Fluorescent dye leading to
FT fluorescent resonance energy transfer"
XX
XX JP10127300-A.
XX
XX 19-MAY-1998.
XX
XX 31-OCT-1996; 96JP-00290235.
XX
XX 31-OCT-1996; 96JP-00290235.
XX (HAMM ) HAMAMATSU PHOTONICS KK.
XX
XX WPI; 1998-340670/30.
XX
XX Detection of point mutation and detection of gene abnormality - using
XX probe with base sequence and fluorescent dye.
XX
XX Disclosure; Page 6; 14pp; Japanese.
XX
XX Oligonucleotide probes AAV29709-48 were used to exemplify the method of
XX the invention. This method detects the presence of a point mutation in a
XX specific sequence of a target nucleic acid. The method comprises using a
XX probe which is labelled at 5' and 3' ends with 2 different labels that
XX form fluorescent resonance energy transfer (FRET). The ratio of
XX fluorescence between both fluorescent dyes at the maximum fluorescent
XX absorption wavelength is measured. The fluorescence ratio indicated the
XX ratio of target/probe
XX
XX Sequence 11 BP; 1 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 7 GCTGTTGGCG 16
XX |||||
XX 2 GCTGGTGGCG 11
XX
XX
XX RESULT 238
XX AAV29730/C
XX ID AAV29730 standard; DNA; 11 BP.
XX
XX AC AAV29730;
XX
XX 03-AUG-1998 (first entry)
XX
XX Probe used to exemplify the method of the invention.
XX
XX Probe; point mutation; fluorescent resonance energy transfer; FRET;
XX fluorescent dye; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /note= "labelled with a Fluorescent dye leading to
XX fluorescent resonance energy transfer"
XX
XX modified_base 11
XX /*tag= a
XX /note= "labelled with a Fluorescent dye leading to
XX fluorescent resonance energy transfer"
XX
XX JP10127300-A.
XX
XX 19-MAY-1998.
```

```
PF 31-OCT-1996; 96JP-00290235.
XX
XX 31-OCT-1996; 96JP-00290235.
XX
XX (HAMM ) HAMAMATSU PHOTONICS KK.
XX
XX WPI; 1998-340670/30.
XX
XX Detection of point mutation and detection of gene abnormality - using
XX probe with base sequence and fluorescent dye.
XX
XX Disclosure; Page 6; 14pp; Japanese.
XX
XX Oligonucleotide probes AAV29709-48 were used to exemplify the method of
XX the invention. This method detects the presence of a point mutation in a
XX specific sequence of a target nucleic acid. The method comprises using a
XX probe which is labelled at 5' and 3' ends with 2 different labels that
XX form fluorescent resonance energy transfer (FRET). The ratio of
XX fluorescence between both fluorescent dyes at the maximum fluorescent
XX absorption wavelength is measured. The fluorescence ratio indicated the
XX ratio of target/probe
XX
XX Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 7 GCTGTTGGCG 16
XX |||||
XX 10 GCTGGTGGCG 1
XX
XX
XX RESULT 239
XX AAA72648/C
XX ID AAA72648 standard; DNA; 11 BP.
XX
XX AC AAA72648;
XX
XX 01-DEC-2000 (first entry)
XX
XX K-ras SW480 UDG-digest fragment SEQ ID #5.
XX
XX Uracil DNA glycosylase; UDG; infectious disease detection; cancer;
XX sickle cell anaemia; cystic fibrosis; thalassaemia; muscular dystrophy;
XX Tay-Sachs disease; K-ras; ss.
XX
XX Synthetic.
XX
XX OS US6090553-A.
XX
XX PN 18-JUL-2000.
XX
XX 29-OCT-1997; 97US-00959853.
XX
XX 29-OCT-1997; 97US-00959853.
XX
XX (BECI ) BECKMAN COULTER INC.
XX
XX Matson RS;
XX
XX WPI; 2000-531416/48.
XX
XX Detecting specific nucleic acid sequence in sample containing nucleic
XX acids involves amplifying nucleic acid, cleaving amplified products with
XX uracil-DNA glycosylase to obtain DNA segments and detecting segments.
XX
XX Example 2; Col 17; 21pp; English.
XX
XX A new method for detecting specific nucleic acid sequences in a sample
XX involves amplifying the nucleic acid sample by PCR and then cleaving the
XX amplified products with uracil DNA glycosylase (UDG), the resulting DNA
XX fragments are detected using reverse blot hybridisation techniques. The
```

CC method can be used to distinguish between two different sequences, for
 CC example for the detection of a DNA fragment carrying a mutation. The
 CC method is useful for detecting the presence or absence of a nucleic acid
 CC sequence containing a polymorphic restriction site associated with a
 CC disease such as cystic fibrosis disease, and may be used for detecting
 CC infectious diseases. Genetic disorders such as sickle cell anemia,
 CC cystic fibrosis, alpha or beta thalassemia, muscular dystrophy, and Tay-
 CC Sachs disease may also be detected using the method. Oncogenes such as
 CC RAS may also be detected using the method, for the diagnosis of certain
 CC cancers. The present sequence represents a fragment of the K-ras gene
 CC created by UNG cleavage. This sequence is used in an example of the
 CC invention and contains the position of a mutation site in K-ras SW480.
 CC This fragment and the corresponding mutant containing fragment (AAA72649)
 CC can be used to produce probes specifically to identify the mutation,
 CC which can then be used in the method of the invention

XX SQ Sequence 11 BP; 3 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
 |||||
 Db 11 GCTGTTGGCG 2

RESULT 240
 ABV65344/c
 ID ABV65344 standard; cDNA; 11 BP.

XX AC ABV65344;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 3130.

XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX DR WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 112; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14
 |||||
 Db 10 AGACTGTGG 1

RESULT 241
 ABV63110/c
 ID ABV63110 standard; cDNA; 11 BP.

XX AC ABV63110;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 896.

XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX DR WPI; 2002-590638/63.

XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 50; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
 |||||
 Db 11 GGCTGTGGC 2

```

RESULT 242
ABV68127
ID ABV68127 standard; cDNA; 11 BP.
XX
XX ABV68127;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 5913.
DE
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Disclosure; Page 189; 1345pp; German.
PS
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTTGCGA 17
DB 1 CTGTTGTGA 10

RESULT 243
ABV70531/c
ID ABV70531 standard; cDNA; 11 BP.
XX
XX ABV70531;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human skin EST 8317.
DE
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
PN
XX 11-JUL-2002.
PD
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX 03-JAN-2001; 2001DE-01000127.
PR
XX (HENK ) HENKEL KGAA.
PA

```

```
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 137; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGT 11
Db 1 TTGAGGCTGT 10
RESULT 245
ABV65312
ID ABV65312 standard; cDNA; 11 BP.
XX AC ABV65312;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3098.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
XX KW immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX PS WPI; 2002-590638/63.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX PS Disclosure; Page 111; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGT 11
Db 1 TTGAGGCTGT 10
RESULT 246
ABV65306
ID ABV65306 standard; cDNA; 11 BP.
XX AC ABV65306;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3092.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
XX KW immunosuppressive; antiinflammatory; cycostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX PS WPI; 2002-590638/63.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
```


KW Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss.

OS Homo sapiens.

PN EPI225233-A2.

XX 24-JUL-2002.

XX 23-JAN-2002; 2002EP-00075264.

XX 23-JAN-2001; 2001EP-00200228.

PR 28-SEP-2001; 2001EP-00203703.

XX 28-SEP-2001; 2001US-0325722P.

PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.

PI Van Der Kuyl AC, Cornelissen M;

XX WPI; 2002-668396/72.

XX Determining presence of a tumor cell or angiogenesis, and the

PT effectiveness of treatment, by detecting the presence of marker genes is

PT useful to detect and monitor treatment of Kaposi's Sarcoma.

XX Claim 12; Page 9; 38pp; English.

PS The present invention describes a method for determining if an individual
 CC has a tumour cell or site of angiogenesis, or if a treatment is effective
 CC in changing angiogenesis or changing a status of a set of target cells,
 CC comprising determining if a sample of the subject has an expression
 CC product of at least one marker gene. Also described is a compound capable
 CC of altering the expression or activity of Keratin 14, TIE 1, Salivohesin
 CC or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed
 CC Keratin 14, TIE 1, Salivohesin or Siglec, and kits containing them from
 CC the present invention can be used in a diagnostic method, particularly as
 CC an indicator of angiogenesis or to determine presence of a tumour cell.
 CC The method of the invention is suitable to determine within a few days if
 CC a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
 CC ABQ82006 represent nucleotide sequence used in the exemplification of the
 CC present invention

XX Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14

Db 2 AGGCTGTGG 11

RESULT 250

AAT47119/c

ID AAT47119 standard; DNA; 12 BP.

XX AAT47119;

XX 21-MAR-1997 (first entry)

XX K-ras exon 1 variant specific reverse primer, 407.

XX K-ras; exon 1; variation; hot spot; detection; primer; PCR;

XX polymerase chain reaction; amplification; asymmetric; determination;

XX ultra-violet; absorbance; variation detector; ss.

XX Synthetic.

XX JP08298998-A.

XX 19-NOV-1996.

XX 02-MAY-1995; 95JP-00108379.

XX 02-MAY-1995; 95JP-00108379.

XX (SUZM) SUZUKI KK.

XX WPI; 1997-045827/05.

XX Detection of gene variation, determined by UV absorbance - using a new

XX low cost DNA variation detector.

XX Example; Fig 4; 6pp; Japanese.

XX Codons 1 to 21 of K-ras exon 1 contain a variation hot spot, which can be
 CC detected using the method of the invention. The wild type (AAT47112) and
 CC variant (AAT47113) K-ras sequences are non-specifically amplified using
 CC the primers AAT47114/15, which are complementary to sequences at either
 CC side of the hot spot. An asymmetric PCR is carried out with the centrally
 CC placed hot spot of the K-ras DNA placed in between, using the primers
 CC AAT47116-19 in the pairings AAT47116/18, AAT47117/19, AAT47116/19 and
 CC AAT47117/18. The resulting asymmetric PCR prods. are then annealed with
 CC oligonucleotides having sequences complementary to the base sequence of
 CC the wild type DNA. The resultant double stranded DNA is then heated, and
 CC the change in absorbance due to the rise in temp. analysed, to detect a
 CC variation in the DNA. The method determines variations in DNA sequences
 CC based on UV absorbance values, pref. using a novel low cost DNA variation
 CC detector

XX Sequence 12 BP; 3 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16

Db 11 GCTGATGGCG 2

RESULT 251

AAT47118/c

ID AAT47118 standard; DNA; 12 BP.

XX AAT47118;

XX 21-MAR-1997 (first entry)

XX K-ras exon 1 wild type specific reverse primer, 406.

XX K-ras; exon 1; variation; hot spot; detection; primer; PCR;

XX polymerase chain reaction; amplification; asymmetric; determination;

XX ultra-violet; absorbance; variation detector; ss.

XX Synthetic.

XX JP08298998-A.

XX 19-NOV-1996.

XX 02-MAY-1995; 95JP-00108379.

XX 02-MAY-1995; 95JP-00108379.

XX (SUZM) SUZUKI KK.

XX WPI; 1997-045827/05.

XX Detection of gene variation, determined by UV absorbance - using a new

XX low cost DNA variation detector.

XX Example; Fig 4; 6pp; Japanese.

XX Codons 1 to 21 of K-ras exon 1 contain a variation hot spot, which can be

XX detected using the method of the invention. The wild type (AAT47112) and

CC variant (AAT47113) K-ras sequences are non-specifically amplified using
CC the primers AAT47114/15, which are complementary to sequences at either
CC side of the hot spot. An asymmetric PCR is carried out with the centrally
CC placed hot spot of the K-ras DNA placed in between, using the primers
CC AAT47116-19 in the pairings AAT47116/18, AAT47117/19, AAT47116/19 and
CC AAT47117/18. The resulting asymmetric PCR prods. are then annealed with
CC oligonucleotides having sequences complementary to the base sequence of
CC the wild type DNA. The resultant doubled stranded DNA is then heated, and
CC the change in absorbance due to the rise in temp. analysed, to detect a
CC variation in the DNA. The method determines variations in DNA sequences
CC based on UV absorbance values, pref. using a novel low cost DNA variation
CC detector

XX SQ Sequence 12 BP; 3 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 11 GCTGGTGGCG 2

RESULT 252
AAT47116
ID AAT47116 standard; DNA; 12 BP.
XX AC AAT47116;
XX DT 21-MAR-1997 (first entry)
XX DE K-ras exon 1 wild type specific forward primer, 404.
XX KW K-ras; exon 1; variation; hot spot; detection; primer; PCR;
XX KW polymerase chain reaction; amplification; asymmetric; determination;
XX KW ultra-violet; absorbance; variation detector; ss.
XX OS Synthetic.
XX JF08298998-A.
XX PD 19-NOV-1996.
XX PF 02-MAY-1995; 95JP-00108379.
XX PR 02-MAY-1995; 95JP-00108379.
XX PA (SUZM) SUZUKI KK.
XX WPI; 1997-045827/05.
XX Detection of gene variation, determined by UV absorbance - using a new
XX low cost DNA variation detector.
XX Example; Fig 4; 6pp; Japanese.

CC Codons 1 to 21 of K-ras exon 1 contain a variation hot spot, which can be
CC detected using the method of the invention. The wild type (AAT47112) and
CC variant (AAT47113) K-ras sequences are non-specifically amplified using
CC the primers AAT47114/15, which are complementary to sequences at either
CC side of the hot spot. An asymmetric PCR is carried out with the centrally
CC placed hot spot of the K-ras DNA placed in between, using the primers
CC AAT47116-19 in the pairings AAT47116/18, AAT47117/19, AAT47116/19 and
CC AAT47117/18. The resulting asymmetric PCR prods. are then annealed with
CC oligonucleotides having sequences complementary to the base sequence of
CC the wild type DNA. The resultant doubled stranded DNA is then heated, and
CC the change in absorbance due to the rise in temp. analysed, to detect a
CC variation in the DNA. The method determines variations in DNA sequences
CC based on UV absorbance values, pref. using a novel low cost DNA variation
CC detector

XX SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 2 GCTGGTGGCG 11

RESULT 253
AAV06831
ID AAV06831 standard; DNA; 12 BP.
XX AC AAV06831;
XX DT 01-JUL-1998 (first entry)
XX DE Amino derivatised K-ras wild-type oligonucleotide.
XX KW H-ras; wild-type; immobilising; diagnosis; ethylene acrylic acid;
XX KW ethylene methacrylic acid; polypropylene; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*note= "H2N-Cytosine"
XX PN WO9746597-A1.
XX PD 11-DEC-1997.
XX PF 22-MAY-1997; 97WO-US008880.
XX PR 05-JUN-1996; 96US-00658664.
XX PA (BECI) BECKMAN INSTR INC.
XX PI Milton RC;
XX WPI; 1998-051910/05.
XX Polymetric reagents for immobilising biopolymers - are stable under
XX synthesis conditions.
XX Example 3; Page 26; 66pp; English.

CC This sequence is shown in the specification. The invention relates to a
CC new reagent for immobilising a biopolymer. It comprises a solid support
CC fabricated from a polymeric material having at least one surface
CC comprising pendant acyl fluoride functionalities. The reagent is stable
CC under conditions for synthesising and immobilising biopolymers and is
CC stable under conditions used to analyse the biopolymers. The reagents can
CC be formed into devices which are physically rugged and inexpensive which
CC can be used in analytical and diagnostic procedures

XX SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCG 16
Db 1 GCTGGTGGCG 10

RESULT 254
AAV32277/c
ID AAV32277 standard; DNA; 12 BP.


```

XX AC AAV32277;
XX DT 18-AUG-1998 (first entry)
XX DE Random primed reverse transcription PCR primer 185.
XX KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
XX KW differential gene expression; ss.
XX OS Synthetic.
XX OS WO9813521-A1.
XX PN 02-APR-1998.
XX PD 26-SEP-1997; 97WO-EP005290.
XX PF 27-SEP-1996; 96GB-00020216.
XX PR (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX PS Consalez G, Fesce R;
XX PI WPI; 1998-230725/20.
XX CC Differential screening of gene expression by reverse transcription
XX CC polymerase chain reaction - uses random priming with primers selected for
XX CC high efficiency and selectivity by computer screening of database(s).
XX CC Claim 9; Page 24; 37pp; English.
XX CC The invention provides a method for the differential screening of gene
XX CC expression by random primed reverse transcription PCR (RT-PCR). The
XX CC primer sequences are generated by stimulating PCR reactions on non-
XX CC redundant mammalian nucleotide sequence databank entries containing at
XX CC least 1,000 bp of coding region. The primers selected, such as the
XX CC present one, had to meet various criteria such as having an efficiency
XX CC index between 2-10, having a selectivity index higher than 1, being 12 bp
XX CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others
XX CC in at least 5 of the 8 bases at the 3'-end. The invention claims the
XX CC selected primers make it possible to use internally primed, PCR-based RNA
XX CC fingerprinting for simple, exhaustive and systematic analysis of
XX CC differential gene expression as an advantageous alternative to
XX CC differential display. The method can also be useful for isolating new
XX CC coding sequences and to compare known and new genes
XX CC Sequence 12 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 1 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 75.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX Qy 6 GGCTGTTGGCGA 17
XX Db :|||||
XX 12 SGCTGGTGACCA 1
XX RESULT 255
XX ID AAV32276/c
XX ID AAV32276 standard; DNA; 12 BP.
XX AC AAV32276;
XX DT 18-AUG-1998 (first entry)
XX DE Random primed reverse transcription PCR primer 580.
XX KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
XX KW differential gene expression; ss.
XX OS Synthetic.
XX OS

```

```

PN WO9813521-A1.
XX 02-APR-1998.
XX 26-SEP-1997; 97WO-EP005290.
XX 27-SEP-1996; 96GB-00020216.
XX (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX Consalez G, Fesce R;
XX WPI; 1998-230725/20.
XX Differential screening of gene expression by reverse transcription
XX polymerase chain reaction - uses random priming with primers selected for
XX high efficiency and selectivity by computer screening of database(s).
XX Claim 9; Page 24; 37pp; English.
XX The invention provides a method for the differential screening of gene
XX expression by random primed reverse transcription PCR (RT-PCR). The
XX primer sequences are generated by stimulating PCR reactions on non-
XX redundant mammalian nucleotide sequence databank entries containing at
XX least 1,000 bp of coding region. The primers selected, such as the
XX present one, had to meet various criteria such as having an efficiency
XX index between 2-10, having a selectivity index higher than 1, being 12 bp
XX long i.e. 8 C or G and 4 T or A, and each primer differed from the others
XX in at least 5 of the 8 bases at the 3'-end. The invention claims the
XX selected primers make it possible to use internally primed, PCR-based RNA
XX fingerprinting for simple, exhaustive and systematic analysis of
XX differential gene expression as an advantageous alternative to
XX differential display. The method can also be useful for isolating new
XX coding sequences and to compare known and new genes
XX Sequence 12 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 1 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 75.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX Qy 6 GGCTGTTGGCGA 17
XX Db :|||||
XX 12 SGCTGTTGGCCA 1
XX RESULT 256
XX ABI05176
XX ID ABI05176 standard; DNA; 12 BP.
XX AC ABI05176;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 305149 for detecting SNP TSC0021316.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX OS WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI

```

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 305149; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 2 TGAGGTTGTT 11
|||||
|
RESULT 257
ABH96455/c
ID ABH96455 standard; DNA; 12 BP.
XX AC ABH96455;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 296448 for detecting SNP TSC0017086.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 296448; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 10 TGAGGCTGTT 1
|||||
|
RESULT 258
ABH73096
ID ABH73096 standard; DNA; 12 BP.
XX AC ABH73096;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 273081 for detecting SNP TSC0003039.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 273081; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;


```

XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PF 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 355310; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 2 TTGAGGCTGT 11
XX Db 10 TTGAGGTTGT 1
XX
XX RESULT 262
XX ABI74401/C
XX ID ABI74401 standard; DNA; 12 BP.
XX XX
XX AC ABI74401;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 374374 for detecting SNP TSC0060659.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 355310; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 2 TTGAGGCTGT 11
XX Db 10 TTGAGGTTGT 1
XX
XX RESULT 262
XX ABI74401/C
XX ID ABI74401 standard; DNA; 12 BP.
XX XX
XX AC ABI74401;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 374374 for detecting SNP TSC0060659.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 374374; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 3 TGAGGCTGTT 12
XX Db 12 TGAGGCTGTT 3
XX
XX RESULT 263
XX ABI63160
XX ID ABI63160 standard; DNA; 12 BP.
XX XX
XX AC ABI63160;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 363133 for detecting SNP TSC0053673.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 363133; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence

```

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
 |||||
 Db 2 TGAGGATGTT 11

RESULT 264
 ABI1963/c
 ID ABI1963 standard; DNA; 12 BP.

XX AC ABI1963;

XX XX 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 361936 for detecting SNP TSC0052957.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 361936; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
 XX Best Local Similarity 90.0%; Pred. No. 2e+02;
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
 |||||
 Db 10 GAGGTTGTTG 1

RESULT 265
 ABH82840/c

XX ID ABH82840 standard; DNA; 12 BP.

XX AC ABH82840;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 282833 for detecting SNP TSC0011017.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 282833; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
 XX Best Local Similarity 90.0%; Pred. No. 2e+02;
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
 |||||
 Db 11 AGGTGTTGG 2

RESULT 266
 ABH92756/c

XX ID ABH92756 standard; DNA; 12 BP.

XX AC ABH92756;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 292749 for detecting SNP TSC0015336.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGAC 18
 Db 2 TGTGGCGAC 11
 ||||| |||

RESULT 269

ABI65785/c
 ID ABI65785 standard; DNA; 12 BP.

XX AC ABI65785;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 365758 for detecting SNP TSC0055316.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 365758; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGT 11
 Db 12 TTGAGGTTGT 3
 ||||| |||

RESULT 270

ABH78619/c
 ID ABH78619 standard; DNA; 12 BP.

XX AC ABH78619;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 278612 for detecting SNP TSC0006177.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 278612; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
 Db 11 TGAGGATGTT 2
 ||||| |||

RESULT 271

ABI31077/c
 ID ABI31077 standard; DNA; 12 BP.

```
XX AC ABI31077;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 331050 for detecting SNP TSC0035938.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286163 for detecting SNP TSC0012605.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX DE Oligonucleotide primer SEQ ID NO 269382 for detecting SNP TSC0001730.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX DE Oligonucleotide primer SEQ ID NO 269382 for detecting SNP TSC0001730.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR
```

```
PN WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX Claim 1; SEQ ID NO 286163; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TTGAGGCTGT 11
DB 1 TTGAGGATGT 10
RESULT 273
ABH69405
ID ABH69405 standard; DNA; 12 BP.
XX AC ABH69405;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 269382 for detecting SNP TSC0001730.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR
```


XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 269382; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
XX
Qy 2 TTGAGGCTGT 11
Db 2 TTGAGGCTGT 11
XX
RESULT 274
ABH92262/C
ID ABH92262 standard; DNA; 12 BP.
XX
AC ABH92262;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 292255 for detecting SNP TSC0015143.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 292255; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
XX
Qy 3 TGAGGCTGTT 12
Db 11 TGAGGCTGTT 2
XX
RESULT 275
ABI74119
ID ABI74119 standard; DNA; 12 BP.
XX
AC ABI74119;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 374092 for detecting SNP TSC0060486.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 374092; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

```
QY 2 TTGAGGCTGT 11
XX ||||| |||
Db 1 TTGAGGTTGT 10
XX ||||| |||

RESULT 276
ABI63944
ID ABI63944 standard; DNA; 12 BP.
XX
AC ABI63944;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 363917 for detecting SNP TSC0054129.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 363917; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTGG 14
XX ||||| |||
Db 3 AGGTTGTGG 12
XX ||||| |||

RESULT 277
ABI24997
ID ABI24997 standard; DNA; 12 BP.
XX
AC ABI24997;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297499 for detecting SNP TSC0017609.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
```

```
DE Oligonucleotide primer SEQ ID NO 324970 for detecting SNP TSC0032326.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 324970; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTGG 14
XX ||||| |||
Db 3 AGGTTGTGG 12
XX ||||| |||

RESULT 278
ABH97506/c
ID ABH97506 standard; DNA; 12 BP.
XX
AC ABH97506;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297499 for detecting SNP TSC0017609.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
```

XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 297499; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TTGAGGCTGT 11
Db 10 TTTGAGGATGT 1
RESULT 279
ABI01343/C
ID ABI01343 standard; DNA; 12 BP.
XX AC ABI01343;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 301316 for detecting SNP TSC0019452.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX

PS Claim 1; SEQ ID NO 301316; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TTGAGGCTGT 11
Db 12 TTTGAGGTTGT 3
RESULT 280
ABZ58912
ID ABZ58912 standard; DNA; 12 BP.
XX AC ABZ58912;
XX DT 28-APR-2003 (first entry)
XX DE Human JAM3 intron 1/exon 2 junction sequence.
XX JAM3 Junctional adhesion molecule; JAM3; JAM2; antiasthmatic; antirheumatic;
XX antiarthritic; antithyroid; immunosuppressive; thyromimetic; virucide;
XX hepatotropic; antiinflammatory; antidiabetic; haemostatic; antipsoriatic;
XX antiallergic; human; chromosome 11q25; ds.
XX Homo sapiens.
XX WO2003006673-A2.
XX 23-JAN-2003.
XX 10-JUL-2002; 2002WO-US021697.
XX 11-JUL-2001; 2001US-0304603P.
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX Cunningham S;
XX WPI; 2003-210431/20.
XX Identifying compounds that bind to junctional adhesion molecules (JAM3 or
XX JAM2) or modulators of binding between JAM and other molecules for
XX treating or alleviating e.g. arthritis, hepatitis, Crohn's disease or
XX graft rejection.
XX Example 2B; Page 60; 90pp; English.
XX The invention relates to identifying compounds that bind to junctional
XX adhesion molecule 3 (JAM3), JAM2, or modulators of binding between JAM3,
XX JAM2 and other junctional adhesion molecules by detecting binding between
XX JAM3 and a test compound, or detecting binding between JAM3 and other
XX molecules. The identified compounds or modulators may be employed for
XX treating or alleviating e.g. arthritis, asthma, rheumatoid arthritis,
XX systemic lupus erythematosus, thrombocytopenia, Grave's disease,
XX Hashimoto's thyroiditis, hepatitis, diabetes mellitus, Crohn's disease,
XX psoriasis, allergic rhinitis, idiopathic pulmonary fibrosis, graft

```
CC rejection or graft-versus-host disease. Sequences ABZ58911-926 represent
CC human JAM3 exon and intron splice-site junction sequences
XX
SQ Sequence 12 BP; 1 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCTG 10
Db ||| |||||
1 CTTGAGGCTG 10

RESULT 281
ACA61780
ID ACA61780 standard; DNA; 12 BP.
XX
AC ACA61780;
XX
DT 20-AUG-2003 (first entry)
XX
DE Sample preparation and multiplex detection apparatus DNA #40.
XX
KW Multiplex detection; ss; spacer element; three dimensional capture probe.
XX
OS Unidentified.
XX
PN US2003032029-A1.
XX
PD 13-FEB-2003.
XX
PF 12-MAR-2002; 2002US-00096718.
XX
PR 21-DEC-1998; 98US-00217472.
XX
PS (NANO-) NANOGEN INC.
XX
PI Collins ML;
XX
DR WPI; 2003-466222/44.
XX
PT Apparatus for carrying out sample preparation and detection of panels of
PT target nucleic acids and antigens in a sample, has sample preparation
PT zone, three dimensional capture probe platforms and spacer elements.
XX
PS Disclosure; Page 21; 41pp; English.
XX
CC The invention relates to an apparatus for carrying out sample preparation
CC and multiplex detection of panels of target nucleic acids and antigens in
CC a sample, comprising a sample preparation zone, several three dimensional
CC capture probe platforms for capturing specific classes of target
CC molecules and spacer elements for separating the sets of three
CC dimensional capture probe platforms. The apparatus is useful for carrying
CC out multiplex detection of panels of target nucleic acids and antigens in
CC a sample, by providing a sample containing target nucleic acids and/or
CC antigens of interest, treating the sample with a sample buffer to form a
CC pre-processed sample, passing the pre-processes sample over the
CC apparatus, capturing the target nucleic acids and antigens by capture
CC probes of the apparatus, reacting a label with a signal probe, the signal
CC probe having specificity for at least one other signal probe that is
CC specific for the target and detecting the reacted level. Sequences
CC ACA61741-ACA61800 and ACD17023-ACD17041 represent DNA molecules used in
CC the scope of the invention
XX
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
Db ||| |||||
```

```
Db 3 GATGCTGTTG 12

RESULT 282
ACA61760/c
ID ACA61760 standard; DNA; 12 BP.
XX
AC ACA61760;
XX
DT 20-AUG-2003 (first entry)
XX
DE Sample preparation and multiplex detection apparatus DNA #20.
XX
KW Multiplex detection; ss; spacer element; three dimensional capture probe.
XX
OS Unidentified.
XX
PN US2003032029-A1.
XX
PD 13-FEB-2003.
XX
PF 12-MAR-2002; 2002US-00096718.
XX
PR 21-DEC-1998; 98US-00217472.
XX
PS (NANO-) NANOGEN INC.
XX
PI Collins ML;
XX
DR WPI; 2003-466222/44.
XX
PT Apparatus for carrying out sample preparation and detection of panels of
PT target nucleic acids and antigens in a sample, has sample preparation
PT zone, three dimensional capture probe platforms and spacer elements.
XX
PS Example 1; Page 9; 41pp; English.
XX
CC The invention relates to an apparatus for carrying out sample preparation
CC and multiplex detection of panels of target nucleic acids and antigens in
CC a sample, comprising a sample preparation zone, several three dimensional
CC capture probe platforms for capturing specific classes of target
CC molecules and spacer elements for separating the sets of three
CC dimensional capture probe platforms. The apparatus is useful for carrying
CC out multiplex detection of panels of target nucleic acids and antigens in
CC a sample, by providing a sample containing target nucleic acids and/or
CC antigens of interest, treating the sample with a sample buffer to form a
CC pre-processed sample, passing the pre-processes sample over the
CC apparatus, capturing the target nucleic acids and antigens by capture
CC probes of the apparatus, reacting a label with a signal probe, the signal
CC probe having specificity for at least one other signal probe that is
CC specific for the target and detecting the reacted level. Sequences
CC ACA61741-ACA61800 and ACD17023-ACD17041 represent DNA molecules used in
CC the scope of the invention
XX
SQ Sequence 12 BP; 4 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
Db ||| |||||
10 GATGCTGTTG 1

RESULT 283
AAA80787
ID AAA80787 standard; DNA; 8 BP.
XX
AC AAA80787;
XX
DT 24-NOV-2000 (first entry)
XX
```

```
DE A. thaliana primer walking octamer SEQ ID NO: 100.
KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
XX Arabidopsis thaliana.
XX
XX US6083695-A.
XX
XX 04-JUL-2000.
XX
XX 21-MAY-1997; 97US-00859954.
XX
XX 15-APR-1996; 96US-00632782.
XX
XX (UYHO-) UNIV HOUSTON.
XX (HARD/) HARDIN S H.
XX
XX Hardin PE, Hardin SH, Homayouni R;
XX
XX WPI; 2000-474852/41.
XX
XX Sequencing an unknown DNA molecule for the polymerase chain reaction and
XX other primer processes comprises primer walking of octamer
XX oligonucleotides.
XX
XX Example 8; Col 75-76; 161pp; English.
XX
XX This invention describes a novel method for sequencing an unknown DNA
XX molecule which comprises selecting a library primer from an octamer
XX oligonucleotide library consisting of 48 8-bp sequences and corresponding
XX complementary sequences, where the library primer is complementary to a
XX known sequence adjacent to the unknown sequence or is complementary to a
XX sequence in a known extension product. The method is useful for DNA
XX nucleotide sequencing, in PCR, and in other processes which make use of
XX primers. The octamers are used to identify coding sequences. Primer
XX walking using the octamer libraries is advantageous over other sequencing
XX methods because it does not require multiple cloning steps nor subsequent
XX template preparations, and it is a directed and methodical approach.
XX AAA80688-A81253 represent the octamer primers used in the primer walking
XX method of the invention
XX
XX Sequence 8 BP; 1 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGAGGCT 9
DB 1 TTGAGGCT 8
RESULT 284
ABQ72028
ID ABQ72028 standard; DNA; 9 BP.
XX
XX AC ABQ72028;
XX
XX 28-AUG-2002 (first entry)
XX
XX Zinc finger protein related oligonucleotide target SEQ ID NO:2326.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 60; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subsite. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subsite, selecting the F2 zinc finger such that it
XX binds to the S2 target subsite, and selecting the F3 zinc finger such
XX that it binds to the S3 target subsite, thus designing (I) that binds to
XX a target site. (I) is useful for recognition of triplet target subsites
XX having the nucleotide G in the 5'-most position of the subsite. (I) is
XX useful in studying gene function, and for human therapeutics and plant
XX engineering. (I), (II) or (III) is useful in therapeutic methods to
XX modulate the expression of a target region within a subject, in
XX diagnostic methods for sequence specific detection of target nucleic acid
XX in a sample, and in assays to determine the phenotype and function of
XX gene expression. (I) has improved affinity and specificity for their
XX target sequences, as well as enhanced biological activity. ABQ71213 to
XX ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX finger peptides which are given in the exemplification of the present
XX invention
XX
XX Sequence 9 BP; 0 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGTC 15
DB 1 CTGTGTC 8
RESULT 285
ABQ72029
ID ABQ72029 standard; DNA; 9 BP.
XX
XX AC ABQ72029;
XX
XX 28-AUG-2002 (first entry)
XX
XX Zinc finger protein related oligonucleotide target SEQ ID NO:2327.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX WO200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
```

```
PI Liu Q;
XX WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 60; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (I), a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F2 zinc finger such that it
CC binds to the S1 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S2 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 0 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGGC 15
DB 1 CTGTTGGC 8

RESULT 286
ABQ71854
ID ABQ71854 standard; DNA; 9 BP.
XX
AC ABQ71854;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2152.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PR (SANG-) SANGAMO BIOSCIENCES INC.
XX
PA
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
```

```
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 56; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (I), a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 0 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 16
DB 2 TGTGGCG 9

RESULT 287
ADA64355
ID ADA64355 standard; DNA; 9 BP.
XX
AC ADA64355;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #813.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
OS US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
XX
PR 24-MAR-1999; 99US-0126239P.
XX
PR 30-JUL-1999; 99US-0146595P.
XX
PR 30-JUL-1999; 99US-0146615P.
XX
PR 23-MAR-2000; 2000US-00535008.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
```

```
DR WPI; 2003-567233/53.
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
XX Disclosure; Page 25; 34pp; English.
XX
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
XX Sequence 9 BP; 0 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGGC 15
Db 1 CTGTTGGC 8
RESULT 288
ADA64356
ID ADA64356 standard; DNA; 9 BP.
XX
XX ADA64356;
XX
XX 20-NOV-2003 (first entry)
XX
XX Zinc finger target sequence DNA #814.
XX
XX ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
XX Synthetic.
XX
XX OS
XX US2003068675-A1.
XX
XX 10-APR-2003.
XX
XX 20-NOV-2001; 2001US-00990186.
XX
XX 24-MAR-1999; 99US-0126238P.
XX
XX 24-MAR-1999; 99US-0126239P.
XX
XX 30-JUL-1999; 99US-0146595P.
XX
XX 30-JUL-1999; 99US-0146615P.
XX
XX 23-MAR-2000; 2000US-00535008.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX (LIUQ/) LIU Q.
XX
XX Liu Q;
XX
XX WPI; 2003-567233/53.
XX
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
XX Disclosure; Page 23; 34pp; English.
XX
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
XX Sequence 9 BP; 0 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGCG 16
Db 2 TGTGGCG 9
RESULT 290
AAQ97101/c
ID AAQ97101 standard; DNA; 10 BP.
XX
XX AAQ97101;
XX
```



```

XX Claim 14; Page 197; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise Os field)
XX
XX Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTGAGGCT 9
Db 8 TTGAGGCT 1
RESULT 293
AAZ78512/c
ID AAZ78512 standard; DNA; 10 BP.
XX
XX AAZ78512;
AC
DT 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag, SEQ ID NO:940:
DE
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTU;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-0089911P.
XX 19-JUN-1998; 98US-0089922P.
XX 19-JUN-1998; 98US-0089932P.
XX 19-JUN-1998; 98US-0089939P.
XX 19-JUN-1998; 98US-0089944P.
XX 19-JUN-1998; 98US-0089957P.
XX 19-JUN-1998; 98US-0089999P.
XX 19-JUN-1998; 98US-0090000P.
XX 19-JUN-1998; 98US-0090003P.
XX 19-JUN-1998; 98US-0090036P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX 19-JUN-1998; 98US-0090042P.
XX 19-JUN-1998; 98US-0090043P.
XX 19-JUN-1998; 98US-0090044P.
XX 19-JUN-1998; 98US-0090045P.
XX 19-JUN-1998; 98US-0090047P.
XX 19-JUN-1998; 98US-0090048P.
XX 19-JUN-1998; 98US-0090072P.
XX 19-JUN-1998; 98US-0090076P.
XX 19-JUN-1998; 98US-0090077P.
XX 19-JUN-1998; 98US-0090078P.
XX 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 92; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding or
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
XX Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCTG 10
Db 10 TGAGGCTG 3
RESULT 294
AAZ82715/c
ID AAZ82715 standard; DNA; 10 BP.
XX
XX AAZ82715;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #1949.
DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

```

XX Homo sapiens.
 OS WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE//) ROBERTS B L.
 PA (SHAN//) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 111; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 GGCTGTTG 13
 Db 9 GGCTGTTG 2
 |||||
 RESULT 295
 AAZ83636
 ID AAZ83636 standard; DNA; 10 BP.
 XX AC
 XX AAZ83636;
 XX 07-APR-2000 (first entry)
 DT
 XX Metastatic breast tumour cell upregulated transcript tag #2870.
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 PN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE//) ROBERTS B L.
 PA (SHAN//) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 135; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GCTGTTGG 14
 Db 3 GCTGTTGG 10
 |||||
 RESULT 296
 AAC74142
 ID AAC74142 standard; cDNA; 10 BP.
 XX AC
 XX AAC74142;
 XX 02-FEB-2001 (first entry)
 DT Human monocyte and dendritic cell expressed gene oligonucleotide #229.
 KW

XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmune disease; tumour; ss.
 XX Homo sapiens.
 XX WO200060074-A1.
 XX 12-OCT-2000.
 XX 30-MAR-2000; 2000WO-JP002019.
 XX 01-APR-1999; 99JP-00095481.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Hashimoto S, Matsushima K, Suzuki T;
 XX WPI; 2000-619172/59.
 XX Groups of genes expressed in human dendritic cells at a greater or lesser
 PT extent than in monocytes for investigation and diagnosis of autoimmune
 PT disease and tumors.
 XX Claim 19; Page 15; 95pp; Japanese.
 XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases
 XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 SQ Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CTGTTGGC 15
 DB |||||
 1 CTGTTGGC 8
 RESULT 297
 AAA56180
 ID AAA56180 standard; DNA; 10 BP.
 XX AAA56180;
 AC
 DT 07-SEP-2000 (first entry)
 XX Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:74.
 DE
 XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.
 XX Homo sapiens.
 OS
 XX WO200024892-A1.
 PN
 XX 04-MAY-2000.
 XX Hashimoto S, Matsushima K, Suzuki T;

PF 28-OCT-1999; 99WO-JP005982.
 XX 28-OCT-1998; 98JP-00307532.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Hashimoto S, Matsushima K, Suzuki T;
 XX WPI; 2000-350734/30.
 XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.
 XX Claim 1; Page 54; 138pp; Japanese.
 XX The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody
 CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
 CC specifically claimed oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages
 XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 SQ Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CTGTTGGC 15
 DB |||||
 1 CTGTTGGC 8
 RESULT 298
 AAA56502
 ID AAA56502 standard; DNA; 10 BP.
 XX AAA56502;
 AC
 DT 07-SEP-2000 (first entry)
 XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:396.
 DE
 XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.
 XX Homo sapiens.
 OS
 XX WO200024892-A1.
 PN
 XX 04-MAY-2000.
 XX 28-OCT-1999; 99WO-JP005982.
 XX 28-OCT-1998; 98JP-00307532.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Hashimoto S, Matsushima K, Suzuki T;

```

XX WPI; 2000-350734/30.
XX
XX Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
XX Claim 37; Page 118; 138pp; Japanese.
XX
XX The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGGC 15
Db 1 CTGTTGGC 8
RESULT 299
AAH64421
ID AAH64421 standard; cDNA; 10 BP.
XX
XX AAH64421;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1261.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UUYO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VB, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 13; Page 68; 94pp; English.
XX
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGGC 15
Db 1 CTGTTGGC 8
RESULT 300
AAH63452/C
ID AAH63452 standard; cDNA; 10 BP.
XX
XX AAH63452;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 292.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UUYO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VB, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 13; Page 45; 94pp; English.
XX
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GGCTGTTG 13
Db 9 GGCTGTTG 2

```

```
RESULT 301
AAH32904
ID AAH32904 standard; cDNA; 10 BP.
XX
AC AAH32904;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:277.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-304369/32.
XX
FT LPS activated human monocyte expression gene group.
XX
PS Claim 19; Page 45; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGCC 15
Db 1 CTGTTGCC 8
| | | | |
| | | | |

RESULT 302
AAF43753
ID AAF43753 standard; DNA; 10 BP.
XX
AC AAF43753;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11892.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW not previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
```

```
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with arial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 374; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTGG 14
Db 3 GCTGTTGG 10
| | | | |
| | | | |

RESULT 303
AAD25887
ID AAD25887 standard; DNA; 10 BP.
XX
XX AAD25887;
XX
XX 26-MAR-2002 (first entry)
XX
XX Primer #9 to detect polymorphisms in human DTR gene.
XX
XX Human; polymorphic site; PS; diphtheria toxin receptor; DTR; haplotype;
XX heparin-binding epidermal growth factor-like growth factor; therapy;
XX chromosome 5q23; transgenic animal; drug screening; tumour growth;
XX
```

KW smooth muscle hyperplasia; atherosclerosis; primer; ss.
 XX Homo sapiens.
 OS WO200179233-A2.
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US012302.
 XX 14-APR-2000; 2000US-0197375P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Choi JY, Kliem SE, Koshy B, Parks KE, Stephens JC;
 XX WPI; 2002-082745/11.
 XX New nucleotide polymorphisms in the human diphtheria toxin receptor,
 PT heparin-binding epidermal growth factor-like growth factor (DTR) gene,
 PT useful for screening or expressing proteins for treating diseases related
 PT to DTR activity.
 XX Claim 18; Page 12; 66pp; English.
 XX The present invention relates to an isolated polynucleotide, comprising
 CC polymorphisms in the human diphtheria toxin receptor, heparin-binding
 CC epidermal growth factor-like growth factor (DTR) gene. DTR gene is
 CC located on chromosome 5q23. The polynucleotide comprising polymorphisms
 CC in the DTR gene is useful in studying the expression and function of DTR,
 CC and in expressing DTR protein for use in screening candidate drugs to
 CC treat diseases related to DTR activity. The methods and haplotypes are
 CC useful in improving the efficiency and output of several steps in the
 CC drug discovery and development process, including target validation,
 CC identifying lead compounds, and early phase clinical trials. The kit and
 CC method are useful for determining if an individual has one of the
 CC haplotypes or haplotype pairs. The transgenic animals are useful for
 CC studying expression of the DTR isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against DTR protein, and for testing the
 CC efficacy of therapeutic agents and compounds for tumour growth, smooth
 CC muscle hyperplasia or atherosclerosis in a biological system. The present
 CC sequence is a primer to detect polymorphisms in human DTR gene
 XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 AGGCTGTT 12
 Db |||||
 2 AGGCTGTT 9
 RESULT 304
 AAS99181/C
 ID AAS99181 standard; DNA; 10 BP.
 AC AAS99181;
 XX 12-MAR-2002 (first entry)
 XX UDP glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #48.
 DE UDP glycosyltransferase 1 (UGT1A1); human; haplotyping; ss;
 KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;
 KW allele-specific oligonucleotide.
 XX Homo sapiens.
 OS WO200179230-A2.
 XX 25-OCT-2001.
 XX 13-APR-2001; 2001WO-US012273.
 XX 18-APR-2000; 2000US-0197514P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Koshy B, Rounds E;
 XX WPI; 2002-075063/10.
 XX Genotyping a human UDP glycosyltransferase 1 gene of an individual for
 PT determining the haplotype of an individual, involves determining the
 PT identity of a nucleotide pair at specific polymorphic sites for two
 PT copies of the gene.
 XX Claim 18; Page 14; 81pp; English.
 XX The invention relates to genotyping a human UDP glycosyltransferase
 CC (UGT1A1) gene of an individual, involving determining for the two copies
 CC of the UGT1A1 gene present in the individual, the identity of the
 CC nucleotide pair at one or more polymorphic sites. The new method is
 CC useful for determining whether an individual has a haplotype or haplotype
 CC pairs, given in the specification. It is useful for improving the
 CC efficacy and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with UGT1A1
 CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to
 CC validate UGT1A1 as a candidate agent for treating a specific condition or
 CC disease predicted to be associated with UGT1A1 activity, and in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease predicted to be associated with UGT1A1 activity. The
 CC method is useful to screen for compounds targeting UGT1A1 to treat a
 CC specific condition or disease associated with UGT1A1 activity. A nucleic
 CC acid (I) comprising a polymorphic variant of a reference sequence for the
 CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the
 CC expression and function of UGT1A1, and in expressing UGT1A1 protein for
 CC use in screening for candidate drugs to treat diseases related to UGT1A1
 CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a
 CC recombinant organism comprising (II) is useful for studying expression of
 CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against UGT1A1 protein, and for testing the efficacy of
 CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-
 CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP
 CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the
 CC method of the invention
 XX SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TTGAGGCT 9
 Db |||||
 9 TTGAGGCT 2
 RESULT 305
 AAS19963
 ID AAS19963 standard; DNA; 10 BP.
 XX AAS19963;
 XX 26-MAR-2002 (first entry)
 XX Primer-extension oligonucleotide #15 to detect human DNAL4 polymorphisms.
 DE Human; single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
 XX dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
 KW neuroprotective; neurological disorder; primer; ss.
 XX Homo sapiens.
 OS

PN WO200179235-A2.
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US012304.
 XX 17-APR-2000; 2000US-0197460P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Chew A, Choi JY, Koshy B;
 XX WPI; 2002-075065/10.
 XX Genotyping human dynein, axonemal light polypeptide chain 4 gene of
 PT individual, useful for determining haplotype of individual, comprises
 PT determining identity of nucleotide pair at specific polymorphic sites for
 PT two copies of gene.
 XX Claim 18; Page 14; 79pp; English.
 XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4)
 CC gene located on chromosome 2q13.1, and methods for haplotyping and/or
 CC genotyping the DNAL4 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the DNAL4 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC the treatment of diseases associated with DNAL4 activity, such as
 CC neurological disorders. AAS19949-AAS19976 represent primer-extension
 CC oligonucleotides for detecting human DNAL4 gene polymorphisms
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TGAGGCTG 10
 DB 2 TGAGGCTG 9
 |||||
 RESULT 306
 AAS95967
 ID AAS95967 standard; DNA; 10 BP.
 XX AAS95967;
 AC AAS95967;
 XX 26-FEB-2002 (first entry)
 DT Human CALM1 gene allele-specific oligonucleotide #76.
 DE
 DE Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
 KW haplotyping; SCVA3; Alzheimer's disease; drug screening;
 KW calcium-dependent signal transduction; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200179218-A2.
 PN 25-OCT-2001.
 XX 09-APR-2001; 2001WO-US011509.
 XX 12-APR-2000; 2000US-0196340P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
 XX WPI; 2002-049190/06.
 DR
 XX

PT New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
 PT expressing CALM1 protein for use in screening for candidate drugs to
 PT treat diseases related to CALM1 activity such as Alzheimer's disease.
 XX Claim 17; Page 14; 82pp; English.
 XX The invention relates to an isolated polynucleotide comprising a sequence
 CC selected from a polymorphic variant of calmodulin 1 (CALM1). The
 CC polymorphic variant comprises an CALM1 isogene defined by a haplotype
 CC selected from haplotypes 1-21 given in the specification. The
 CC polymorphisms are useful for studying the biological function of CALM1 as
 CC well as in identifying drugs targeting this protein for the treatment of
 CC a disorder related to its abnormal expression or function. The
 CC polymorphic variants may also be used in screening for compounds
 CC targeting CALM1 to treat a specific condition or disease predicted to be
 CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype
 CC pair of an individual is useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with SCVA3 activity, e.g. Alzheimer's
 CC disease and diseases involving defects in calcium-dependent signal
 CC transduction. Haplotyping the CALM1 gene in an individual is also useful
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease predicted to be associated with CALM1
 CC activity. AAS95892-AAS96018 represent human CALM1 allele-specific
 CC oligonucleotides and PCR primers of the invention
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TGAGGCTG 10
 DB 2 TGAGGCTG 9
 |||||
 RESULT 307
 AAT18106/C
 ID AAT18106 standard; DNA; 11 BP.
 XX AAT18106;
 AC AAT18106;
 XX 30-AUG-1996 (first entry)
 DT M. kansasii species specific amplification primer. B1.
 DE
 DE Species-specific amplification; M. kansasii; probe; pMK1-9;
 KW strand displacement amplification; SDA; primers; Mycobacterium;
 KW cross-react; Nocardia asteroides; Rhodococcus rhodochrous; ss.
 XX Synthetic.
 OS
 XX US5500341-A.
 PN 19-MAR-1996.
 XX 19-SEP-1994; 94US-00308892.
 XX 19-SEP-1994; 94US-00308892.
 XX (BECT) BECTON DICKINSON CO.
 XX Spears PA;
 XX WPI; 1996-171042/17.
 DR
 XX Primers for species-specific amplification of Mycobacterium kansasii -
 PT detect double stranded target sequences with no cross-reactivity between
 PT species.
 XX Claim 3; Col 15; 15pp; English.
 XX

CC The sequences given in AAT18103-11 are primers which may be used in the
 CC species-specific amplification of *M. kansasii* DNA. These primers bind to
 CC a fragment, bases 51-220, of the clone p6123. p6123 is a cloned probe
 CC which hybridises to all *M. kansasii* strains, including the subgroup which
 CC is negative to binding with the probe pMK1-9 (M.Yang et al. 1993. J.
 CC Clin. Microbid. 31, 2769-2772). These primers are pref. used in strand
 CC displacement amplification (SDA). These primers showed a positive
 CC reaction with 74 *M. kansasii* isolates tested, but did not cross react
 CC with any other *Mycobacterium* species. In addition, these primers did not
 CC cross-react with *Nocardia* asteroides or *Rhodococcus* rhodochrous. This
 CC primer binds around bases 93-103 of the p6123 fragment
 XX
 SQ Sequence 11 BP; 3 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
 Db 11 CTGTGGC 4

RESULT 308
 AAV61928/c
 ID AAV61928 standard; DNA; 11 BP.
 XX
 AC AAV61928;
 XX
 XX 04-JAN-1999 (first entry)
 XX
 XX Molecular weight marker element 5' EcoRI subunit of 100mer #1 DNA.
 XX
 XX dsDNA ladder; RNA ladder; ssDNA ladder; multimer template; size marker;
 KW molecular weight marker; gel electrophoresis; ss.
 XX
 OS Synthetic.
 XX
 XX US5824787-A.
 PN
 XX 20-OCT-1998.
 PD
 XX
 XX 02-FEB-1996; 96US-00597467.
 XX
 XX 03-DEC-1993; 93US-00161901.
 PR
 XX (GENS-) GENSURA LAB INC.
 PA
 XX Singer PA;
 PI
 XX WPI; 1998-582625/49.
 DR
 XX

XX Nucleic acid multimer template - for generating electrophoretic size
 PT markers of specific size.
 PT
 XX Disclosure; Col 25-26; 20pp; English.
 PS
 XX AAV61914-V61933 are sequences used a method resulting in the production
 CC of a nucleic acid multimer template for generating a size marker. The
 CC method is used to make molecular weight markers for use in gel
 CC electrophoresis (kits provided), especially in the high MW range, e.g.
 CC >500 bp. It can also be used to create radiolabelled RNA markers, which
 CC are currently not available. The method allows the construction of size
 CC markers of specific, predetermined size. Current markers are constructed
 CC from digestion of DNA e.g. lambda DNA, and their sizes depend on
 CC restriction sites in the DNA. Additionally, DNA does not migrate linearly
 CC in agarose, requiring extrapolation of sizes if a product falls between 3
 CC markers. The method allows construction of a marker of exact length to a
 CC desired product
 XX

SQ Sequence 11 BP; 4 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
 Db 11 TTGAGGCT 4

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGGC 8
 Db 9 CTTGAGGC 2

RESULT 309
 AAA11725/c
 ID AAA11725 standard; DNA; 11 BP.
 XX
 AC AAA11725;
 XX
 XX 14-JUL-2000 (first entry)
 DT
 XX Human prothrombin 20210 A allele PCR primer #3.
 DE
 XX Prothrombin; human; thrombosis; mutation; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX US6043035-A.
 PN
 XX 28-MAR-2000.
 PD
 XX 03-NOV-1997; 97US-00962790.
 PF
 XX 03-NOV-1997; 97US-00962790.
 PR
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Bertina RM, Reitsma PH, Rosendaal FR, Poort SR;
 PI
 XX WPI; 2000-270338/23.
 DR
 XX

XX Determining increased risk for thrombosis by determining prothrombin
 PT level, or by detecting the presence or absence of genetic mutation
 PT correlated with elevated prothrombin levels.
 PT
 XX Example 2; Col 11-12; 1lpp; English.

XX This invention describes a novel method for determining an increased risk
 CC for thrombosis in an individual by determining the prothrombin level, or
 CC by detecting the presence or absence of a genetic mutation correlated
 CC with elevated prothrombin levels in individuals with the mutation, and
 CC where an increased prothrombin level indicates increased risk for
 CC thrombosis. INDEPENDENT CLAIMS are also included for the following: (1) a
 CC kit for determining whether an individual is at an increased risk for
 CC thrombosis comprising at least one primer which specifically hybridizes
 CC adjacent to the region of the prothrombin gene that contains a G to A
 CC mutation at position 20210, and suitable amplification reagents; and (2)
 CC an isolated polynucleotide comprising a mutated prothrombin gene, in
 CC which G at position 20210 is replaced by A, or a fragment of the gene
 CC which includes the G to A transition mutation at position 20210. The
 CC method is also used for screening and diagnosis of thrombophilia,
 CC especially, hereditary thrombophilia. AAA11723-AAA11726 represent PCR
 CC primers used in the method of the invention
 XX

SQ Sequence 11 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 1 Other;
 Query Match 44.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 310
 ABV68951
 ID ABV68951 standard; cDNA; 11 BP.


```

XX AC ABV68951;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 6737.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENKEL ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX PF WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 212; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma of sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 1 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTGG 14
Db 3 GCTGTTGG 10

RESULT 311
ABV69622
ID ABV69622 standard; cDNA; 11 BP.
XX AC ABV69622;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 7408.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PI
XX PI Palliugaard N, Hokland P;

PN WO200253774-A2.
PD 11-JUL-2002.
PF 20-DEC-2001; 2001WO-EP015179.
PR 03-JAN-2001; 2001DE-01000127.
PA (HENKEL ) HENKEL KGAA.
PI Petersohn D, Conradt M, Hofmann K;
PF WPI; 2002-590638/63.
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
PS Disclosure; Page 232; 1345pp; German.
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
Db 1 CTGTGGC 8

RESULT 312
AAV40927/c
ID AAV40927 standard; DNA; 12 BP.
XX AC AAV40927;
XX DT 25-SEP-1998 (first entry)
XX DE Primer AFX1:70L12 for abnormality detection.
XX KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
XX KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
XX KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9824928-A2.
XX PD 11-JUN-1998.
XX PF 08-DEC-1997; 97WO-DK000556.
XX PR 06-DEC-1996; 96DK-00001401.
XX PA (PALLI/) PALLISGAARD N.
XX PI Palliugaard N, Hokland P;
XX PI

```

```

DR WPI; 1998-333344/29.
XX
XX Detection of chromosomal abnormalities - by subjecting patient sample
PT nucleic acids to a multiplex molecular amplification procedure using
PT primers specific for characteristic nucleic acid sequence.
XX
XX Claim 73; Page 67; 126pp; English.
XX
CC This sequence represents a primer used in the method of the invention for
CC the detection of the presence or absence of chromosomal abnormalities,
CC each abnormality being associated with a condition in a subject and each
CC being defined by at least one characteristic nucleic acid sequence. The
CC method comprises: (a) obtaining a sample of nucleic acids derived from a
CC subject which may harbour one of the chromosomal abnormalities; (b)
CC subjecting the sample to a multiplex molecular amplification (MMA)
CC procedure, where a number of the characteristic sequences, if present in
CC a sufficient amount, will be amplified; (c) retrieving the product (s)
CC from step (b), and detecting the presence and/or absence of an amplicon
CC characteristic of the abnormal sequences to detect the presence or
CC absence of corresponding chromosomal abnormalities; where the MMA
CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
CC in one single reaction mixture, each of the primers defining an end of at
CC least one characteristic nucleic acid sequence, and where at least one of
CC the primers defines the first end of at least two characteristic nucleic
CC acid sequences, the characteristic nucleic acid sequences each being
CC determined in their opposite ends by MDP selected from the remainder of
CC the MDP. The methods can be used for detecting chromosomal abnormalities
CC associated with diseases including numerous leukaemia's, lymphoma's,
CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX
XX Sequence 12 BP; 5 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTTGGC 15
DB 12 CTGTTGGC 5
|||||||
RESULT 313
ABH71139
ID ABH71139 standard; DNA; 12 BP.
XX
AC ABH71139;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 271116 for detecting SNP TSC0002403.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
methylation status.

```

```

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271116; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 TGTGTGGC 16
DB 1 TGTGTGGC 8
|||||||
RESULT 314
ABI31650/c
ID ABI31650 standard; DNA; 12 BP.
XX
AC ABI31650;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 331623 for detecting SNP TSC0036370.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 331623; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

```

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTTGGCG 16
 |||||

Db 11 TGTTGGCG 4

RESULT 315
 AB11193/c

ID AB11193 standard; DNA; 12 BP.

XX AC AB11193;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 311166 for detecting SNP TSC0024340.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 311166; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTTGGCG 16
 |||||

Db 12 TGTTGGCG 5

RESULT 316

ID AB171666/c

XX ID AB171666 standard; DNA; 12 BP.

XX AC AB171666;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 371639 for detecting SNP TSC0009763.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 371639; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTGGCGA 17
 |||||

Db 11 GTTGGCGA 4

RESULT 317

ID ABH71141
 ID ABH71141 standard; DNA; 12 BP.

XX AC ABH71141;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 271118 for detecting SNP TSC0002403.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271118; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 TGTGGCG 16
Db 1 TGTGGCG 8
|||||
RESULT 318
AB130029
ID ABI30029 standard; DNA; 12 BP.
XX
XX AC ABI30029;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 330002 for detecting SNP TSC0035269.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX

XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 330002; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTTGGCGA 17
Db 4 GTTGGCGA 11
|||||
RESULT 319
ABH95942/C
ID ABH95942 standard; DNA; 12 BP.
XX
XX AC ABH95942;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 295935 for detecting SNP TSC0016808.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 295935; 29pp + Sequence Listing; German.
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 1 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGCG 16
Db 8 TGTGGCG 1

RESULT 320
ABI49660
ID ABI49660 standard; DNA; 12 BP.
XX AC ABI49660;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 349633 for detecting SNP TSC0046242.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 349633; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 0 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGCG 16
Db 2 TGTGGCG 9

RESULT 321
AAQ48916
ID AAQ48916 standard; DNA; 11 BP.
XX AC AAQ48916;
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1994 (first entry)
XX DE Cross-linking oligonucleotide 12.
XX KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
XX KW bulge; fixation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_binding /*tag= b
FT /note= "crosslinked to base 6 of (AAQ48906) via O-(CH2)8-
FT NH-O-CH2- as in example 11b"
FT modified_base 6
FT /*tag= a
FT /mod_base= octyl-hydroxylamine functional_cytidine_(sic)
FT /note= "ref: Example 4-A"
XX PN W09318052-A1.
XX PD 16-SEP-1993.
XX PF 05-MAR-1993; 93WO-US002059.
XX PR 05-MAR-1992; 92US-00846376.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cook PD, Manoharan M, Bruice T;
XX WPI; 1993-303395/38.
XX New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
PT structures or hairpin loop, stem loop, interior loop, bulge or other
PT structures.
XX Disclosure; Page 67; 145pp; English.
XX Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
CC number of crosslinking methods are claimed, which are used to fix
CC separate ON strands in duplex structures or to fix a single ON strand in
CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-
CC order structures. Fixing a strand or strands in a duplex structure also
CC can disrupt the normal function of a single stranded nucleic acid-binding
CC protein by forming nuclease resistant mimics of the protein binding
CC receptors. The ONs have diagnostic, therapeutic and prophylactic
CC applications as well as being used as research agents. (Updated on 25-MAR
CC -2003 to correct PN field.)
XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY      6 GGCTGTTGGCG 16
Db      |||||: |||
        1 GGCTGUCTGCG 11

RESULT 322
AAQ48917
ID AAQ48917 standard; DNA; 11 BP.
XX AC AAQ48917;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1994 (first entry)
XX DE Cross-linking oligonucleotide 13.
XX XX
XX KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
XX KW bulge; fixation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_binding 6 /*tag= b
XX FT /note= "crosslinked to base 6 of (AAQ48906) via O-(CH2)8-
XX FT NH-NH-CH2- as in example 11c"
XX FT modified_base 6 /*tag= a
XX FT /mod_base= penty-N-semicarbazide_functional_uridine
XX FT with an oxygen linking atom
XX FT /note= "ref: example 4-A"
XX XX
XX DN WO9318052-A1.
XX XX
XX PD 16-SEP-1993.
XX XX
XX PP 05-MAR-1993; 93WO-US002059.
XX XX
XX PR 05-MAR-1992; 92US-00846376.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cook PD, Manoharan M, Bruce T;
XX PS WPI; 1993-303395/38.
XX DR
XX FT New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX FT structures or hairpin loop, stem loop, interior loop, bulge or other
XX FT structures.
XX PS Disclosure; Page 68; 145pp; English.
XX CC Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
XX CC number of crosslinking methods are claimed, which are used to fix
XX CC separate ON strands in duplex structures or to fix a single ON strand in
XX CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-
XX CC order structures. Fixing a strand or strands in a duplex structure also
XX CC can disrupt the normal function of a single stranded nucleic acid-binding
XX CC protein by forming nuclease resistant mimics of the protein binding
XX CC receptors. The ONs have diagnostic, therapeutic and prophylactic
XX CC applications as well as being used as research agents. (Updated on 25-MAR
XX CC -2003 to correct PN field.)
XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
      Query Match 43.3%; Score 7.8; DB 1; Length 11;
      Best Local Similarity 72.7%; Pred. No. 2.6e+02;
      Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      |||||: |||
        1 GGCTGUCTGCG 11

RESULT 324
AAQ48925
ID AAQ48925 standard; DNA; 11 BP.
XX AC AAQ48925;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1994 (first entry)
XX DE Cross-linking oligonucleotide 24.
XX XX
XX KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
XX KW bulge; fixation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1. .11 /*tag= b
XX FT /note= "see comments for details about backbone bonds"
XX FT modified_base 6 /*tag= a
XX FT /mod_base= 2'-O-(hexylamino)_uridine
XX FT WO9318052-A1.
XX XX
XX PN 16-SEP-1993.
XX XX
XX PP 05-MAR-1993; 93WO-US002059.
XX XX
XX PR 05-MAR-1992; 92US-00846376.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cook PD, Manoharan M, Bruce T;
XX PS WPI; 1993-303395/38.
XX DR
XX FT New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX FT structures or hairpin loop, stem loop, interior loop, bulge or other
XX FT structures.
XX PS Disclosure; Page 80; 145pp; English.
XX CC The bases are linked as follows. Where - is a phosphodiester backbone. =
XX CC is a phosphorothioate backbone. G=C-T-G-X-C-T-G-C-G sequences (AAQ48905
XX CC -28) consist of novel crosslinked oligo-nucleotides. A number of
XX CC crosslinking methods are claimed, which are used to fix separate ON
XX CC strands in duplex structures or to fix a single ON strand in a hairpin
XX CC loop, stem loop, interior loop, bulge or other similar higher-order
XX CC structures. Fixing a strand or strands in a duplex structure also can
XX CC disrupt the normal function of a single stranded nucleic acid-binding
XX CC protein by forming nuclease resistant mimics of the protein binding
XX CC receptors. The ONs have diagnostic, therapeutic and prophylactic
XX CC applications as well as being used as research agents. (Updated on 25-MAR
XX CC -2003 to correct PN field.)
XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
      Query Match 43.3%; Score 7.8; DB 1; Length 11;
      Best Local Similarity 72.7%; Pred. No. 2.6e+02;
      Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      |||||: |||
        1 GGCTGUCTGCG 11

RESULT 324
AAQ48925
ID AAQ48925 standard; DNA; 11 BP.

```



```
FT FT /*tag= a
FT FT /mod_base= 2'-O-(hexylamino)_uridine
XX PN WO9318052-A1.
XX XX
XX PD 16-SEP-1993.
XX XX
XX PF 05-MAR-1993; 93WO-US002059.
XX XX
XX PR 05-MAR-1992; 92US-00846376.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cook PD, Manoharan M, Bruice T;
XX XX WPI; 1993-303395/38.
XX DR
XX PF New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX PT structures or hairpin loop, stem loop, interior loop, bulge or other
XX PT structures.
XX XX
XX PS Disclosure; Page 80; 145pp; English.
XX CC
XX CC Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
XX CC number of crosslinking methods are claimed, which are used to fix
XX CC separate ON strands in duplex structures or to fix a single ON strand in
XX CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-
XX CC order structures. Fixing a strand or strands in a duplex structure also
XX CC can disrupt the normal function of a single stranded nucleic acid-binding
XX CC protein by forming nuclease resistant mimics of the protein binding
XX CC receptors. The ONs have diagnostic, therapeutic and prophylactic
XX CC applications as well as being used as research agents. (Updated on 25-MAR
XX CC -2003 to correct PN field.)
XX XX
XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 72.7%; Pred. No. 2.6e+02;
XX Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 6 GGCTGTTGGCG 16
Db |||||: |||
1 GGCTGUCTGCG 11
XX
XX RESULT 327
XX AAQ48918
XX ID AAQ48918 standard; DNA; 11 BP.
XX AC AAQ48918;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1994 (first entry)
XX XX
XX DE Cross-linking oligonucleotide 14.
XX XX
XX KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
XX KW bulge; fixation; ss.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT misc_binding 6
XX FT /*tag= b
XX FT /note= "crosslinked to base 6 of (AAQ48906) via O-(CH2)7-
XX FT O-CH(OH) - as in example 11d"
XX FT modified_base 6
XX FT /*tag= a
XX FT /mod_base= heptan-7-ol functional_uridine
XX FT /note= "ref: example 4-A"
XX XX
XX PN WO9318052-A1.
XX XX
XX PD 16-SEP-1993.
XX XX
XX PF 05-MAR-1993; 93WO-US002059.
XX XX
XX PR 05-MAR-1992; 92US-00846376.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PF 05-MAR-1993; 93WO-US002059.
XX XX
XX XX
```

```
FT FT /*tag= a
FT FT /mod_base= 2'-O-(hexylamino)_uridine
XX PN WO9318052-A1.
XX XX
XX PD 16-SEP-1993.
XX XX
XX PF 05-MAR-1993; 93WO-US002059.
XX XX
XX PR 05-MAR-1992; 92US-00846376.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Cook PD, Manoharan M, Bruice T;
XX XX WPI; 1993-303395/38.
XX DR
XX PF New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX PT structures or hairpin loop, stem loop, interior loop, bulge or other
XX PT structures.
XX XX
XX PS Disclosure; Page 80; 145pp; English.
XX CC
XX CC Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
XX CC number of crosslinking methods are claimed, which are used to fix
XX CC separate ON strands in duplex structures or to fix a single ON strand in
XX CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-
XX CC order structures. Fixing a strand or strands in a duplex structure also
XX CC can disrupt the normal function of a single stranded nucleic acid-binding
XX CC protein by forming nuclease resistant mimics of the protein binding
XX CC receptors. The ONs have diagnostic, therapeutic and prophylactic
XX CC applications as well as being used as research agents. (Updated on 25-MAR
XX CC -2003 to correct PN field.)
XX XX
XX SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 72.7%; Pred. No. 2.6e+02;
XX Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 6 GGCTGTTGGCG 16
Db |||||: |||
1 GGCTGUCTGCG 11
XX
XX RESULT 327
XX AAQ48918
XX ID AAQ48918 standard; DNA; 11 BP.
XX AC AAQ48918;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1994 (first entry)
XX XX
XX DE Cross-linking oligonucleotide 14.
XX XX
XX KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
XX KW bulge; fixation; ss.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 6
XX FT /*tag= a
XX FT /mod_base= ethyl hydrazide_functional_uridine
XX FT with oxygen linking atom
XX FT /note= "ref: example 4-A"
XX XX
XX PN WO9318052-A1.
XX XX
XX PD 16-SEP-1993.
XX XX
XX PF 05-MAR-1993; 93WO-US002059.
XX XX
XX XX
```



```

PI Cook PD, Manoharan M, Bruice T;
XX WPI; 1993-303395/38.
XX
XX New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX structures or hairpin loop, stem loop, interior loop, bulge or other
XX structures.
XX
XX Disclosure; Page 68; 145pp; English.
XX
XX Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
XX number of crosslinking methods are claimed, which are used to fix
XX separate ON strands in duplex structures or to fix a single ON strand in
XX a hairpin loop, stem loop, interior loop, bulge or other similar higher-
XX order structures. Fixing a strand or strands in a duplex structure also
XX can disrupt the normal function of a single stranded nucleic acid-binding
XX protein by forming nuclease resistant mimics of the protein binding
XX receptors. The ONs have diagnostic, therapeutic and prophylactic
XX applications as well as being used as research agents. (Updated on 25-MAR
XX -2003 to correct PN field.)
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 329
AAV06685
ID AAV06685 standard; DNA; 11 BP.
XX
XX AAV06685;
AC
XX
XX 25-MAR-2003 (revised)
DT 26-MAY-1998 (first entry)
XX
XX Oligonucleotide used in covalently cross-linked nucleic acid.
DE
XX Covalent cross-link; RNA mimic; spatial configuration; abasic site; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 6
XX modified_base 6
XX /tag= a
XX /note= "2'-O-(octylhydrazino)-uridine"
XX
XX US5543507-A.
XX
XX 06-AUG-1996.
XX
XX 02-MAR-1994; 94US-00205507.
XX
XX 05-MAR-1992; 92US-00846376.
XX 05-MAR-1993; 93WO-US002059.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bruice T, Manoharan M, Cook PD;
XX WPI; 1996-370682/37.
XX
XX Crosslinked nucleic acids and oligo-nucleotide(s) - used as RNA mimics
XX that are fixed in specific spatial configurations.
XX

```

```

PS Example 15; Col 42; 44pp; English.
XX
XX This sequence represents an oligonucleotide shown in the specification. A
XX crosslinked nucleic acid comprises: a 1st nucleotide (N1) located on a
XX 1st oligonucleotide (ON) strand; a 1st bond means (B1) located on a sugar
XX moiety of N1, a 2nd nucleotide (N2) located on a 2nd ON strand; a 2nd
XX bond means (B2) located on a sugar moiety of N2; and a covalent cross-
XX linkage (CCL) between B1 and B2; provided that at least one of B1 and B2
XX is located at a non-terminal nucleotide and further provided that CCL is
XX not between the 3' carbon of a sugar moiety of N1 and the 5' carbon of a
XX sugar moiety of N2; is not between the 3' carbon of a sugar group of N2
XX and the 5' carbon of a sugar gp. Of N1; and does not include a
XX nucleosidic base. The oligonucleotides can be used as RNA mimics that are
XX fixed in specific spatial conformations via crosslinking covalent bonds.
XX The covalently crosslinked ON's have the same sequence as known nuclease-
XX resistant mimics of binding receptors for nucleic acid binding proteins.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 330
AAV06675
ID AAV06675 standard; DNA; 11 BP.
XX
XX AAV06675;
AC
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Modified oligonucleotide in covalently cross-linked nucleic acid.
DE
XX Covalent cross-link; modified oligonucleotide; abasic site;
XX space spanning group; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 6
XX modified_base 6
XX /tag= b
XX /label= uracil
XX
XX /tag= a
XX /note= "nucleotide modified to incorporate a 2'-O-
XX (octylhydrazino), octyl-hydroxylamino, pentyl-N-
XX semicarbazide, ethylhydrazide, heptan-7-ol or a
XX hexylamino functionality. Nucleotide may be 2'-
XX deoxyuridine"
XX
XX US5719271-A.
XX
XX 17-FEB-1998.
XX
XX 30-AUG-1994; 94US-00295743.
XX
XX 05-MAR-1992; 92US-00846376.
XX 05-MAR-1993; 93WO-US002059.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Bruice T, Cook PD;
XX WPI; 1998-158831/14.
XX
XX Covalently cross-linked nucleic acids - in which 2'- or 3'-hydroxy groups
XX

```

PT on sugar moieties of nucleotide(s), on one or more oligonucleotide
 PT strands, are linked by a non-phosphorus linkage.
 XX
 PS Example 10; Col 39; 36pp; English.
 XX
 CC This sequence represents an oligonucleotide shown in the patent. The
 CC invention relates to a cross-linked nucleic acid, which comprises: (a) a
 CC first nucleotide located on a first oligonucleotide strand having a first
 CC bond site located on either a 2'- or 3'-OH of the sugar moiety; (b) a
 CC second nucleotide located on a second oligonucleotide strand having a
 CC second bond site located on either a 2'- or 3'-OH of the sugar moiety.
 CC The first strand is linked to the second strand via a non-phosphorus
 CC covalent cross-linkage between the first and second bond sites, where not
 CC both sites may be on a 3'-OH or a terminal nucleotide. The cross-linked
 CC nucleic acids include materials in which oligonucleotide strands are
 CC covalently cross-linked to themselves or to other strands. Such materials
 CC can be used, e.g., as RNA mimics which are fixed in specific spatial
 CC conformations. These materials may be used as therapeutic agents,
 CC research reagents and diagnostic agents. (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX
 SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 2.6e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 6 GGCTGTGGCG 16
 Db ||||| ||||
 1 GGCTGUCTGCG 11
 RESULT 331
 AAZ18935/C
 ID AAZ18935 standard; DNA; 11 BP.
 XX
 AC AAZ18935;
 DT 22-OCT-1999 (first entry)
 XX Murine MRL SAGE tag 76753.
 DE
 XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
 XX
 OS Mus sp.
 XX
 XX WO9941364-A2.
 XX
 XX 19-AUG-1999.
 XX
 XX 12-FEB-1999; 99WO-US002962.
 XX
 XX 13-FEB-1998; 98US-0074737P.
 PR 26-AUG-1998; 98US-0097937P.
 PR 28-SEP-1998; 98US-0102051P.
 XX
 XX (WIST-) WISTAR INST.
 PA
 XX Heber-Katz E;
 PI
 XX WPI; 1999-494533/41.
 DR
 XX New mammalian model for enhanced wound healing - useful for identifying
 PT enhanced wound healing genes.
 PT
 XX Claim 13; Page 72; 136pp; English.
 PS
 XX This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.

CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGAGGCTGTT 12
 Db ||||| |||||
 11 TTGAACCTGTT 1
 RESULT 332
 AAZ19008
 ID AAZ19008 standard; DNA; 11 BP.
 XX
 AC AAZ19008;
 DT 22-OCT-1999 (first entry)
 XX Murine MRL SAGE tag 3059451.
 DE
 XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
 XX
 OS Mus sp.
 XX
 XX WO9941364-A2.
 PN
 XX 19-AUG-1999.
 PD
 XX 12-FEB-1999; 99WO-US002962.
 PF
 XX 13-FEB-1998; 98US-0074737P.
 PR 26-AUG-1998; 98US-0097937P.
 PR 28-SEP-1998; 98US-0102051P.
 XX
 XX (WIST-) WISTAR INST.
 PA
 XX Heber-Katz E;
 PI
 XX WPI; 1999-494533/41.
 DR
 XX New mammalian model for enhanced wound healing - useful for identifying
 PT enhanced wound healing genes.
 PT
 XX Claim 13; Page 74; 136pp; English.
 PS
 XX This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.

CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AA218591-219036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention

XX SQ Sequence 11 BP; 0 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
Db 1 GTGGGTGTTGG 11

RESULT 333
AAZ95239
ID AAZ95239 standard; DNA; 11 BP.

AC AAZ95239;

DT 05-JUN-2000 (first entry)

DE Sequence used in thermal melt analysis of modified oligonucleotides.

XX Antisense oligonucleotide; phosphorothioate; gene therapy;
KW research reagent; therapeutic; thermal melt analysis; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 6

FT /*tag= a
FT /note= "Site of 2'-aminolinker or 3'-aminolinker
FT attachment"

XX WO200004189-A1.

XX 27-JAN-2000.

XX 13-JUL-1999; 99WO-US015886.

XX 14-JUL-1998; 98US-00115043.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Cook PD;

XX WPI; 2000-182445/16.

XX Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents.

XX Example 53; Page 57; 75pp; English.

XX This sequence represents a modified oligonucleotide used in the thermal
CC melt analysis of 2',5'-linked oligonucleotides versus 3',5'-linked
CC oligonucleotides. The 2',5'-linkages demonstrate a higher melting
CC temperature against an RNA target compared to a DNA target. The invention
CC relates to oligonucleotides comprising nucleotides covalently linked
CC together by internucleotide linkages where at least 1 nucleotide is
CC linked to adjacent nucleotide by a 2',5'-internucleotide linkage and
CC bears a 3'-substituent. The oligonucleotides can be used in gene therapy
CC and are also useful in antisense methodologies, diagnostics, therapeutics
CC and as research reagents

XX Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 1 GGCTGUCTGG 11

RESULT 334

AAA88944

ID AAA88944 standard; DNA; 11 BP.

XX AAA88944;

DT 05-MAR-2001 (first entry)

DE 3',5'-linked oligonucleotide A.

XX Oligonucleotide; DNA-RNA hybrid; nuclease resistance; psoriasis;
KW antipsoriatic; dermatological; cytostatic; virucide; antibacterial;
KW fungicide; therapy; diagnosis; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 6

FT /*tag= b
FT /label= RNA

FT modified_base 6

FT /*tag= a

FT /label= OTHER

XX /note= "2'-aminolinker-uridine"

XX WO200066609-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000WO-US011913.

XX 03-MAY-1999; 99US-00303586.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Mohan V;

XX WPI; 2000-672833/65.

XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.

XX Example 53; Page 67; 132pp; English.

XX Oligonucleotide A is a 3',5'-linked phosphodiester
CC oligodeoxyribonucleotide including a 2'-aminolinker. It was used in an
CC experiment that demonstrated the higher melting temperatures of 2',5'-
CC linked versus 3',5'-linked oligonucleotides. Novel oligonucleotides of
CC the invention have both A- and B-form conformational geometry. The A-form
CC geometry modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications

XX Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16

```
Db          1 GGCTGUCTGCG 11
|||||: |||
|||||: |||
1 GGCTGUCTGCG 11

RESULT 335
AAA88945
ID AAA88945 standard; DNA; 11 BP.
XX
AC AAA88945;
XX
DT 05-MAR-2001 (first entry)
XX
DE 3',5'-linked oligonucleotide B.
XX
KW Oligonucleotide; DNA-RNA hybrid; nuclease resistance; psoriasis;
KW antipsoriatic; dermatological; cytostatic; virucide; antibacterial;
KW fungicide; therapy; diagnosis; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 1 /*tag= c
FT /mod_base= gm
FT modified_base 2 /*tag= d
FT /mod_base= gm
FT modified_base 3 /*tag= e
FT /mod_base= cm
FT modified_base 4 /*tag= f
FT /mod_base= OTHER
FT /note= "2'-O-methylthymidine"
FT modified_base 6 /*tag= g
FT /mod_base= cm
FT misc_RNA 6 /*tag= b
FT /label= RNA
FT modified_base 6 /*tag= a
FT /label= OTHER
FT modified_base 8 /*tag= h
FT /mod_base= OTHER
FT modified_base 9 /*tag= i
FT /mod_base= gm
FT modified_base 10 /*tag= j
FT /mod_base= cm
FT modified_base 12 /*tag= k
FT /mod_base= gm
XX
PN WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to

treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
bacterial infections, bind to single stranded RNA or DNA.

Example 53; Page 68; 132pp; English.

Oligonucleotide B is a 3',5'-linked phosphodiester
oligodeoxyribonucleotide including a 2'-aminolinker. It was used in an
experiment that demonstrated the higher melting temperatures of 2',5'-
linked versus 3',5'-linked oligonucleotides. Novel oligonucleotides of
the invention have both A- and B-form conformational geometry. The A-form
geometry modulates the binding affinity and nuclease resistance of the
oligonucleotide. The B-form geometry allows the oligonucleotide to serve
as substrate for RNase-H when bound to a target nucleic acid strand. The
oligonucleotides can be used to treat psoriasis and other inflammatory
skin conditions, skin cancers and viral, bacterial and fungal infections,
and in various diagnostic applications

SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 336
AAA88946
ID AAA88946 standard; DNA; 11 BP.
XX
AC AAA88946;
XX
DT 05-MAR-2001 (first entry)
XX
DE 3',5'-linked oligonucleotide C.
XX
KW Oligonucleotide; DNA-RNA hybrid; nuclease resistance; psoriasis;
KW antipsoriatic; dermatological; cytostatic; virucide; antibacterial;
KW fungicide; therapy; diagnosis; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT misc_RNA 6 /*tag= b
FT /label= RNA
FT modified_base 6 /*tag= a
FT /label= OTHER
FT /note= "2'-aminolinker-uridine, 2',5'-linkage"
XX
PN WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
bacterial infections, bind to single stranded RNA or DNA.

Example 53; Page 68; 132pp; English.

New oligonucleotides containing sequences with A and B geometry, used to
treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
bacterial infections, bind to single stranded RNA or DNA.

Example 53; Page 68; 132pp; English.
```

CC Oligonucleotide A is a 2',5'-linked phosphodiester
CC oligodeoxyribonucleotide including a 2'-aminolinker. It was used in an
CC experiment that demonstrated the higher melting temperatures of 2',5'-
CC linked versus 3',5'-linked oligonucleotides. Novel oligonucleotides of
CC the invention have both A- and B-form conformational geometry. The A-form
CC geometry modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTGGCG 16
Db 1 GGCTGTGGCG 11

RESULT 337
AAF31260/c
ID AAF31260 standard; DNA; 11 BP.
XX
AC AAF31260;
XX
DT 09-APR-2001 (first entry)
XX
DE GC-rich template cycle sequencing mixture related sequence #4.
XX
KW GC-rich template; cycle sequencing; 7-deaza dGTP; dITP;
KW DNA amplification; ds.
XX
OS Synthetic.
XX
PN WO200102602-A2.
XX
PD 11-JAN-2001.

XX 05-JUL-2000; 2000WO-EP006349.
XX
XX 05-JUL-1999; 99EP-00112943.
XX
XX (LION-) LION BIOSCIENCE AG.
XX
XX Motz M, Voss H;
XX
XX WPI; 2001-138153/14.
XX
XX Use of a mixture comprising 7-deaza dGTP and dITP for direct exponential
PT amplification and sequencing of nucleic acids, particularly guanosine
PT cytosine rich templates.
XX
XX Disclosure; Fig 2; 18pp; English.

XX The present invention describes a mixture comprising 7-deaza dGTP and
CC dITP, which can be used in the cycle sequencing of GC-rich templates. In
CC addition, the mixture can be used in DNA amplification. Sequences
CC AAF31257-AAF31267 are examples of compression prone sequences
XX
SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGGCTGTGGC 15
Db 11 AGGCTGTGGC 1

RESULT 338
AAH25736
ID AAH25736 standard; DNA; 11 BP.
XX
AC AAH25736;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H thermal melt assay oligonucleotide.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW Gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.

PH Key Location/Qualifiers
FT misc_RNA 6 /*tag= b
FT modified_base 6 /*tag= a
FT /*mod_base= OTHER
FT /*note= "modified by 2'-aminolinker"

XX WO200123613-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-US026729.
XX
XX 30-SEP-1999; 99US-00409926.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX
XX WPI; 2001-343164/36.

XX Chimeric oligonucleotides that can serve as substrates for human RNase
PT H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
XX Example 53; Page 86; 178pp; English.

XX The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase H1 (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an oligonucleotide used
CC in the exemplification of the invention

SQ Sequence 11 BP; 0 A; 3 C; 5 G; 2 T; 1 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 1 GGCTGTGGCG 11

RESULT 339
ABQ86744
ID ABQ86744 standard; cDNA; 11 BP.
XX
AC ABQ86744;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 499.
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

```

XX OS Homo sapiens.
XX PN W0200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX Claim 8; Page 57; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 CTGTTGGCGAC 18
Db 1 CTGCTGCCAC 11
|||||
RESULT 340
ABV67690/c
XX ID ABV67690 standard; cDNA; 11 BP.
XX AC ABV67690;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 5476.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;

```

```

XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 176; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGCGTGTGG 14
Db 11 GAAGCTGCTGG 1
|||||
RESULT 341
ABV67410/c
XX ID ABV67410 standard; cDNA; 11 BP.
XX AC ABV67410;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 5196.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 168; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.

```

CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 11 AGGTGGGCG 1

RESULT 342
ABV62451
ID ABV62451 standard; cDNA; 11 BP.
XX
AC ABV62451;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 237.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 32; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 11 AGGTGGGCG 1

RESULT 344
ABV68093
ID ABV68093 standard; cDNA; 11 BP.
XX
AC ABV68093;
XX

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGGCTCTGGC 11

RESULT 343
ABV66069
ID ABV66069 standard; cDNA; 11 BP.
XX
AC ABV66069;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3855.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 131; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGGATGTGGC 11

RESULT 344
ABV68093
ID ABV68093 standard; cDNA; 11 BP.
XX
AC ABV68093;
XX

DT 21-OCT-2002 (first entry)
 XX Human skin EST 5879.
 DE
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 XX Disclosure; Page 188; 1345pp; German.
 XX
 XX The invention relates to in vitro identification (M1) of genes expressed
 XX in the skin of humans or animals by subjecting a mixture of genetically
 XX encoded factors from skin, to serial analysis of gene expression (SAGE)
 XX so as to identify skin-expressed genes and quantify their expression.
 XX (M1) is useful for identifying genes involved in skin homeostasis; to
 XX determine skin homeostasis and to test agent (A) that maintains or
 XX promotes skin homeostasis or that can be used for treating skin
 XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 XX skin. The present sequence is that of a human expressed sequence tag
 XX (EST) of the invention
 XX
 XX Sequence 11 BP; 2 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTGG 13
 DB 1 TGATGATGTG 11
 RESULT 345
 ABV69872
 ID ABV69872 standard; cDNA; 11 BP.
 AC ABV69872;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 7658.
 DE
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 XX
 XX Claim 24; Page 242; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 XX in the skin of humans or animals by subjecting a mixture of genetically
 XX encoded factors from skin, to serial analysis of gene expression (SAGE)
 XX so as to identify skin-expressed genes and quantify their expression.
 XX (M1) is useful for identifying genes involved in skin homeostasis; to
 XX determine skin homeostasis and to test agent (A) that maintains or
 XX promotes skin homeostasis or that can be used for treating skin
 XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 XX skin. The present sequence is that of a human expressed sequence tag
 XX (EST) of the invention
 XX
 XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 AGGCTGTGGC 15
 DB 1 AGGCTCTGGC 11
 RESULT 346
 ABV65916
 ID ABV65916 standard; cDNA; 11 BP.
 XX
 XX ABV65916;
 AC
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 3702.
 DE
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against

PT e.g. skin cancer.
 PS Disclosure; Page 127; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GAGCTCTGTCG 14
 Db 1 GAGCTCTGTCG 11
 RESULT 347
 ABV63034
 ID ABV63034 standard; cDNA; 11 BP.
 AC ABV63034;
 XX
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 820.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 48; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GAGCTCTGTCG 14
 Db 1 GAGCTCTGTCG 11
 RESULT 348
 ABV67617/c
 ID ABV67617 standard; cDNA; 11 BP.
 AC ABV67617;
 XX
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 5403.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR
 XX (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 174; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTT 12
 Db 11 TTGAAGCAGTT 1

```
RESULT 349
ABV62588/c
ID   ABV62588 standard; cDNA; 11 BP.
XX   AC   ABV62588;
XX   DT   21-OCT-2002 (first entry)
XX   DE   Human skin EST 374.
XX   KW   Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX   KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX   KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX   OS   Homo sapiens.
XX   PN   WO200253774-A2.
XX   PD   11-JUL-2002.
XX   PF   20-DEC-2001; 2001WO-EP015179.
XX   PR   03-JAN-2001; 2001DE-01000127.
XX   PA   (HENK ) HENKEL KGAA.
XX   PI   Petersohn D, Conradt M, Hofmann K;
XX   PS   WPI; 2002-590638/63.
XX   CC   The invention relates to in vitro identification (M1) of genes expressed
XX   CC   in the skin of humans or animals by subjecting a mixture of genetically
XX   CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
XX   CC   so as to identify skin-expressed genes and quantify their expression.
XX   CC   (M1) is useful for identifying genes involved in skin homeostasis; to
XX   CC   determine skin homeostasis and to test agent (A) that maintains or
XX   CC   promotes skin homeostasis or that can be used for treating skin
XX   CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX   CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX   CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX   CC   skin. The present sequence is that of a human expressed sequence tag
XX   CC   (EST) of the invention
XX   SQ   Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
XX   Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX   Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX   Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX   QY 5 AGCGTGTGGC 15
XX   DB 11 ACGCGTGTGGC 1
XX   RESULT 350
XX   ABV65487/c
XX   ID   ABV65487 standard; cDNA; 11 BP.
XX   AC   ABV65487;
XX   DT   21-OCT-2002 (first entry)
XX   DE   Human skin EST 3273.
XX   KW   Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX   KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX   KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX   OS   Homo sapiens.
XX   PN   WO200253774-A2.
XX   PD   11-JUL-2002.
XX   PF   20-DEC-2001; 2001WO-EP015179.
XX   PR   03-JAN-2001; 2001DE-01000127.
XX   PA   (HENK ) HENKEL KGAA.
XX   PI   Petersohn D, Conradt M, Hofmann K;
XX   PS   WPI; 2002-590638/63.
XX   CC   The invention relates to in vitro identification (M1) of genes expressed
XX   CC   in the skin of humans or animals by subjecting a mixture of genetically
XX   CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
XX   CC   so as to identify skin-expressed genes and quantify their expression.
XX   CC   (M1) is useful for identifying genes involved in skin homeostasis; to
XX   CC   determine skin homeostasis and to test agent (A) that maintains or
XX   CC   promotes skin homeostasis or that can be used for treating skin
XX   CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX   CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX   CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX   CC   skin. The present sequence is that of a human expressed sequence tag
XX   CC   (EST) of the invention
XX   SQ   Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
XX   Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX   Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX   Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX   QY 7 GCTGTGTGGCGA 17
XX   DB 11 GGTGTGTGGCAA 1
XX   RESULT 351
XX   ABV70455
XX   ID   ABV70455 standard; cDNA; 11 BP.
XX   AC   ABV70455;
XX   DT   21-OCT-2002 (first entry)
XX   DE   Human skin EST 8241.
XX   KW   Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX   KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX   KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX   OS   Homo sapiens.
XX   PN   WO200253774-A2.
XX   PD   11-JUL-2002.
XX   PF   20-DEC-2001; 2001WO-EP015179.
XX   PR   03-JAN-2001; 2001DE-01000127.
XX   PA   (HENK ) HENKEL KGAA.
XX   PI   Petersohn D, Conradt M, Hofmann K;
XX   PS   WPI; 2002-590638/63.
XX   CC   The invention relates to in vitro identification (M1) of genes expressed
XX   CC   in the skin of humans or animals by subjecting a mixture of genetically
XX   CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
XX   CC   so as to identify skin-expressed genes and quantify their expression.
XX   CC   (M1) is useful for identifying genes involved in skin homeostasis; to
XX   CC   determine skin homeostasis and to test agent (A) that maintains or
XX   CC   promotes skin homeostasis or that can be used for treating skin
XX   CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX   CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX   CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX   CC   skin. The present sequence is that of a human expressed sequence tag
XX   CC   (EST) of the invention
XX   SQ   Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
XX   Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX   Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX   Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX   QY 7 GCTGTGTGGCGA 17
XX   DB 11 GGTGTGTGGCAA 1
```

PA (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 264; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
 Db 1 CTGTTGGCGAC 11
 ||| |||||
 ||| |||||

RESULT 352
 ABV68204
 ID ABV68204 standard; cDNA; 11 BP.
 XX AC ABV68204;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 5990.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 191; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
 Db 1 TGGATGCTGTT 11
 ||| |||||
 ||| |||||

RESULT 353
 ABV70009/c
 ID ABV70009 standard; cDNA; 11 BP.
 XX AC ABV70009;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 7795.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 248; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match	43.3%;	Score 7.8;	DB 1;	Length 11;
Best Local Similarity	81.8%;	Pred. No. 2.6e+02;		
Matches	9;	Conservative	0; Mismatches	2; Indels
Gaps	0;			

QY	-	5 AGGCTGTGGC	15
DB	-		
	11	ACCGCGTTGC	1

RESULT 354

ABV64798

ID ABV64798 standard; cDNA; 11 BP.

XX AC

XX AC

XX AC

DT 21-OCT-2002 (first entry)

XX XX

DE Human skin EST 2584.

XX XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX XX

PN WO200253774-A2.

XX XX

PD 11-JUL-2002.

XX XX

PF 20-DEC-2001; 2001WO-EP015179.

XX PR

PR 03-JAN-2001; 2001DE-01000127.

XX XX

PA (HENK) HENKEL KGAA.

XX PA

PI Petersohn D, Conradt M, Hofmann K;

XX PI

XX WPI; 2002-590638/63..

DR XX

PT In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

PT PT

PS Disclosure; Page 97; 1345pp; German.

XX PS

CC The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX XX

SQ Sequence 11 BP; 2 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match	43.3%;	Score 7.8;	DB 1;	Length 11;
Best Local Similarity	81.8%;	Pred. No. 2.6e+02;		
Matches	9;	Conservative	0; Mismatches	2; Indels
Gaps	0;			

QY	-	4 GAGCGTGTGG	14
DB	-		
	1	GAGGCGTTGG	11

RESULT 355

ABL91967

ID ABL91967 standard; cDNA; 11 BP.

KW DNA mismatch; oxidising agent; mutation identification; polymorphism; ds.
XX Synthetic.
XX WO200266674-A1.
XX 29-AUG-2002.
XX 19-FEB-2002; 2002WO-AU000171.
XX 19-FEB-2001; 2001AU-00003205.
PR 20-MAR-2001; 2001AU-00003855.
XX (GENO-) GENOMIC DISORDERS RES CENT.
XX Cotton RGH, Bui CT, Lambrinakos A;
XX WPI; 2002-674958/72.
XX
XX Detecting base pairing differences between nucleic acid molecules, useful
XX in detecting diseases and genetically modified organisms, comprises the
XX use of oxidizing agents on mismatched or unmatched bases in the duplex.
XX
XX Example 3; Page 33; 82pp; English.
XX
XX The present invention relates to a method of detecting a base pairing
XX difference between two nucleic acid molecules in a test nucleic acid
XX duplex, comprising treating the duplex with an oxidising agent to oxidise
XX a mismatched or unmatched base in the duplex, monitoring the formation
XX and/or consumption, or their rates, of the reaction products or starting
XX agents, respectively, and determining the difference in the formation
XX and/or consumption between test and control duplexes. The methods are
XX useful in detecting the presence of genetic mutations and variations or
XX damage to the integrity of the cellular DNA and RNA, thus, aiding in the
XX diagnosis, prognosis or choice of optimal therapy of disease states, e.g.
XX infections, in the detection of genetically modified organisms, and in
XX research, commercial or pharmaceutical purposes. The methods may also be
XX used to enable quality control of nucleotide constructs for gene therapy,
XX antisense oligonucleotide therapy, DNA vaccine production or other
XX therapeutic modalities, and for industrial applications. The present
XX sequence is an oligonucleotide used to demonstrate the method of the
XX invention
SQ Sequence 11 BP; 3 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 11 GGCTGTTGGCG 1

RESULT 357
AAL49632
ID AAL49632 standard; DNA; 11 BP.
AC AAL49632;
XX
XX 27-NOV-2002 (first entry)
XX
XX DNA mismatch identification method related oligonucleotide #7.
XX
XX DNA mismatch; oxidising agent; mutation identification; polymorphism; ds.
XX Synthetic.
XX WO200266674-A1.
XX 29-AUG-2002.
XX 19-FEB-2002; 2002WO-AU000171.

XX 19-FEB-2001; 2001AU-00003205.
PR 20-MAR-2001; 2001AU-00003855.
XX (GENO-) GENOMIC DISORDERS RES CENT.
XX Cotton RGH, Bui CT, Lambrinakos A;
XX WPI; 2002-674958/72.
XX
XX Detecting base pairing differences between nucleic acid molecules, useful
XX in detecting diseases and genetically modified organisms, comprises the
XX use of oxidizing agents on mismatched or unmatched bases in the duplex.
XX
XX Example 3; Page 33; 82pp; English.
XX
XX The present invention relates to a method of detecting a base pairing
XX difference between two nucleic acid molecules in a test nucleic acid
XX duplex, comprising treating the duplex with an oxidising agent to oxidise
XX a mismatched or unmatched base in the duplex, monitoring the formation
XX and/or consumption, or their rates, of the reaction products or starting
XX agents, respectively, and determining the difference in the formation
XX and/or consumption between test and control duplexes. The methods are
XX useful in detecting the presence of genetic mutations and variations or
XX damage to the integrity of the cellular DNA and RNA, thus, aiding in the
XX diagnosis, prognosis or choice of optimal therapy of disease states, e.g.
XX infections, in the detection of genetically modified organisms, and in
XX research, commercial or pharmaceutical purposes. The methods may also be
XX used to enable quality control of nucleotide constructs for gene therapy,
XX antisense oligonucleotide therapy, DNA vaccine production or other
XX therapeutic modalities, and for industrial applications. The present
XX sequence is an oligonucleotide used to demonstrate the method of the
XX invention
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGTTGGCG 11

RESULT 358
AAD32705
ID AAD32705 standard; DNA; 11 BP.
XX
XX AAD32705;
XX
XX 01-JUL-2002 (first entry)
XX
XX pWB plasmid DNA half-site.
XX
XX Gene construct; pWB plasmid; half-site; ds.
XX Unidentified.
XX US2002025561-A1.
XX
XX 28-FEB-2002.
XX
XX 17-APR-2001; 2001US-00836737.
XX
XX 17-APR-2000; 2000US-0197882P.
XX (HODG/) HODGSON C P.
XX Hodgson CP;
XX WPI; 2002-280094/32.

PT Assembling gene constructs from a number of DNA fragments, and the
PT plasmid produced (pWB) which is useful for assembling synthetic genes,
PT constructs, vectors and chromosomes.
XX
PS Claim 14; Page 9; 12pp; English.
XX
CC The patent discloses methods for assembling gene constructs from a number
CC of DNA fragments to produce the plasmid (pWB). The vectors produced (pWB)
CC are used for the construction of a gene, vector, construct, combinatorial
CC library or chromosome and for trimming one or more bases from the ends of
CC insert fragments. The vectors of the invention facilitates the placement
CC of unique, non-palindromic address tags at the ends of the fragments and
CC allows validation of the fragments prior to assembly to assure that the
CC resulting construct is free of mutations. The present sequence is pWB
CC plasmid DNA half-site. This sequence is a combination of a SapI site with
CC an overlapping NruI site. This combination allows trimming of three bases
CC from one end of a nucleic acid molecule cloned in the NruI site
XX
SQ Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 17
DB 1 GCTGTGGCGA 11
|||||

RESULT 359
ABX71892
ID ABX71892 standard; DNA; 11 BP.
XX
AC ABX71892;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA tag used to identify human gene encoding PEM 65.
XX
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS Homo sapiens.
XX
XX WO200283874-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US008253.
XX
XX 11-APR-2001; 2001US-0282850P.
XX
XX 06-FEB-2002; 2002US-0354262P.
XX
XX (UJO) UNIV JOHNS HOPKINS.
XX
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX
XX New purified human transmembrane protein, designated as tumor endothelial
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
XX psoriasis.
XX
XX Disclosure; Page 97; 374pp; English.
XX
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal

CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neovascularization or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC represent DNA tags for human PEM, TEM or NEM genes
XX
SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGCCTGTGGC 15
DB 1 AGCCTGTGGC 11
|||||

RESULT 360
ACD82358/c
ID ACD82358 standard; DNA; 11 BP.
XX
AC ACD82358;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #59.
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
XX US2003044791-A1.
XX
XX 06-MAR-2003.
XX
XX 13-JUN-2001; 2001US-00880313.
XX
XX 13-JUN-2001; 2001US-00880313.
XX
XX (FLEM/) FLEMINGTON E K.
XX
XX Flemington EK;
XX
XX WPI; 2003-521745/49.
XX
XX New adaptor molecules, useful for cloning nucleic acid molecules that
XX does not require the design and synthesis of oligonucleotides or PCR
XX primers.
XX
XX Claim 12; Fig 1; 100pp; English.
XX
XX The invention describes adaptor molecules, where each end of the adaptor
XX is compatible with a nucleic acid digested with a restriction enzyme or a
XX nucleic acid comprising an end that is compatible with a nucleic acid
XX digested with a restriction enzyme. The adaptor molecules, compositions,
XX kits and arrays are useful for cloning nucleic acid molecules that does
XX not require the design and synthesis of oligonucleotides or PCR primers.
XX The adaptors, kits and arrays are also useful for ligating two ends of a
XX single nucleic acid molecule, or ligating two or more nucleic acid
XX molecules. The kits can also be used for performing internal deletion
XX mutagenesis analysis. The adaptor molecules are ligated to a cloning
XX vehicle, making the cloning procedure more rapid and efficient, and less
XX error-prone. This sequence represents a nucleic acid cloning associated
XX adaptor molecule
XX
XX Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 2.6e+02; Mismatches 0; Gaps 0; Indels 0;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
 ||||| |||||
 Db 11 GGCTGCAGGCG 1

RESULT 361
 AAT03078
 ID AAT03078 standard; DNA; 12 BP.
 AC AAT03078;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAY-1996 (first entry)
 XX
 DE E. coli small ribosomal subunit 16S rRNA antisense oligo (529-518).
 XX
 KW E. coli; small ribosomal subunit; 16S; rRNA; antisense; retrovirus; HIV;
 KW HTLV type 1; pol gene; ribosomal frameshifting; huamn; 18S; ss.
 XX
 OS Synthetic.
 XX WO9527054-A1.
 XX
 XX 12-OCT-1995.
 XX
 XX 28-MAR-1995; 95WO-CA000169.
 XX
 PR 30-MAR-1994; 94US-00220604.
 PR 23-MAR-1995; 95US-00409852.
 XX
 PA (UTMO-) UNIV MONTREAL.
 XX
 FI Brakier-Gingras L, Melancon P, Cote M, Payant C;
 XX
 DR WPI; 1995-366159/47.
 XX
 PT New anti-sense DNA oligomers - which decrease ribosomal frame-shifting
 PT and inhibit the expression of viral enzymatic proteins.
 XX
 PS Claim 2; Page 25; 34pp; English.
 XX
 CC The antisense oligonucleotides AAT03073-80 are targeted against specific
 CC regions in the 16S and 18S rRNA of the E. coli and human small ribosomal
 CC subunit, respectively. They can be used to inhibit enzymatic protein
 CC expression by a retrovirus in a host, and are therefore useful in the
 CC treatment of retroviral infections, e.g. HIV, HTLV type 1 or human
 CC retroviruses requiring ribosomal frameshifting for the expression of the
 CC pol gene. The antisense sequences are shown 3' to 5' in the
 CC specification. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
 ||||| |||||
 Db 2 GCGGCTGCTGG 12

RESULT 362
 AAV04828
 ID AAV04828 standard; cDNA; 12 BP.
 AC AAV04828;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Antisense DNA oligomer targeted against the 16S rRNA of E. coli.

XX Antisense oligomer; 16S rRNA; small ribosomal subunit; human; 18S rRNA;
 KW ribosomal frameshifting; expression; HIV enzymatic protein;
 KW HIV infection; ss.
 XX
 OS Synthetic.
 XX US5707866-A.
 XX
 PD 13-JAN-1998.
 XX
 DP 21-MAY-1996; 96US-00651835.
 XX
 PR 30-MAR-1994; 94US-00220604.
 PR 23-MAR-1995; 95US-00409852.
 XX
 PA (UTMO-) UNIV MONTREAL.
 XX
 FI Cote M, Payant C, Brakier-Gingras L, Melancon P;
 XX
 DR WPI; 1998-100350/09.
 XX
 PT Antisense oligonucleotide(s) complementary to human 18S rRNA - for
 PT inhibiting HIV ribosomal frameshifting and enzyme expression.
 XX
 PS Claim 2; Col 5; 14pp; English.
 XX
 CC Antisense oligomers AAV04822-29 are targeted against specific regions in
 CC the 16S rRNA of Escherichia coli small ribosomal subunit. These regions
 CC correspond to the human 18S rRNA nucleotides 595-641. The present
 CC oligomer is targeted toward positions 529-518. The oligonucleotides
 CC decrease the occurrence of ribosomal frameshifting and inhibits the
 CC expression of HIV enzymatic proteins. The antisense oligonucleotides are
 CC used for treating HIV infections
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
 ||||| |||||
 Db 2 GCGGCTGCTGG 12

RESULT 363
 AAV32292/C
 ID AAV32292 standard; DNA; 12 BP.
 XX
 AC AAV32292;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE Random primed reverse transcription PCR primer 42.
 XX
 KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
 KW differential gene expression; ss.
 XX
 OS Synthetic.
 XX WO9813521-A1.
 XX
 PD 02-APR-1998.
 XX
 PF 26-SEP-1997; 97WO-EP005290.
 XX
 PR 27-SEP-1996; 96GB-00020216.
 XX
 PA (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
 XX
 FI Consalez G, Fesce R;
 XX

DR WPI; 1998-230725/20.
XX Differential screening of gene expression by reverse transcription
PT polymerase chain reaction - uses random priming with primers selected for
PT high efficiency and selectivity by computer screening of database(s).
XX
PS Claim 9; Page 24; 37pp; English.
XX
CC The invention provides a method for the differential screening of gene
CC expression by random primed reverse transcription PCR (RT-PCR). The
CC primer sequences are generated by stimulating PCR reactions on non-
CC redundant mammalian nucleotide sequence databank entries containing at
CC least 1,000 bp of coding region. The primers selected, such as the
CC present one, had to meet various criteria such as having an efficiency
CC index between 2-10, having a selectivity index higher than 1, being 12 bp
CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others
CC in at least 5 of the 8 bases at the 3'-end. The invention claims the
CC selected primers make it possible to use internally primed, PCR-based RNA
CC fingerprinting for simple, exhaustive and systematic analysis of
CC differential gene expression as an advantageous alternative to
CC differential display. The method can also be useful for isolating new
CC coding sequences and to compare known and new genes
XX
SQ Sequence 12 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 1 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCG 16
||| |||||
DB 11 GGCAATTGGCG 1

RESULT 364
AAV05439
ID AAV05439 standard; DNA; 12 BP.
XX
AC AAV05439;
XX
CC 05-JUN-1998 (first entry)
DT
DE Primer used in protein-protein interaction detection.
DE
KW PCR primer; protein-protein interaction; detection; ss.
XX
OS Synthetic.
XX
PN W09747763-A1.
XX
PD 18-DEC-1997.
XX
PF 13-JUN-1997; 97WO-US010392.
XX
PR 14-JUN-1996; 96US-00663824.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;
XX WPI; 1998-052326/05.
XX
PT Identification and comparison of protein-protein interactions - useful
PT for assembling and processing unified databases of sequences.
XX
PS Example; Page 277; 426pp; English.
XX
CC The present sequence was used in the development of a novel method for
CC the detection of one or more protein-protein interactions. The method can
CC be used for comparative analysis of protein-protein interactions that
CC occur in two or more different tissue/cell-types, disease states or
CC stages of development. The genes encoding the proteins involved in these
CC interactions, can be identified and isolated rapidly. The method can also

CC be used for concurrent identification of inhibitors of the protein-
CC protein interactions that characterise a given population, and which have
CC therapeutic value
XX
SQ Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTTGGCGA 17
||||| |||
DB 2 GCTGTCGGTGA 12

RESULT 365
AAZ41828
ID AAZ41828 standard; DNA; 12 BP.
XX
AC AAZ41828;
XX
DT 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX
DE Organic material detecting primer 189.
XX
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX
OS Synthetic.
XX
PN DE19914461-A1.
XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99DE-01014461.
XX
PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
PT Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
PS Example 1; Page 22; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-241855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

Qy 5 AGGCTGTTGGC 15
Db 1 AAGCTGTGGC 11

RESULT 366
AAZ41696
ID AAZ41696 standard; DNA; 12 BP.
XX AC AAZ41696;
XX AC
XX XX
XX XX
DT 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX XX
XX XX
DE Organic material detecting primer 57.
XX XX
XX XX
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX OS
XX OS
XX XX
XX DE19914461-A1.
XX XX
PD 21-OCT-1999.
XX XX
PF 30-MAR-1999; 99DE-01014461.
XX XX
PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX XX
PI Inoue T;
XX XX
DR WPI; 1999-592157/51.
XX XX
XX Novel polymerase chain reaction method, for differentiating between
XX microorganisms and for detecting contaminants.
XX
XX Example 1; Page 17; 78pp; German.
XX
XX This invention describes a novel method for the amplification of DNA
XX comprising (i) preparing many primers (p) with different probabilities of
XX amplification and (ii) simultaneous polymerase chain reaction (PCR) of
XX many different DNA using these primers. The method is used (i) to
XX differentiate between different microorganisms in a mixed population and
XX (ii) to determine presence/absence of an impurity (pollutant), or its
XX concentration, in e.g. soil, foods, compost etc., typically metals,
XX agricultural chemicals, polymers, organochlorine compounds etc. A
XX particular use is monitoring composting of organic material.
XX Amplification with many primers produces a lot of information, so
XX reliability of the test is improved, and many samples may be tested
XX quickly. AAZ41640-241855 represent the primers described in the method of
XX the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
XX Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
Db 1 AAGCTGTGGC 11

RESULT 367
AAZ41612
ID AAZ41612 standard; DNA; 12 BP.
XX AC AAZ41612;

19-JAN-2000 (first entry)
Microbe detection in organic waste arbitrarily primed PCR primer #189.
Microbe; detection; organic waste; arbitrarily primer PCR;
random amplified polymorphic DNA; amplification; PCR primer; ss.
Synthetic.
JPI11276176-A.
12-OCT-1999.
31-MAR-1998; 98JP-00087652.
31-MAR-1998; 98JP-00087652.
(SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
WPI; 1999-626940/54.
Amplification of a DNA fragment - in order to establish the state of
existence of a microbe.
Example; Page 10; 40pp; Japanese.
A method has been developed for the amplification of a DNA fragment in
which amplification is carried out on the DNA fragments of a number of
different DNAs. The method comprises a PCR reaction repeatedly carrying
out a heat-denaturing step, a primer annealing step and a polymerase
extending step, to amplify the DNA fragments of a plural of different
DNAs. The method can detect the existence of a microbe in organic waste.
AAZ41424 to AAZ41639 represent PCR primers used in random amplified
polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
organic waste
Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15
Db 1 AAGCTGTGGC 11

RESULT 368
AAZ41480
ID AAZ41480 standard; DNA; 12 BP.
XX AC AAZ41480;
XX XX
DT 19-JAN-2000 (first entry)
XX XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #57.
XX Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
XX OS Synthetic.
XX XX
XX JPI11276176-A.
XX XX
PD 12-OCT-1999.
XX XX
PF 31-MAR-1998; 98JP-00087652.
XX XX
PR 31-MAR-1998; 98JP-00087652.
XX XX
PA (SAOL ) SANYO ELECTRIC CO LTD.

```

PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
 XX WPI; 1999-626940/54.
 XX Amplification of a DNA fragment - in order to establish the state of
 PT existence of a microbe.
 XX
 XX Claim 1; Page 8; 40pp; Japanese.
 XX
 CC A method has been developed for the amplification of a DNA fragment in
 CC which amplification is carried out on the DNA fragments of a number of
 CC different DNAs. The method comprises a PCR reaction repeatedly carrying
 CC out a heat-denaturing step, a primer annealing step and a polymerase
 CC extending step, to amplify the DNA fragments of a plural of different
 CC DNAs. The method can detect the existence of a microbe in organic waste.
 CC AA241424 to AA241639 represent PCR primers used in random amplified
 CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
 CC organic waste
 XX
 SQ Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 AGCTGTGGC 15
 DB 1 AGCTGTGGC 11
 RESULT 369
 AAA55875
 ID AAA55875 standard; DNA; 12 BP.
 AC AAA55875;
 XX
 XX 04-SEP-2000 (first entry)
 XX Hind III adapter primer SEQ ID NO:33.
 XX
 XX Yeast; detection; protein-protein interaction; DNA-binding domain;
 KW characterisation; identification; protein pathway information;
 KW protein interaction domain; screening; PCR primer; adapter; linker;
 KW fusion protein; inhibitor; regulation; ss.
 XX
 OS Synthetic.
 XX
 XX US6057101-A.
 XX
 XX 02-MAY-2000.
 XX
 XX 13-JUN-1997; 97US-00874825.
 XX
 XX 14-JUN-1996; 96US-00663824.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;
 XX WPI; 2000-349567/30.
 XX
 XX Identifying, comparing and detecting inhibitors of protein-protein
 PT interactions within population of host cells, involves detecting
 PT regulation of transcription of nucleic acid sequence by fusion protein
 PT interaction.
 XX
 XX Example; Col 155; 161pp; English.
 PS
 XX The present invention describes a method for detecting (D) at least 1
 CC protein-protein interaction (PPI) by recombinantly expressing within a
 CC population of host cells, populations of first and second fusion proteins
 CC comprising DNA binding domain (DBD) and transcriptional regulatory domain
 CC (TRD) respectively and detecting the regulation of transcription of

CC nucleotide sequence of host cells operably linked to a promoter driven by
 CC DBD. The detection method (D) is useful for identifying inhibitors of PPI
 CC for therapeutic use, and for detecting specific cell types, tissue types,
 CC stage of development and disease states. From the population of the
 CC proteins characteristic of the particular tissue or a cell-type, all
 CC possible detectable PPI that occur can be identified and genes encoding
 CC these proteins can be isolated. Thus, parallel analysis of two cell types
 CC enumerates PPI that are common to both and those that are specific to
 CC both. This analysis has significant value since PPI specific to a disease
 CC state can serve as therapeutic points of intervention. Inhibitors of PPI
 CC can also be isolated in rapid fashion. The number of false positives and
 CC low throughput are reduced. AAA55843 to AAA55963 and AA190961 are
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 GCTGTGGCGA 17
 DB 2 GCTGTGGCGA 12
 RESULT 370
 AAZ55846/c
 ID AAZ55846 standard; DNA; 12 BP.
 XX AAZ55846;
 AC
 XX 10-APR-2000 (first entry)
 XX Human retinaldehyde binding protein cDNA clone HRGR33 DNA insertion.
 XX
 XX Retinaldehyde binding protein; rgr gene; all-trans retinal; chromophore;
 KW photoreceptor; G protein-coupled receptor; human; insertion; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6008338-A.
 XX
 XX 28-DEC-1999.
 XX
 XX 05-JUN-1998; 98US-00090947.
 XX
 XX 16-DEC-1994; 94US-00358171.
 XX (FONG/) FONG H K W.
 XX Fong HK;
 PI
 XX WPI; 2000-096388/08.
 DR P-PSDB; AA58461.
 XX
 XX Isolated nucleic acid molecule encoding a photoreceptive retinaldehyde-
 PT binding protein for use in antisense therapeutics.
 PT
 PS Disclosure; Col 3; 40pp; English.
 XX
 XX The invention relates to mammalian retinaldehyde binding proteins and
 CC nucleotides encoding them. Retinaldehyde binding protein is the first
 CC light-absorbing vertebrate protein identified to stably and
 CC preferentially bind the all-trans-retinal chromophore. Retinaldehyde
 CC binding proteins have distant homology to other G protein-coupled
 CC receptors, possessing seven transmembrane domains. The nucleic acid and
 CC encoded protein are useful for assaying changes in the structure or the
 CC retinaldehyde-binding proteins which would be indicative of a molecular
 CC aberration in the retinal pigment epithelium, visual system or brain. The
 CC nucleic acid is also useful in antisense therapeutics and in the
 CC recombinant expression of retinaldehyde-binding protein. This sequence
 CC represents an inserted sequence that is present in human retinaldehyde
 CC binding protein cDNA clone HRGR33 at a position corresponding to

```
CC nucleotide 275 in the native cDNA sequence
XX Sequence 12 BP; 2 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
SQ

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
Db 12 CTGTGGGAGAC 2

RESULT 371
AAA73387
ID AAA73387 standard; DNA; 12 BP.
XX
XX AAA73387;
AC AAA73387;
DT 09-FEB-2001 (first entry)
XX
XX Yeast PCR primer #8.
DE PCR primer; yeast; two-hybrid system; protein-protein interaction;
XX PCR cancer; ss.
KW Saccharomyces cerevisiae.
XX
XX US083693-A.
XX 04-JUL-2000.
XX 14-JUN-1996; 96US-00663824.
XX 14-JUN-1996; 96US-00663824.
XX (CURA-) CURAGEN CORP.
XX Nandabalan K, Rothberg JM;
XX WPI; 2000-464335/40.
XX
XX Detecting protein-protein interactions in protein populations useful for
XX identifying genes encoding the proteins, and inhibitors of the
XX interactions, by detecting transcriptional regulation leading to reporter
XX gene activation.
XX Example; Col 126; 135pp; English.
XX
XX The present invention relates to methods for detecting and isolating
XX genes encoding proteins that interact with each other, via the
XX reconstitution of a transcription factor and hence reporter gene
XX activation. Proteins are fused to either the yeast DNA-binding domain of
XX a transcriptional activator or to the activation domain of a
XX transcriptional activator. The present sequence is a PCR primer used in
XX the present invention to amplify yeast fusion genes. The present method
XX may be used to identify protein-protein interactions and genes encoding
XX the interacting proteins relevant to a particular tissue, stage or
XX disease e.g. cancer
XX
XX Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGCGCA 17
Db 2 GCTGTGCGTGA 12

RESULT 372
AAC97831
ID AAC97831 standard; DNA; 12 BP.
XX
XX AAC97831;
AC AAC97831;
DT 28-FEB-2001 (first entry)
XX
XX Primer used to illustrate DNA amplification method SEQ ID 57.
DE Primer; amplification; selective; ss.
XX Synthetic.
XX JP2000270867-A.
XX 03-OCT-2000.
XX 19-MAR-1999; 99JP-00076844.
XX 19-MAR-1999; 99JP-00076844.
XX (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX WPI; 2001-011047/02.
XX
XX Amplification of a DNA fragment and its apparatus.
XX Example 1; Page 8; 32pp; Japanese.
XX
XX This invention relates to a method for amplifying a DNA fragment. The
XX method comprises successive repetitions of heat-denaturing, annealing of
XX a primer and an extending step using a DNA polymerase. The method makes
XX use of a cDNA pool in which the primer is one primer or a pair of primer
XX sets and has an amplification probability which allows it to amplify a
XX DNA fragment from a limited number of the cDNAs among the DNA pool (where
XX the limited number is in the range of 1 to 25). Also included in the
XX invention are apparatus used for carrying out the method, a primer and a
XX DNA polymerase and a kit used for amplifying a DNA fragment. The method
XX can be used to amplify a limited number of cDNAs from a pool in which a
XX wide variety of cDNAs are present. Oligonucleotides AAC9775 - AAC97990
XX represent primers used in an example illustrating the method of the
XX invention
XX
XX Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGCCTGTGGC 11

RESULT 373
AAC97963
ID AAC97963 standard; DNA; 12 BP.
XX
XX AAC97963;
AC AAC97963;
DT 28-FEB-2001 (first entry)
XX
XX Primer used to illustrate DNA amplification method SEQ ID 189.
DE Primer; amplification; selective; ss.
XX Synthetic.
XX JP2000270867-A.
XX 03-OCT-2000.
XX 19-MAR-1999; 99JP-00076844.
XX
```

XX 19-MAR-1999; 99JP-00076844.
XX (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUI SAN SENTAN GIJUTSU SANGYO.
XX WPI; 2001-011047/02.
XX Amplification of a DNA fragment and its apparatus.
XX Example 1; Page 11; 32pp; Japanese.
XX This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the
CC invention
XX Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGCTGTGGC 15
Db 1 AAGCTGTGGC 11
RESULT 374
AAF26620
ID AAF26620 standard; DNA; 12 BP.
AC AAF26620;
XX 27-MAR-2001 (first entry)
DE Mu opioid receptor SNP oligonucleotide probe SEQ ID NO:4.
XX Mu opioid receptor; MOR; single nucleotide polymorphism; SNP;
KW neurotransmitter factor dysfunction; detection; polymorphism; addiction;
KW alcohol dependence; probe; identification; schizophrenia;
KW neurological disorder; Tourette's syndrome; drug abuse; anxiety; stroke;
KW attention deficit disorder; depression; obsessive-compulsive disorder;
KW obesity; pain response; hypertension; vascular disorder; migraine;
KW nausea; Alzheimer's disease; aggressive behaviour; Parkinson's disease;
KW premenstrual syndrome; diabetic neuropathy; ss.
XX Homo sapiens.
OS
XX WO200077261-A1.
PN
XX 21-DEC-2000.
PD
XX 16-JUN-2000; 2000WO-US016706.
PF
XX 16-JUN-1999; 99US-00334113.
PR
XX (UYVR) UNIV ROCKEFELLER.
PA
XX Kreek MJ, Laforge KS, Spangler R;
PI
XX WPI; 2001-071285/08.
DR
XX Identifying genes of interest and relevance to neurological disorders or
PT

PT dysfunctions such as Parkinson's disease involves use of biological array
PT including all genes associated with neurotransmitter molecules.
XX Disclosure; Page 38; 76pp; English.
XX The present invention describes a method for identifying genetic
CC predisposition to, susceptibility to development of, characteristics of,
CC or persistence of physiological or pathological response to, a
CC neurotransmitter factor-related condition (NFC). The method comprises
CC identifying genetic polymorphisms in neurotransmitter genes associated
CC with NFC, using a multiple biological sample array. The method can be
CC used for making a biological chip plate which is useful for identifying
CC genetic predisposition to, susceptibility to development of,
CC characteristics of, or persistence of physiological or pathological
CC response to a NFC, genetic polymorphisms or gene expression in several
CC neurotransmitter genes, preferably opioid system genes, associated with
CC the NFC. The chip plates are useful in prognosis of neurological
CC disorders such as addiction, schizophrenia, Tourette's syndrome, drug
CC abuse, attention deficit disorder, anxiety, depression, obsessive-
CC compulsive disorder, stroke, obesity, response to pain, hypertension,
CC vascular disorders, migraine, nausea, Alzheimer's disease, aggressive
CC behaviour, premenstrual syndrome, diabetic neuropathy, suppression of
CC alcohol intake, and Parkinson's disease. A DNA array can determine the
CC particular strain of a pathogenic organism based on characteristic DNA
CC sequences of the strain. The present sequence represents an
CC oligonucleotide probe for a single nucleotide polymorphism (SNP) in the
CC mu opioid receptor (MOR), which is used in the exemplification of the
CC present invention
XX Sequence 12 BP; 0 A; 1 C; 7 G; 4 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GGCTGTGGC 16
Db 1 GGCTGTGGC 11
RESULT 375
ABH94426
ID ABH94426 standard; DNA; 12 BP.
AC ABH94426;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 294419 for detecting SNP TSC0016106.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT

XX PS Claim 1; SEQ ID NO 294419; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 2 TTGGGATGTT 12
|||||
|||||

RESULT 376
ABH70592/C
ID ABH70592 standard; DNA; 12 BP.
XX AC
XX ABH70592;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 270569 for detecting SNP TSC0002184.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 270569 for detecting SNP TSC0002184.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 270569; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 2 TTGGGATGTT 12
|||||
|||||

RESULT 377
ABI06014/C
ID ABI06014 standard; DNA; 12 BP.
XX AC
XX ABI06014;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 305987 for detecting SNP TSC00021731.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 305987; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 14
Db 11 GTGCTTGTGG 1
|||||
|||||

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 11 TTGAGTGTGT 1
|||||
|||||

RESULT 377
ABI06014/C
ID ABI06014 standard; DNA; 12 BP.
XX AC
XX ABI06014;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 305987 for detecting SNP TSC00021731.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 305987; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 14
Db 11 GTGCTTGTGG 1
|||||
|||||

```
RESULT 378
ABI32147/C
ID ABI32147 standard; DNA; 12 BP.
XX AC
XX ABI32147;
XX AC
DT 22-FEB-2002 (first entry)
XX AC
XX 22-FEB-2002 (first entry)
XX AC
DE Oligonucleotide primer SEQ ID NO 332120 for detecting SNP TSC0036718.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 332120; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTT 12
DB 12 TTTAGGCTGTT 2
RESULT 379
ABH88200/C
ID ABH88200 standard; DNA; 12 BP.
XX AC
XX ABH88200;
XX AC
DT 22-FEB-2002 (first entry)
XX AC
XX Oligonucleotide primer SEQ ID NO 288193 for detecting SNP TSC0013410.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 288193; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTT 12
DB 11 TTGTGGATGTT 1
RESULT 380
ABI52065/C
ID ABI52065 standard; DNA; 12 BP.
XX AC
XX ABI52065;
XX AC
DT 22-FEB-2002 (first entry)
XX AC
XX Oligonucleotide primer SEQ ID NO 352038 for detecting SNP TSC0047644.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
```

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 352038; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
 XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 Qy 4 GAGGCTGTGG 14
 Db |||||
 11 GAGTTGTGG 1
 RESULT 381
 ABI59850
 ID ABI59850 standard; DNA; 12 BP.
 XX
 AC ABI59850;
 XX
 DT 22-FEB-2002 (first entry)
 DE
 DE Oligonucleotide primer SEQ ID NO 359823 for detecting SNP TSC0051782.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 359823; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
 XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 Qy 4 GAGGCTGTGG 14
 Db |||||
 1 GAAGTTGTGG 11
 RESULT 382
 ABI28030/C
 ID ABI28030 standard; DNA; 12 BP.
 XX
 AC ABI28030;
 XX
 DT 22-FEB-2002 (first entry)
 DE
 DE Oligonucleotide primer SEQ ID NO 328003 for detecting SNP TSC0034025.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 328003; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

```
Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTGAGGCTGTT 12
Db      12 TTGAGGATGTT 2
      ||| || |||
      ||| || |||

RESULT 383
ABH86924/c
ID      ABI31258 standard; DNA; 12 BP.
XX
AC      ABI31258;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 331231 for detecting SNP TSC0036064.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 331231; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGGCTGTTGG 14
Db      12 GAGGAGTGTGG 2
      ||| || |||
      ||| || |||

RESULT 384
ABH86924/c
ID      ABH86924 standard; DNA; 12 BP.
XX
AC      ABH87174;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 287167 for detecting SNP TSC0012879.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
```



```
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 287167; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 3 TGAGGCTGTTG 13
XX Db 1 TGAGGTGTAG 11
XX
XX RESULT 386
XX ABI59322/c
XX ID ABI59322 standard; DNA; 12 BP.
XX
XX AC ABI59322;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 359295 for detecting SNP TSC0051543.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 359295 for detecting SNP TSC0051543.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX
```

```
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 359295; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 4 GAGGCTGTTG 14
XX Db 11 GAAGTGTGTTG 1
XX
XX RESULT 387
XX ABI59541
XX ID ABI59541 standard; DNA; 12 BP.
XX
XX AC ABI59541;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 359514 for detecting SNP TSC0051635.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 359514; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
```

```
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTGG 14
  ||||| |||||
Db 1 GAGGTTGGTG 11
  ||||| |||||
RESULT 388
ABH76783
ID ABH76783 standard; DNA; 12 BP.
XX
AC ABH76783;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 276776 for detecting SNP TSC0004282.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 276776; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
  ||||| |||||
```

```
Db 2 TTGGGGTGTGT 12
  ||||| |||||
RESULT 389
ABI01895/c
ID ABI01895 standard; DNA; 12 BP.
XX
AC ABI01895;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 301868 for detecting SNP TSC0019678.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 301868; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
  ||||| |||||
Db 12 TAGAGGCGGTT 2
  ||||| |||||
RESULT 390
ABH88028/c
ID ABH88028 standard; DNA; 12 BP.
XX
AC ABH88028;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 288021 for detecting SNP TSC0013341.
```

```
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 288021; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 6 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TTGAGGCTGTT 12
XX ||||| |||||
XX 11 TTGCGGTGTT 1
XX
XX RESULT 391
XX ABH89209/C
XX ID ABH89209 standard; DNA; 12 BP.
XX
XX AC ABH89209;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 289202 for detecting SNP TSC0013835.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 342341; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TTGAGGCTGTT 12
XX ||||| |||||
XX 11 TTGAGGTAGTT 1
XX
XX RESULT 392
XX ABI42368
XX ID ABI42368 standard; DNA; 12 BP.
XX
XX AC ABI42368;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 342341 for detecting SNP TSC0042502.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 342341; 29pp + Sequence Listing; German.
```

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTG 12
Db 2 TTGAGGAAGTT 12
RESULT 393
ABI74572/C
ID ABI74572 standard; DNA; 12 BP.
XX
AC ABI74572;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 374545 for detecting SNP TSC0060771.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 374545; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTGG 14
Db 11 GAGGCTTTGG 1
RESULT 394
ABI18927
ID ABI18927 standard; DNA; 12 BP.
XX
AC ABI18927;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 318900 for detecting SNP TSC0028944.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 318900; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGG 13
Db 1 TGAGTGTGTGG 11
RESULT 395

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 325444; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db ||| ||| |||
2 TTGAGGCTGTT 12

RESULT 398
ABI06881
ID ABI06881 standard; DNA; 12 BP.
XX
AC ABI06881;
XX
XX 22-FEB-2002 (first entry)
DE
DE Oligonucleotide primer SEQ ID NO 306854 for detecting SNP TSC0022206.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 306854; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db ||| ||| |||
1 TTTAGGTTGTT 11

RESULT 399
ABI12111
ID ABI12111 standard; DNA; 12 BP.
XX
AC ABI12111;
XX
XX 22-FEB-2002 (first entry)
DE
DE Oligonucleotide primer SEQ ID NO 312084 for detecting SNP TSC0024853.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 312084; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;


```

XX 06-APR-2001; 2001WO-IB000713.
PP
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 363894; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTGG 14
DB 2 GAGGATGTTTG 12
|||||
|||||
RESULT 403
ABI19328
ID ABI19328 standard; DNA; 12 BP.
XX
XX ABI19328;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 319301 for detecting SNP TSC0029157.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 363894; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTGG 14
DB 2 GAGGATGTTTG 12
|||||
|||||
RESULT 403
ABI19328
ID ABI19328 standard; DNA; 12 BP.
XX
XX ABI19328;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 319301 for detecting SNP TSC0029157.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 319301; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTT 12
DB 1 TTGAGGCTGTTT 11
|||||
|||||
RESULT 404
ABI20414/C
ID ABI20414 standard; DNA; 12 BP.
XX
XX ABI20414;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 320387 for detecting SNP TSC0029686.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 320387; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence

```


CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 4 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 11 GGGGTGTGG 1

RESULT 405

ABI00728
ID ABI00728 standard; DNA; 12 BP.
XX AC
XX ABI00728;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO.300701 for detecting SNP TSC0019147.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 300701; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 1 GAGGTGTGG 11

RESULT 406
ABI25879
ID ABI25879 standard; DNA; 12 BP.
XX AC
XX ABI25879;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 325852 for detecting SNP TSC0032758.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 300701; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 1 GAGGTGTGG 11

RESULT 407
ABH88026/C
ID ABH88026 standard; DNA; 12 BP.
XX AC
XX ABH88026;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 288019 for detecting SNP TSC0013341.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW

SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 1 GAGGTGTGG 11

RESULT 408
ABI00728
ID ABI00728 standard; DNA; 12 BP.
XX AC
XX ABI00728;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO.300701 for detecting SNP TSC0019147.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 300701; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 1 GAGGTGTGG 11

RESULT 409
ABH88026/C
ID ABH88026 standard; DNA; 12 BP.
XX AC
XX ABH88026;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 288019 for detecting SNP TSC0013341.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW

SQ Sequence 12 BP; 1 A; 0 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||
Db 2 GAGGGGTGG 12

```
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 288019; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TTGAGGCTGTT 12
XX ||||| |||||
XX 11 TTGTGGTGT 1
XX
XX RESULT 408
XX ABI41864/C
XX ID ABI41864 standard; DNA; 12 BP.
XX
XX AC ABI41864;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 341837 for detecting SNP TSC0005942.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 341837; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 7 GCTGTGGCGA 17
XX ||||| ||
XX 12 GTTGTGGGCA 2
XX
XX RESULT 409
XX ABI55024/C
XX ID ABI55024 standard; DNA; 12 BP.
XX
XX AC ABI55024;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 354997 for detecting SNP TSC0049413.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 354997; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
```

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
 || || || || || || || ||
 Db 11 TTTAGGATGTT 1

RESULT 410
 ABI61270
 ID ABI61270 standard; DNA; 12 BP.
 XX
 AC ABI61270;
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 361243 for detecting SNP TSC0052515.
 XX
 KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

XX WO200177384-A2.
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 361243; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
 || || || || || || || || ||
 Db 2 TGAGGGAGTTG 12

RESULT 411
 ABI77278
 ID ABI77278 standard; DNA; 12 BP.

XX
 AC ABI77278;
 XX
 DT 22-FEB-2002 (first entry)
 XX

DE Oligonucleotide primer SEQ ID NO 377251 for detecting SNP TSC0062216.
 XX
 KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 377251; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
 || || || || || || || ||
 Db 2 TTGGGGCTGTT 12

RESULT 412
 ABH70295/C
 ID ABH70295 standard; DNA; 12 BP.

```
XX AC ABH70295;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 270272 for detecting SNP TSC0002069.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 270272; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
XX XX
XX CC Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX CC Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX CC Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX QY 4 GAGGCTCTTG 14
XX Db |||||
XX 11 GAGGCTCTTG 1
XX XX
XX RESULT 413
XX ABH95346
XX ID ABH95346 standard; DNA; 12 BP.
XX XX
XX AC ABH95346;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 295339 for detecting SNP TSC0016538.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
```

```
PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 295339; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
XX XX
XX CC Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX CC Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX CC Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX QY 2 TTCGAGCTGTT 12
XX Db |||||
XX 2 TTAAGGTTGTT 12
XX XX
XX RESULT 414
XX ABH70593/C
XX ID ABH70593 standard; DNA; 12 BP.
XX XX
XX AC ABH70593;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 270570 for detecting SNP TSC0002184.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 270570; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 11 TTGAGGCTGTT 1
RESULT 415
ABH71521/C
ID ABH71521 standard; DNA; 12 BP.
XX
XX ABH71521;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 271498 for detecting SNP TSC0002525.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271498; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAGGCTGTTG 14
Db 12 GAGGCGGTTG 2
RESULT 416
ABI24777
ID ABI24777 standard; DNA; 12 BP.
XX
XX ABI24777;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 324750 for detecting SNP TSC0032206.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 324750; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      6 GGCTGTGGCG 16
Db      1 GGTGTAGGCG 11

RESULT 417
ABI04440/c
ID ABI04440 standard; DNA; 12 BP.
XX
AC ABI04440;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 304413 for detecting SNP TSC0020911.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 304413; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 TGAGGCTGTGG 13
Db      11 TGAGGCTGTAG 1

RESULT 418
ABI32952
ID ABI32952 standard; DNA; 12 BP.
XX
AC ABI32952;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 283914 for detecting SNP TSC0011567.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

```

```

DE Oligonucleotide primer SEQ ID NO 332925 for detecting SNP TSC0037270.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 332925; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 TGAGGCTGTGG 13
Db      1 TAAGGTGTGG 11

RESULT 419
ABH83921/c
ID ABH83921 standard; DNA; 12 BP.
XX
AC ABH83921;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 283914 for detecting SNP TSC0011567.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

```



```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 1 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
Db 1 GAGGGCGTTGG 11
||||| |||||

RESULT 422
AB141857/c
ID AB141857 standard; DNA; 12 BP.
XX
AC AB141857;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341830 for detecting SNP TSC0009164.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341830 for detecting SNP TSC0009164.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 341830; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
Db 12 GATGGTGTGG 2
||||| |||||

RESULT 423
AB172757/c
ID AB172757 standard; DNA; 12 BP.
XX
AC AB172757;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 372730 for detecting SNP TSC0059583.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 372730; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 11 TTGAGTTTGT 1
||||| |||||

RESULT 424
AB160455/c
ID AB160455 standard; DNA; 12 BP.
XX
AC AB160455;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 360428 for detecting SNP TSC0052076.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```



```
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 360428; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABCF9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 2 TTGAGGCTGTT 12
Db 12 TTGATGTTGTT 2
RESULT 425
ABI63529/c
XX ID ABI63529 standard; DNA; 12 BP.
XX AC ABI63529;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 363502 for detecting SNP TSC0053890.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 363502; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABCF9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 2 TTGAGGCTGTT 12
Db 12 TTGATGTTGTT 2
RESULT 426
ABI30747/c
XX ID ABI30747 standard; DNA; 12 BP.
XX AC ABI30747;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 330720 for detecting SNP TSC0035702.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 330720; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
```

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTG 13
 DB 11 TGATGTTGTTG 1
 ||| | |||||
 ||| | |||||

RESULT 427
 ABI31406
 ID ABI31406 standard; DNA; 12 BP.
 XX AC
 AC ABI31406;
 XX
 DT 22-FEB-2002 (first entry)
 DE
 DE Oligonucleotide primer SEQ ID NO 331379 for detecting SNP TSC0036164.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 331379; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
 DB 2 TTAAGGATGTT 12
 ||| | |||||
 ||| | |||||

RESULT 428
 ABH84137
 ID ABH84137 standard; DNA; 12 BP.
 XX AC
 AC ABH84137;
 XX
 DT 22-FEB-2002 (first entry)
 DE
 DE Oligonucleotide primer SEQ ID NO 284130 for detecting SNP TSC0011676.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 284130; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
 DB 1 TTGAGGCTTTT 11
 ||||| | |||||
 ||||| | |||||

RESULT 429
 ABH84138/C
 ID ABH84138 standard; DNA; 12 BP.
 XX AC
 AC ABH84138;

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 323503; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 7 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCG 16
Db 11 GTCGTGTGGCG 1
|||||
|
RESULT 432
ABI25770
ID ABI25770 standard; DNA; 12 BP.
XX
AC ABI25770;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 325743 for detecting SNP TSC0032693.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 325743; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 7 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCG 16
Db 11 GTCGTGTGGCG 1
|||||
|
RESULT 433
ABI09805/c
ID ABI09805 standard; DNA; 12 BP.
XX
AC ABI09805;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 309778 for detecting SNP TSC0023668.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 309778; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCGTGTGG 14
Db 1 GACTATGTGG 11
|||||
|
RESULT 434
ABI09805/c
ID ABI09805 standard; DNA; 12 BP.
XX
AC ABI09805;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 309778 for detecting SNP TSC0023668.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 309778; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCGTGTGG 14
Db 1 GACTATGTGG 11
|||||
|

```

Db      11 GAGGCTTTGG 1
RESULT 434
ABI50807/C
ID      ABI50807 standard; DNA; 12 BP.
XX      AC      ABI50807;
XX      XX      22-FEB-2002 (first entry)
XX      DE      Oligonucleotide primer SEQ ID NO 350780 for detecting SNP TSC0046874.
XX      KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX      KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX      KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX      OS      Homo sapiens.
XX      XX      WO200177384-A2.
XX      PD      18-OCT-2001.
XX      PF      06-APR-2001; 2001WO-IB000713.
XX      PR      07-APR-2000; 2000DE-01019173.
XX      PA      (EPIG-) EPIGENOMICS AG.
XX      PI      Olek A, Piepenbrock C, Berlin K;
XX      WI      WPI; 2001-657177/75.
XX      PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
XX      PT      designed to detect single-nucleotide polymorphisms and cytosine
XX      PT      methylation status.
XX      PS      Claim 1; SEQ ID NO 350780; 29pp + Sequence Listing; German.
XX      CC      This invention describes novel oligonucleotide primers or peptide nucleic
XX      CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX      CC      and cytosine methylation status in chemically pretreated genomic DNA. The
XX      CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX      CC      range of diseases including immune system, gastrointestinal, respiratory,
XX      CC      central nervous system, cardiovascular and metabolic disorders. The
XX      CC      oligomers are also used for detecting cell type differentiation. ABC00010
XX      CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX      CC      represent the oligomers described in the invention. NOTE: The sequence
XX      CC      data for this patent did not form part of the printed specification, but
XX      CC      was obtained in electronic format from WIPO at
XX      CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GCTGTTGGCGA 17
Db      12 GTTGTGGAGA 2
          |||||
          |||||

RESULT 435
ABI69356/C
ID      ABI69356 standard; DNA; 12 BP.
XX      AC      ABI69356;
XX      XX      22-FEB-2002 (first entry)
XX      DE      Oligonucleotide primer SEQ ID NO 369329 for detecting SNP TSC0057583.
XX      KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX      KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX      KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX      OS      Homo sapiens.
XX      XX      WO200177384-A2.
XX      PD      18-OCT-2001.
XX      PF      06-APR-2001; 2001WO-IB000713.
XX      PR      07-APR-2000; 2000DE-01019173.
XX      KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX      KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX      KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX      OS      Homo sapiens.
XX      XX      WO200177384-A2.
XX      PD      18-OCT-2001.
XX      PF      06-APR-2001; 2001WO-IB000713.
XX      PR      07-APR-2000; 2000DE-01019173.

```

```
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 358332; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 TTGAGGCTGTG 13
XX Db 12 TTAGGTTGTG 2
XX
XX RESULT 437
XX ABI22393/C
XX ID ABI22393 standard; DNA; 12 BP.
XX AC ABI22393;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 322366 for detecting SNP TSC0030824.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 322366; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TTGAGGCTGTG 12
XX Db 11 TTGAGGCTTTT 1
XX
XX RESULT 438
XX ABH98561
XX ID ABH98561 standard; DNA; 12 BP.
XX AC ABH98561;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 298554 for detecting SNP TSC0018170.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 298554; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
```

```

SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
   |||||
Db 1 GAGGAAGTTGG 11

RESULT 439
ABH80581
ID ABH80581 standard; DNA; 12 BP.
XX
AC ABH80581;
XX
DT 22-FEB-2002 (first entry)
XX
Oligonucleotide primer SEQ ID NO 280574 for detecting SNP TSC0008780.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 22-FEB-2002 (first entry)
XX
Oligonucleotide primer SEQ ID NO 280574 for detecting SNP TSC0008780.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WIPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
Claim 1; SEQ ID NO 280574; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   |||||
Db 2 TGAGGATGTCG 12

RESULT 440
ABI09990
ID ABI09990 standard; DNA; 12 BP.
XX
AC ABI09990;
XX
DT 22-FEB-2002 (first entry)
XX
Oligonucleotide primer SEQ ID NO 309963 for detecting SNP TSC0023755.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WIPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
Claim 1; SEQ ID NO 309963; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGTC 15
   |||||
Db 2 AGGTTGTTGTC 12

RESULT 441
ABI48685/C
ID ABI48685 standard; DNA; 12 BP.
XX
AC ABI48685;
XX
DT 22-FEB-2002 (first entry)
XX
Oligonucleotide primer SEQ ID NO 348658 for detecting SNP TSC0001217.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.

```

```

XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 348658; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCGTGTTCG 14
Db 11 GAGGTTGTCG 1
|||||
|

RESULT 442
ABI48873
ID ABI48873 standard; DNA; 12 BP.
XX AC ABI48873;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 348846 for detecting SNP TSC0045785.
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 348846 for detecting SNP TSC0008646.
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352572 for detecting SNP TSC0008646.
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352572; 29pp + Sequence Listing; German.
XX PS Claim 1; SEQ ID NO 348846; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCGTGTTCG 14
Db 2 GAGGTTGTTAG 12
|||||
|

RESULT 443
ABI52599/c
ID ABI52599 standard; DNA; 12 BP.
XX AC ABI52599;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352572 for detecting SNP TSC0008646.
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 352572; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

```


CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
 Db 11 TTGGGGTGT 1

RESULT 444
 ABI58547/C
 ID ABI58547 standard; DNA; 12 BP.

XX AC ABI58547;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 358520 for detecting SNP TSC0007206.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 358520; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTCTTGG 14
 Db 12 GAGGCTTGG 2

RESULT 445
 ABH92986/C
 ID ABH92986 standard; DNA; 12 BP.

XX AC ABH92986;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 292979 for detecting SNP TSC0015441.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 292979; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTCTTGG 14
 Db 12 GAGTCTTGG 2

RESULT 446
 ABH69192
 ID ABH69192 standard; DNA; 12 BP.

XX AC ABH69192;

XX DT 22-FEB-2002 (first entry)

```
XX Oligonucleotide primer SEQ ID NO 269169 for detecting SNP TSC0001644.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 269169; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 TTGAGGCTGTT 12
XX 1 TTTAGGCTGTT 11
XX
XX
XX RESULT 447
XX ABI20668/C
XX ID ABI20668 standard; DNA; 12 BP.
XX
XX AC ABI20668;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 320641 for detecting SNP TSC0029829.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
```

```
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 320641; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4 GAGGCTGTTGG 14
XX 12 GAAGGTGTTGG 2
XX
XX
XX RESULT 448
XX ABI29816
XX ID ABI29816 standard; DNA; 12 BP.
XX
XX AC ABI29816;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 329789 for detecting SNP TSC0035150.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
```



```
RESULT 451
ABH90077
ID ABH90077 standard; DNA; 12 BP.
XX AC
XX ABH90077;
DT 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 290070 for detecting SNP TSC0014205.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN WO200177384-A2.
XX AC
XX ABH90077;
DT 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 290070 for detecting SNP TSC0014205.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN WO200177384-A2.
XX AC
XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 290070; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTCG 14
DB 1 GAGGGTGTCG 11
RESULT 452
ABI16474/C
ID ABI16474 standard; DNA; 12 BP.
XX AC
XX ABI16474;
DT 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 316447 for detecting SNP TSC0027456.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 316447; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TGAGGCTGTG 13
DB 12 TGAGGGTGTG 2
RESULT 453
ABI16577
ID ABI16577 standard; DNA; 12 BP.
XX AC
XX ABI16577;
XX DT 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 316550 for detecting SNP TSC0027491.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
```

XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 316550; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, cardiovascular, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GATGTTGTGG 11
||| |||||
1 GATGTTGTGG 11

RESULT 454
ABH67250/C
ID ABH67250 standard; DNA; 12 BP.
XX AC ABH67250;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267227 for detecting SNP TSC0000060.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 267227; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 12 TTGAGGCTGTT 2
||| |||||
12 TTGAGGCTGTT 2

RESULT 455
ABI50913
ID ABI50913 standard; DNA; 12 BP.
XX AC ABI50913;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 350886 for detecting SNP TSC0046952.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 350886; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

```

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
Db 2 TTGATGTGTT 12
    |||||
RESULT 456
ABI75469/C
ID ABI75469 standard; DNA; 12 BP.
XX AC ABI75469;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 375442 for detecting SNP TSC0061250.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PS Claim 1; SEQ ID NO 375442; 29pp + Sequence Listing; German.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 375442; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
Db 12 TTGGGCTGTT 2
    |||||
RESULT 457
ABI62231/C
ID ABI62231 standard; DNA; 12 BP.
XX AC ABI62231;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267424 for detecting SNP TSC0000211.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.

```

```

AC ABI62231;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 362204 for detecting SNP TSC0053079.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 362204; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGGCTGTTG 13
Db 11 TAAGGATGTTG 1
    |||||
RESULT 458
ABH67447
ID ABH67447 standard; DNA; 12 BP.
XX AC ABH67447;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267424 for detecting SNP TSC0000211.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.

```

XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 267424; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGAGGCTGTT 12
 Db 2 TTGGGGTGT 12
 RESULT 459
 ABI19569/c
 ID ABI19569 standard; DNA; 12 BP.
 XX ABI19569;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 319542 for detecting SNP TSC0029289.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 267424; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGAGGCTGTT 12
 Db 2 TTGGGGTGT 12

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 319542; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTGAGGCTGTT 12
 Db 11 TTGGGGTGT 1
 RESULT 460
 ABI21552
 ID ABI21552 standard; DNA; 12 BP.
 XX ABI21552;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 321525 for detecting SNP TSC0030310.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 321525; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 1 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GAGGCTGTGG 14
 Db 2 GGGGATGTGG 12
 |||||
 |||||
 RESULT 461
 ABI25472
 ID ABI25472 standard; DNA; 12 BP.
 XX
 AC ABI25472;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 325445 for detecting SNP TSC0032544.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 325445; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTT 12
 |||||
 |||||

Db 2 TTGCGGTGTT 12
 |||||
 |||||
 RESULT 462
 ABH78395
 ID ABH78395 standard; DNA; 12 BP.
 XX
 AC ABH78395;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 278388 for detecting SNP TSC0005971.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 278388; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTGTT 12
 |||||
 |||||
 Db 1 TTGAAGGTGTT 11
 |||||
 |||||
 RESULT 463
 ABI14003
 ID ABI14003 standard; DNA; 12 BP.
 XX
 AC ABI14003;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 313976 for detecting SNP TSC0026056.


```
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 313976; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGGCTGTTGG 14
Db 1 GATGGTGTGG 11
RESULT 464
ABH89602/C
ID ABH89602 standard; DNA; 12 BP.
XX AC ABH89602;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 289595 for detecting SNP TSC0013999.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX
```

```
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 289595; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGAGGCTGTT 12
Db 11 TTTAGGTTGTT 1
RESULT 465
ABI57686
ID ABI57686 standard; DNA; 12 BP.
XX AC ABI57686;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 357659 for detecting SNP TSC0050723.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 357659; 29pp + Sequence Listing; German.
XX
```

```
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 2 TTGAGGCTGTT 12
  Db 1 TTAAGGTGTT 11
  RESULT 466
  ABI19012/c
  ID ABI19012 standard; DNA; 12 BP.
  XX AC ABI19012;
  XX DT 22-FEB-2002 (first entry)
  DE Oligonucleotide primer SEQ ID NO 318985 for detecting SNP TSC0029004.
  XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
  KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
  KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
  XX OS Homo sapiens.
  XX WO200177384-A2.
  XX PD 18-OCT-2001.
  XX PF 06-APR-2001; 2001WO-IB000713.
  XX PR 07-APR-2000; 2000DE-01019173.
  XX PA (EPIG-) EPIGENOMICS AG.
  PI Olek A, Piepenbrock C, Berlin K;
  DR WPI; 2001-657177/75.
  XX Set of oligonucleotides, useful for diagnosis and cell typing, is
  PT designed to detect single-nucleotide polymorphisms and cytosine
  PT methylation status.
  XX Claim 1; SEQ ID NO 318985; 29pp + Sequence Listing; German.
  XX This invention describes novel oligonucleotide primers or peptide nucleic
  CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  CC and cytosine methylation status in chemically pretreated genomic DNA. The
  CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  CC range of diseases including immune system, gastrointestinal, respiratory,
  CC central nervous system, cardiovascular and metabolic disorders. The
  CC oligomers are also used for detecting cell type differentiation. ABC00010
  CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
  CC represent the oligomers described in the invention. NOTE: The sequence
  CC data for this patent did not form part of the printed specification, but
  CC was obtained in electronic format from WIPO at
  CC ftp.wipo.int/pub/published_pct_sequences
  CC
```

```
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 4 GAGGCTGTTGG 14
  Db 12 GAGGTTGTTAG 2
  RESULT 467
  ABI19356
  ID ABI19356 standard; DNA; 12 BP.
  XX AC ABI19356;
  XX DT 22-FEB-2002 (first entry)
  DE Oligonucleotide primer SEQ ID NO 319329 for detecting SNP TSC0029170.
  XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
  KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
  KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
  XX OS Homo sapiens.
  XX WO200177384-A2.
  XX PD 18-OCT-2001.
  XX PF 06-APR-2001; 2001WO-IB000713.
  XX PR 07-APR-2000; 2000DE-01019173.
  XX PA (EPIG-) EPIGENOMICS AG.
  PI Olek A, Piepenbrock C, Berlin K;
  DR WPI; 2001-657177/75.
  XX Set of oligonucleotides, useful for diagnosis and cell typing, is
  PT designed to detect single-nucleotide polymorphisms and cytosine
  PT methylation status.
  XX Claim 1; SEQ ID NO 319329; 29pp + Sequence Listing; German.
  XX This invention describes novel oligonucleotide primers or peptide nucleic
  CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  CC and cytosine methylation status in chemically pretreated genomic DNA. The
  CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  CC range of diseases including immune system, gastrointestinal, respiratory,
  CC central nervous system, cardiovascular and metabolic disorders. The
  CC oligomers are also used for detecting cell type differentiation. ABC00010
  CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
  CC represent the oligomers described in the invention. NOTE: The sequence
  CC data for this patent did not form part of the printed specification, but
  CC was obtained in electronic format from WIPO at
  CC ftp.wipo.int/pub/published_pct_sequences
  CC
  SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 7 GCTGTTGGCGA 17
  Db 1 GTTGTGTTGCA 11
  RESULT 468
```


XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 279272; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
 Db 12 TTGAGATTGTT 2
 ||||| |||||
 ||||| |||||

RESULT 471
 ABI31459/c
 ID ABI31459 standard; DNA; 12 BP.
 XX AC ABI31459;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 331432 for detecting SNP TSC0036202.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 331432; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
 Db 11 TTGAGGTTGTT 1
 ||||| |||||
 ||||| |||||

RESULT 472
 ABI06804/c
 ID ABI06804 standard; DNA; 12 BP.
 XX AC ABI06804;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 306777 for detecting SNP TSC0022168.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 306777; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;

```

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
    ||||| ||
Db 12 TTGAGGCTATT 2
    ||||| ||

RESULT 473
ABI32404
ID ABI32404 standard; DNA; 12 BP.
XX
AC ABI32404;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 332377 for detecting SNP TSC0036851.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 332377; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
    ||||| ||
Db 2 GAGGATGGTG 12
    ||||| ||

RESULT 474
ABI34318/C
ID ABI34318 standard; DNA; 12 BP.
XX
AC ABI34318;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 310208 for detecting SNP TSC0023863.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX

```

```

DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 334291 for detecting SNP TSC0038060.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 334291; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCGA 17
    ||||| ||
Db 12 GGTGGTGGCGA 2
    ||||| ||

RESULT 475
ABI10235
ID ABI10235 standard; DNA; 12 BP.
XX
AC ABI10235;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 310208 for detecting SNP TSC0023863.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX

```

```

XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310208; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABCG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGAGGCTGTT 12
Db ||||| |||||
2 TTGAAGTTGTT 12
||| |||||

RESULT 476
ABH90677/c
ID ABH90677 standard; DNA; 12 BP.
XX AC ABH90677;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 290670 for detecting SNP TSC0014463.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310208; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABCG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGAGGCTGTT 12
Db ||||| |||||
2 TTGAAGTTGTT 12
||| |||||

RESULT 477
ABI44144
ID ABI44144 standard; DNA; 12 BP.
XX AC ABI44144;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 344117 for detecting SNP TSC0043390.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 344117; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABCG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

```

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
||| ||| |||
Db 2 TTTAGGGTGT 12

RESULT 478

AB145715
ID AB145715 standard; DNA; 12 BP.

XX AC AB145715;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 345688 for detecting SNP TSC0044144.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 345688; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
||||| |||
Db 1 GAGGTTTTTGG 11

RESULT 479

AB177158

XX ID AB177158 standard; DNA; 12 BP.

XX AC AB177158;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 377131 for detecting SNP TSC0062159.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 377131; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTGG 14
||||| |||
Db 1 GAGGAGGTTGG 11

RESULT 480

ABH75413/C

XX ID ABH75413 standard; DNA; 12 BP.

XX AC ABH75413;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 275404 for detecting SNP TSC0003884.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 275404; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4 GAGGCTGTTGG 14
XX 11 GTGGATGTTGG 1
XX
XX
XX RESULT 481
XX ABI25639
XX ID ABI25639 standard; DNA; 12 BP.
XX
XX AC ABI25639;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 325612 for detecting SNP TSC0032626.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX

PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 325612; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4 GAGGCTGTTGG 14
XX 2 GAGGATGTCGG 12
XX
XX
XX RESULT 482
XX ABI03816/c
XX ID ABI03816 standard; DNA; 12 BP.
XX
XX AC ABI03816;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 303789 for detecting SNP TSC0020643.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 303789; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 12 GAGTTTGTGG 2
|||||
|||||

RESULT 483
ABI05325
ID ABI05325 standard; DNA; 12 BP.
AC ABI05325;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 305298 for detecting SNP TSC0021375.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 305298; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 1 TTGAGGGAGTT 11
|||||
|||||

RESULT 484
ABI33073/C
ID ABI33073 standard; DNA; 12 BP.
XX
AC ABI33073;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333046 for detecting SNP TSC0037328.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 333046; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 12 TTGATGGTGT 2
|||||
|||||

RESULT 485
ABI57771/C
ID ABI57771 standard; DNA; 12 BP.

```
XX AC ABI57771;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 357744 for detecting SNP TSC0005411.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 357744; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 GAGGCTGTTGG 14
Db 11 GGGGGTGTGG 1
||| |||||
RESULT 486
ABI58136
ID ABI58136 standard; DNA; 12 BP.
XX AC ABI58136;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 358109 for detecting SNP TSC00050957.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 357744; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 GAGGCTGTTGG 14
Db 11 GGGGGTGTGG 1
||| |||||
RESULT 486
ABI58136
ID ABI58136 standard; DNA; 12 BP.
XX AC ABI58136;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 358109 for detecting SNP TSC00050957.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 358109; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGAGGCTGTT 12
Db 1 TTGAAGTGT 11
||| |||||
RESULT 487
ABI80801
ID ABI80801 standard; DNA; 12 BP.
XX AC ABI80801;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 380774 for detecting SNP TSC0063977.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 380774; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 2 TTGAGTGTGTT 12
RESULT 488
ABI18449/C
ID ABI18449 standard; DNA; 12 BP.
XX
AC ABI18449;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 318422 for detecting SNP TSC0028649.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 318422; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 12 TTAAGGATGTT 2
RESULT 489
ABH71196
ID ABH71196 standard; DNA; 12 BP.
XX
AC ABH71196;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 271173 for detecting SNP TSC0002417.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 271173; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX

```

Qy 2 TTGAGGCTGTT 12
Db 1 TTTAGGCTGTT 11

RESULT 490
ABH99938
ID ABH99938 standard; DNA; 12 BP.
XX AC ABH99938;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299931 for detecting SNP TSC0018813.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PT
XX PS Claim 1; SEQ ID NO 299931; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 2 TTTAGGCTGTT 12

RESULT 491
ABH76685/C
ID ABH76685 standard; DNA; 12 BP.
XX AC ABH76685;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 281616 for detecting SNP TSC0009939.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.

```

```

DE Oligonucleotide primer SEQ ID NO 276678 for detecting SNP TSC0004261.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PT
XX PS Claim 1; SEQ ID NO 276678; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGGCGA 17
Db 11 GATGTTGGCGA 1

RESULT 492
ABH81623
ID ABH81623 standard; DNA; 12 BP.
XX AC ABH81623;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 281616 for detecting SNP TSC0009939.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.

```

XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 281616; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 2 TTGAGGTATT 12
|||||
|||||

RESULT 493
ABI36225/C
ID ABI36225 standard; DNA; 12 BP.
XX AC
XX AC ABI36225;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 336198 for detecting SNP TSC0039243.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 336198 for detecting SNP TSC0039243.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX CC

PS Claim 1; SEQ ID NO 336198; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 12 TTGAGTTGTT 2
|||||
|||||

RESULT 494
ABH86970
ID ABH86970 standard; DNA; 12 BP.
XX AC
XX AC ABH86970;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286963 for detecting SNP TSC0012898.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX DT 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 286963; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 1 TTGAGGAAGTT 11

RESULT 495
ABI13617/C
ID ABI13617 standard; DNA; 12 BP.
XX
AC ABI13617;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 313590 for detecting SNP TSC0025853.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 313590; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 11 TTGAGGTTTT 11

RESULT 496
ABI46100
ID ABI46100 standard; DNA; 12 BP.
XX
AC ABI46100;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 346073 for detecting SNP TSC0044346.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 346073; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 2 TTGAGGTTTT 12

RESULT 497
ABI60184
ID ABI60184 standard; DNA; 12 BP.
XX
AC ABI60184;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 360157 for detecting SNP TSC0051934.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```

XX OS Homo sapiens.
XX XX WO200177384-A2.
XX FN 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PP
XX PR 07-APR-2000; 2000DE-01019173.
XX PS
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 360157; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 TTGAGGCTGTT 12
Db 1 TTGTGGATGTT 11
XX
RESULT 498
ABI74204/c
XX ID ABI74204 standard; DNA; 12 BP.
XX AC ABI74204;
XX DT 22-FEB-2002 (first entry)
XX XX
XX Oligonucleotide primer SEQ ID NO 374177 for detecting SNP TSC0060554.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PS
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 374177; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 4 GAGGCTGTTGG 14
Db 11 GAGGGTGTTAG 1
XX
RESULT 499
ABH97217
XX ID ABH97217 standard; DNA; 12 BP.
XX AC ABH97217;
XX DT 22-FEB-2002 (first entry)
XX XX
XX Oligonucleotide primer SEQ ID NO 297210 for detecting SNP TSC0017484.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PS
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 297210; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 4 GAGGCTGTTGG 14
Db 11 GAGGGTGTTAG 1
XX

```



```

XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 326661 for detecting SNP TSC0033207.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 326661; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 2 TAGAGTGT 12
|||||
|||||

RESULT 503
ABI33755/C
ID ABI33755 standard; DNA; 12 BP.
XX AC ABI33755;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 333728 for detecting SNP TSC0037728.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 326661; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTT 12
Db 2 TAGAGTGT 12
|||||
|||||

RESULT 503
ABI33755/C
ID ABI33755 standard; DNA; 12 BP.
XX AC ABI33755;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 333728 for detecting SNP TSC0037728.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 333728; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTTG 13
Db 12 TGATGATGTTG 2
|||||
|||||

RESULT 504
ABH88565
ID ABH88565 standard; DNA; 12 BP.
XX AC ABH88565;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 288558 for detecting SNP TSC0013573.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

```

PT designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 288558; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;

XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12

Db 2 TTGAGGCTGTT 12

RESULT 505

ABH69193

ID ABH69193 standard; DNA; 12 BP.

XX ABH69193;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 269170 for detecting SNP TSC0001644.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 269170; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;

XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12

Db 1 TTTAGGCTGTT 11

RESULT 506

ABH75818/c

ID ABH75818 standard; DNA; 12 BP.

XX ABH75818;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 275811 for detecting SNP TSC0004010.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX Claim 1; SEQ ID NO 275811; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;

XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13

||| ||| ||| |||

Db 11 TGGGATGTTG 1

RESULT 507

AB129229

ID AB129229 standard; DNA; 12 BP.

XX

AC AB129229;

XX

XX

DT 22-FEB-2002 (first entry)

XX

XX

DE Oligonucleotide primer SEQ ID NO 329202 for detecting SNP TSC0034815.

XX

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

FN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

XX Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

XX

DR Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX

PS Claim 1; SEQ ID NO 329202; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

XX

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;

XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

Qy 2 TTGAGGCTGTT 12

Db 1 TAGAGGTGTT 11

RESULT 508

ABH82959/C

ID ABH82959 standard; DNA; 12 BP.

XX

XX

AC ABH82959;

XX

XX

DT 22-FEB-2002 (first entry)

XX

XX

DE Oligonucleotide primer SEQ ID NO 282952 for detecting SNP TSC0011068.

XX

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

XX WO200177384-A2.

XX

PD 18-OCT-2001.

XX

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

XX Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

XX

DR Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX

PS Claim 1; SEQ ID NO 282952; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

XX

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;

XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

Qy 2 TTGAGGCTGTT 12

Db 1 TAGAGGTGTT 11

RESULT 509

AB11722/C

ID AB11722 standard; DNA; 12 BP.

XX

XX

AC AB11722;

XX

XX

DT 22-FEB-2002 (first entry)

XX

XX

DE Oligonucleotide primer SEQ ID NO 311695 for detecting SNP TSC0024624.

XX

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

XX WO200177384-A2.

XX

PD 18-OCT-2001.

XX

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 311695; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 TTGAGGCTGTT 12
Db 11 TTGAGGGTTT 1
XX
XX RESULT 510
XX ABI14453
XX ID ABI14453 standard; DNA; 12 BP.
XX AC ABI14453;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 314426 for detecting SNP TSC0026351.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 314426; 29pp + Sequence Listing; German.
XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 6 GGCTGTGGCG 16
Db 2 GGATGATGGCG 12
XX
XX RESULT 511
XX ABI47069/C
XX ID ABI47069 standard; DNA; 12 BP.
XX AC ABI47069;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 347042 for detecting SNP TSC0044883.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 347042; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

```

SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 12 TTGAGGATTTT 2

RESULT 512
ABI69559
ID ABI69559 standard; DNA; 12 BP.
AC ABI69559;
XX
XX
DT 22-FEB-2002 (first entry)
DE
DE Oligonucleotide primer SEQ ID NO 369532 for detecting SNP TSC0057698.
KW SNP; single nucleotide polymorphism; human; diagnosis; DNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 369532; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
   ||||| |||
Db 2 TTTAGGTTGTT 12

RESULT 513
AAD45478
ID AAD45478 standard; DNA; 12 BP.
AC AAD45478;
XX
XX 27-DEC-2002 (first entry)
DE
DE Hind III restriction enzyme specific PCR primer #2.
XX Protein-protein interaction; detection; cancer; PCR; primer; ss.
XX
XX Unidentified.
XX
XX US6410239-B1.
XX
XX 25-JUN-2002.
XX
XX 14-DEC-1999; 99US-00461125.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX 13-JUN-1997; 97US-00874825.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;
XX WPI; 2002-654433/70.
XX
XX Detection of protein to protein interactions amongst two protein
XX populations useful e.g. to identify interactions specific for particular
XX tissues or diseases and to identify inhibitors of interactions uses a new
XX genetic method.
XX
XX Example; Col 179; 152pp; English.
XX
XX The present invention relates to novel methods for detecting protein to
XX protein interactions amongst two populations of proteins, each having a
XX complexity of at least 100. The method involves using new genetic methods
XX in which encoded proteins are fused to either the DNA-binding domain of a
XX transcriptional activator or the activation domain of a transcriptional
XX activator. The methods are useful to detect interacting proteins and to
XX identify protein-protein interactions specific for a particular species,
XX tissue, stage of development or disease state, e.g. by comparing protein-
XX protein interactions between populations from cDNA of cancerous or pre-
XX cancerous cells with those from non-cancerous cells. They are also useful
XX to identify inhibitors interfering with protein-protein interactions e.g.
XX potential drug candidates inhibiting interactions specific to cancerous
XX cells. The present DNA sequence is a PCR primer which is specific for
XX Hind III restriction enzyme. This primer is used to illustrate the method
XX of the invention
XX
SQ Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 2.6e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTTGCGGA 17
   ||||| |||
Db 2 GCTGTCGGTGA 12

RESULT 514
ABZ58916
ID ABZ58916 standard; DNA; 12 BP.
AC ABZ58916;
XX
XX 28-APR-2003 (first entry)
DE
DE Human JAM3 intron 3/exon 4 junction sequence.
XX
XX Junctional adhesion molecule; JAM3; JAM2; antiasthmatic; antirheumatic;
XX antiarthritic; antithyroid; immunosuppressive; thyromimetic; virucide;

```

```
KW hepatotropic; antiinflammatory; antidiabetic; haemostatic; antipsoriatic;
KW antiallergic; human; chromosome 11q25; ds.
OS Homo sapiens.
XX WO2003006673-A2.
XX 23-JAN-2003.
XX 10-JUL-2002; 2002WO-US021697.
XX 11-JUL-2001; 2001US-0304603P.
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX Cunningham S;
XX WPI; 2003-210431/20.
XX Identifying compounds that bind to junctional adhesion molecules (JAM3 or
XX JAM2) or modulators of binding between JAM and other molecules for
XX treating or alleviating e.g. arthritis, hepatitis, Crohn's disease or
XX graft rejection.
XX Example 2B; Page 60; 90pp; English.
XX The invention relates to identifying compounds that bind to junctional
XX adhesion molecule 3 (JAM3), JAM2, or modulators of binding between JAM3,
XX JAM2 and other junctional adhesion molecules by detecting binding between
XX JAM3 and a test compound, or detecting binding between JAM3 and other
XX molecules. The identified compounds or modulators may be employed for
XX treating or alleviating e.g. arthritis, asthma, rheumatoid arthritis,
XX systemic lupus erythematosus, thrombocytopenia, Grave's disease,
XX Hashimoto's thyroiditis, hepatitis, diabetes mellitus, Crohn's disease,
XX psoriasis, allergic rhinitis, idiopathic pulmonary fibrosis, graft
XX rejection or graft-versus-host disease. Sequences ABZ58911-926 represent
XX human JAM3 exon and intron splice-site junction sequences
XX Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 8 CTGTGGCGAC 18
DB 1 CTGTGGAGAC 11
XX
RESULT 515
ID AAA33403
XX AAA33403 standard; DNA; 9 BP.
XX AAA33403;
XX
XX 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1092.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
03-AUG-1999; 99WO-US017712.
XX
03-AUG-1998; 98US-0095212P.
XX
(UYEC-) UNIV EAST CAROLINA.
XX
Nyce JW;
XX WPI; 2000-205971/18.
XX
New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.
XX Claim 18; Page 401; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cytostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impeded respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasize to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
XX AAA33992) are specifically claimed ONs from the present invention. N.B.
XX Sequences given in the disclosure of the present invention do not match
XX up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 9 BP; 0 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 9;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 GGCTGTGG 14
DB 1 GGCTGTGG 9
XX
RESULT 516
ID AAF19525
XX AAF19525 standard; DNA; 9 BP.
XX AAF19525;
XX
XX 14-MAR-2001 (first entry)
XX
DE Human ELAM-1 polynucleotide fragment #1092.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplant rejection;
```

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 XX
 PF 06-APR-1999; 99US-0127958P.
 XX
 PR (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 206; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 9 BP; 0 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCTGGTGG 14
 |||||
 Db 1 GGCTGGTGG 9
 RESULT 517
 ABQ72210
 ID ABQ72210 standard; DNA; 9 BP.
 XX
 XX ABQ72210;
 AC
 XX

DT 28-AUG-2002 (first entry)
 XX Zinc finger protein related oligonucleotide target SEQ ID NO:2508.
 DE Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200242459-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 20-NOV-2001; 2001WO-US043438.
 XX
 PR 20-NOV-2000; 2000US-00716637.
 XX
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 XX Liu Q;
 PT
 PT WPI; 2002-500284/53.
 DR
 XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 XX
 XX Example 1; Page 63; 81pp; English.
 PS
 XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 9 BP; 1 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+03;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GAGGCTGCTT 12
 |||||
 Db 1 GAGGCTGCTT 9
 RESULT 518
 ABZ95219
 ID ABZ95219 standard; DNA; 9 BP.
 XX
 XX AC ABZ95219;
 XX
 XX 17-OCT-2003 (first entry)
 XX
 XX Human ELAM-1 antisense fragment no.1085.
 DE
 XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 10461; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cycostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 9 BP; 0 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
Db 1 GGCTGTTGG 9

RESULT 519
ADA64537
ID ADA64537 standard; DNA; 9 BP.
XX
XX ADA64537;
XX
XX 20-NOV-2003 (first entry)
DT
DE Zinc finger target sequence DNA #995.
XX

KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
XX Synthetic.
OS
PN US2003068675-A1.
XX
XX 10-APR-2003.
XX
XX 20-NOV-2001; 2001US-00990186.
XX
XX 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
XX (LIUQ/) LIU Q.
PA
XX
XX Liu Q;
PI
XX
XX WPI; 2003-567233/53.
XX
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
XX Disclosure; Page 28; 34pp; English.
XX
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 1 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 1 GAGGCTCTT 9

RESULT 520
AAQ57343/c
ID AAQ57343 standard; mRNA; 10 BP.
XX
XX AAQ57343;
XX
XX 25-MAR-2003 (revised)
DT 26-JUL-1994 (first entry)
XX
XX Enzymatic RNA molecule ACE mRNA target sequence.
DE
XX
XX Specific; cleavage; target RNA; protein; prophylaxis; expression;
KW inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis;
KW asthma; inflammatory diseases; cardiovascular condition; hypertension;
KW arthritis; restenosis; angiotensin converting enzyme; ss.
XX
XX Synthetic.
OS
XX
XX WO9402595-A1.
XX
XX 03-FEB-1994.
PD
XX
XX 02-JUL-1993; 93WO-US006316.
PF
XX
XX 17-JUL-1992; 92US-00916763.
PR


```

PR 07-DEC-1992; 92US-00987132.
PR 07-DEC-1992; 92US-00989848.
PR 07-DEC-1992; 92US-00989849.
PR 19-JAN-1993; 93US-00008895.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Sullivan SM, Draper KG;
XX
XX WPI; 1994-048853/06.
XX
XX Enzymatic RNA molecules which cleave mRNA - used to treat or prevent
PT inflammatory, arthritic, stenotic or cardiovascular diseases or
PT conditions.
XX
XX Claim 3; Page 22; 65pp; English.
XX
XX This is a ACE mRNA target sequence (nucleotide no. 899) of an enzymatic
CC RNA molecule (ribozyme) which cleaves mRNA associated with the
CC development or maintenance of a cardiovascular condition. The concn. of
CC the ribozyme necessary to effect a therapeutic treatment is lower than
CC that of an antisense oligonucleotide and the specificity of action is
CC higher. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTG 10
Db 9 TTGATGCTG 1
RESULT 521
AAQ96476/c
ID AAQ96476 standard; DNA; 10 BP.
XX
XX AAQ96476;
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 71.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU0000063.
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 189; 301pp; English.
XX

```

```

CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GCTGTGGC 15
Db 10 GCTGTGGC 2
RESULT 522
AAQ96477/c
ID AAQ96477 standard; DNA; 10 BP.
XX
XX AAQ96477;
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 72.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 189; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 GCTGTTGGC 15
Db      9 GCTGCTGGC 1

RESULT 523
AAT29279/c
ID AAT29279 standard; DNA; 10 BP.
XX
AC AAT29279;
XX
DT 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
XX WO9531574-A1.
XX
XX 23-NOV-1995.
XX
XX 12-MAY-1995; 95WO-US006032.
XX
XX 16-MAY-1994; 94US-00242887.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
XX
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
XX amplification and indexing of amplification prods. w.r.t. primers used
XX for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
XX
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
XX from them, which target mammalian G-protein coupled receptor coding
XX sequences, together comprise a PCR primer kit. The kit is used in a new
XX method for the characterisation of nucleic acid sequences obtd. from
XX mammalian biological samples, which comprises PCR amplification and
XX indexing of the prods. w.r.t the primer pair that hybridised to its
XX delineating subsequences. The method may be used in the identification,
XX cloning and analysis of genes, e.g. in genome mapping, and disease
XX diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TTGAGGCTG 10
Db      9 TTGAGGATG 1

RESULT 524
AAT29345/c
ID AAT29345 standard; DNA; 10 BP.
XX
AC AAT29345;
XX
DT 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX

```

```

DE 5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
XX WO9531574-A1.
XX
XX 23-NOV-1995.
XX
XX 12-MAY-1995; 95WO-US006032.
XX
XX 16-MAY-1994; 94US-00242887.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
XX
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
XX amplification and indexing of amplification prods. w.r.t. primers used
XX for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
XX
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
XX from them, which target mammalian G-protein coupled receptor coding
XX sequences, together comprise a PCR primer kit. The kit is used in a new
XX method for the characterisation of nucleic acid sequences obtd. from
XX mammalian biological samples, which comprises PCR amplification and
XX indexing of the prods. w.r.t the primer pair that hybridised to its
XX delineating subsequences. The method may be used in the identification,
XX cloning and analysis of genes, e.g. in genome mapping, and disease
XX diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GTTGGCGAC 18
Db      9 GTTGGTGAC 1

RESULT 525
AAV35919/c
ID AAV35919 standard; DNA; 10 BP.
XX
XX AAV35919;
XX
XX 26-AUG-1998 (first entry)
XX
XX Primer used in RAPD assay of the invention.
XX
XX Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
XX muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
XX Synthetic.
XX
XX Sub sp.
XX
XX WO9815837-A1.
XX
XX 16-APR-1998.
XX
XX 07-OCT-1997; 97WO-GB002741.
XX
XX 07-OCT-1996; 96GB-00020904.
XX

```

```

PR 18-FEB-1997; 97GB-00003350.
PR 20-MAR-1997; 97GB-00005796.
PR 09-SEP-1997; 97GB-00019002.
XX
XX (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
XX Maltin CA, Steven J, Warkup CC;
XX
XX WPI; 1998-240968/21.
XX
XX Assay for alleles or muscle fibre composition characteristic of Duroc
XX type pigs - comprises determination of genotype or muscle fibre
XX properties, used to identify animals for breeding programs and to assess
XX meat quality.
XX
XX Example 3; Page 32; 56pp; English.
XX
XX PCR primers AAV35877-996 were used in a rapid amplification of
XX polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
XX is used to determine if an animal has an allele for, or muscle fibre
XX composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
XX meat of superior quality (particularly tenderness) but are normally less
XX efficient feed converters and fatter than other types. The assay
XX comprises analysing a tissue sample to determine if the genotype
XX comprises the allele, and genetic features typical of animals with Duroc-
XX type MFC are present. The method is used to select animals that have
XX Duroc characteristics for use in breeding programmes (to develop the
XX animals with Duroc pig characteristics), and to assess meat quality
XX
XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 10 GTTGGCGAC 18
Db 9 GTTGTGCAC 1
|||||
|

RESULT 526
AAX19477
ID AAX19477 standard; DNA; 10 BP.
XX
XX AC AAX19477;
XX
XX 21-MAY-1999 (first entry)
XX
XX Human senescence factor p23 primer SEQ ID NO:19.
XX
XX Human; senescence factor; p23; cancer; persistent inflammation;
XX proliferative disorder; degenerative disorder; primer; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX WO9907893-A1.
XX 18-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016343.
XX
XX 08-AUG-1997; 97US-00508873.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Swisselhelm K, Hosier S, Kubbies M;
XX
XX WPI; 1999-167454/14.
XX
XX Newly isolated nucleic acid molecule (designated p23) encoding a p23
XX polypeptide - useful for inducing a senescence phenotype in a cell.
XX

```

```

PS Example 1; Page 19; 44pp; English.
XX
XX The present invention describes human senescence factor p23. An
XX expression vector for p23 is useful for inducing a senescent phenotype in
XX a cell (preferably eukaryotic). This may help in regulating diseases, and
XX including cancer, persistent inflammation, and various proliferative, and
XX degenerative disorders. These transgenic cells are useful in gene therapy
XX for treating cancer, particularly where antisense oligonucleotides are
XX useful for blocking normal or mutant p23 expression in cancer cells or
XX other proliferating cells. Transgenic cells are also useful for producing
XX the p23 polypeptide in large quantities. The antibodies are useful for
XX raising antiserum against p23, and for identifying senescent cells in
XX culture and tissue biopsies. The p23 polynucleotides are useful for
XX modulating or altering p23 activity in a cell, and for identifying and
XX isolating the whole gene encoding p23, and variants of p23. Assays based
XX on p23 elements, which detect p23 levels and activity are useful as
XX diagnostic markers for staging tumours, determining prognosis, and/or
XX predicting therapeutic success. These elements also provide an assay for
XX detecting chromosomal rearrangements in chromosome 3 in a human cell. The
XX isolation of the p23 polynucleotide permits the manipulation of malignant
XX growth in cancer. The present sequence represents a primer used in an
XX example from the present invention
XX
XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 4 GAGCTGTT 12
Db 2 GAGGTGTT 10
|||||
|

RESULT 527
AAX99946/C
ID AAX99946 standard; DNA; 10 BP.
XX
XX AC AAX99946;
XX
XX 21-OCT-1999 (first entry)
XX
XX Human parkin gene intron 11 fragment.
XX
XX Parkinson's disease related gene; parkin gene; variant; gene therapy;
XX intron; ss.
XX
XX Homo sapiens.
XX WO9940191-A1.
XX 12-AUG-1999.
XX
XX 09-FEB-1999; 99WO-JP0000545.
XX
XX 09-FEB-1998; 98JP-00027531.
XX (SHIM/) SHIMIZU N.
XX (MIZU/) MIZUNO Y.
XX
XX Shimizu N, Mizuno Y;
XX WPI; 1999-494295/41.
XX
XX Gene implicated in the pathology of Parkinson's disease, used for
XX treatment of the disease.
XX
XX Claim 11; Page 103; 114pp; English.
XX
XX This sequence represents a fragment of an intron from the gene of the
XX invention. The gene has been designated the parkin gene, and variants of
XX it are implicated in the pathology of Parkinson's disease, and found in
XX parkinson's disease patients. The sequences may be used for the
XX

```

```

CC diagnosis, treatment (including gene therapy) and investigation of
CC Parkinson's disease
XX
SQ Sequence 10 BP; 3 A; 6 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCG 16
Db 10 CTGTTGGCG 2

RESULT 528
AAX99945
ID AAX99945 standard; DNA; 10 BP.
XX
AC AAX99945;
XX
DT 21-OCT-1999 (first entry)
XX
XX Human parkin gene intron 11 fragment.
XX
XX Parkinson's disease related gene; parkin gene; variant; gene therapy;
XX intron; ss.
XX
XX Homo sapiens.
XX
XX WO9940191-A1.
XX
XX 12-AUG-1999.
XX
PF 09-FEB-1999; 99WO-JP0000545.
XX
XX 09-FEB-1998; 98JP-00027531.
XX
XX (SHIM/) SHIMIZU N.
XX (MIZU/) MIZUNO Y.
XX
XX Shimizu N, Mizuno Y;
XX WPI; 1999-494295/41.
XX
XX Gene implicated in the pathology of Parkinson's disease, used for
XX treatment of the disease.
XX
XX Claim 11; Page 103; 114pp; English.
XX
XX This sequence represents a fragment of an intron from the gene of the
XX invention. The gene has been designated the parkin gene, and variants of
XX it are implicated in the pathology of Parkinson's disease, and found in
XX parkinson's disease patients. The sequences may be used for the
XX diagnosis, treatment (including gene therapy) and investigation of
XX Parkinson's disease
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 2 TGAGTCTGT 10

RESULT 529
AAX32315
ID AAX32315 standard; RNA; 10 BP.
XX
AC AAX32315;
XX

```

```

DT 16-JUN-1999 (first entry)
XX
DE Non-activating control RNA isolate no: 8.
XX
KW Transcriptional regulator; DNA-binding moiety; promoter; transcription;
KW initiation; elongation; gene expression; cancer; anemia; erythrocyte;
KW riboactivator; R10 library; ss.
XX
OS Synthetic.
XX
PN WO9910487-A2.
XX
PD 04-MAR-1999.
XX
PF 26-AUG-1998; 98WO-US017691.
XX
PR 27-AUG-1997; 97US-0056857P.
XX
PA (HARD ) HARVARD COLLEGE.
XX (UYBO-) UNIV BOSTON.
XX
PI Jarrell KA, Saha S, Ptashne M;
XX
XX WPI; 1999-204663/17.
XX
XX New RNA transcriptional regulators - used for modulating gene expression
XX in vitro or in vivo, e.g. as therapeutic agents for treating e.g. cancer
XX or anaemia.
XX
XX Example 2; Page 24; 57pp; English.
XX
XX The invention provides novel transcriptional regulators (TR) that are
XX comprised of RNA molecules. The TR comprises a DNA-binding moiety and an
XX RNA linked to the DNA binding moiety, where the RNA has TR activity.
XX Methods of identifying such RNA TRs are also provided. The RNA TRs alter
XX the rate and/or the extent of transcription from a promoter when they are
XX delivered to a site that is operationally linked to that promoter. The
XX TRs can affect transcription initiation, elongation, reinitiation,
XX termination and pausing. They can be used in e.g. bacterial cells, yeast
XX cells, mammalian cells, insect cells, plant cells, reptile cells, for
XX celeronate cells, and protozoan cells. They can be used as agents for
XX controlling gene expression, e.g. to modulate gene expression in vivo in
XX order to alleviate or correct a disease state, e.g. cancer, anemia and
XX other disorders related to erythrocyte production
XX
XX Sequence 10 BP; 0 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
Db 1 GGCTGTTGG 9

RESULT 530
AAX32306
ID AAX32306 standard; RNA; 10 BP.
XX
AC AAX32306;
XX
DT 16-JUN-1999 (first entry)
XX
DE Radioactivator isolate no: 2.
XX
KW Transcriptional regulator; DNA-binding moiety; promoter; transcription;
KW initiation; elongation; gene expression; cancer; anemia; erythrocyte;
KW riboactivator; R10 library; ss.
XX
OS Synthetic.
XX
PN WO9910487-A2.

```

```

XX PD 04-MAR-1999.
XX XX
XX PF 26-AUG-1998; 98WO-US017691.
XX XX
XX PR 27-AUG-1997; 97US-0056857P.
XX XX
XX PA (HARD ) HARVARD COLLEGE.
XX PA (UYBO-) UNIV BOSTON.
XX XX
PI Jarrell KA, Saha S, Ptashne M;
XX WPI; 1999-204663/17.
XX XX
XX CC The invention provides novel transcriptional regulators (TR) that are
XX CC comprised of RNA molecules. The TR comprises a DNA-binding moiety and an
XX CC RNA linked to the DNA binding moiety, where the RNA has TR activity.
XX CC Methods of identifying such RNA TRs are also provided. The RNA TRs alter
XX CC the rate and/or the extent of transcription from a promoter when they are
XX CC delivered to a site that is operationally linked to that promoter. The
XX CC TRs can affect transcription initiation, elongation, reinitiation,
XX CC termination and pausing. They can be used in e.g. bacterial cells, yeast
XX CC cells, mammalian cells, insect cells, plant cells, reptile cells,
XX CC celenterate cells, and protozoan cells. They can be used as agents for
XX CC controlling gene expression, e.g. to modulate gene expression in vivo in
XX CC order to alleviate or correct a disease state, e.g. cancer, anemia and
XX CC other disorders related to erythrocyte production. Sequences AAX32305-312
XX CC represent radioactivator isolate sequences obtained from a R10 library
XX SQ Sequence 10 BP; 1 A; 2 C; 4 G; 0 T; 3 U; 0 Other;
XX
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 9 TGGTGGCGA 17
Db :|:|||||
2 UGUGGCGA 10
XX
RESULT 531
AAX32312
ID AAX32312 standard; RNA; 10 BP.
XX
XX AC AAX32312;
XX
XX DT 16-JUN-1999 (first entry)
XX
XX DE Radioactivator isolate no: 8.
XX
XX KW Transcriptional regulator; DNA-binding moiety; promoter; transcription;
XX KW initiation; elongation; gene expression; cancer; anemia; erythrocyte;
XX KW riboactivator; R10 library; ss.
XX
XX OS Synthetic.
XX
XX PN WO9910487-A2.
XX
XX XX 04-MAR-1999.
XX
XX PF 26-AUG-1998; 98WO-US017691.
XX
XX PR 27-AUG-1997; 97US-0056857P.
XX
XX PA (HARD ) HARVARD COLLEGE.
XX PA (UYBO-) UNIV BOSTON.
XX

```

```

PI Jarrell KA, Saha S, Ptashne M;
XX WPI; 1999-204663/17.
XX XX
XX PT New RNA transcriptional regulators - used for modulating gene expression
XX PT in vitro or in vivo, e.g. as therapeutic agents for treating e.g. cancer
XX PT or anaemia.
XX XX
XX PS Example 2; Page 23; 57pp; English.
XX XX
XX CC The invention provides novel transcriptional regulators (TR) that are
XX CC comprised of RNA molecules. The TR comprises a DNA-binding moiety and an
XX CC RNA linked to the DNA binding moiety, where the RNA has TR activity.
XX CC Methods of identifying such RNA TRs are also provided. The RNA TRs alter
XX CC the rate and/or the extent of transcription from a promoter when they are
XX CC delivered to a site that is operationally linked to that promoter. The
XX CC TRs can affect transcription initiation, elongation, reinitiation,
XX CC termination and pausing. They can be used in e.g. bacterial cells, yeast
XX CC cells, mammalian cells, insect cells, plant cells, reptile cells,
XX CC celenterate cells, and protozoan cells. They can be used as agents for
XX CC controlling gene expression, e.g. to modulate gene expression in vivo in
XX CC order to alleviate or correct a disease state, e.g. cancer, anemia and
XX CC other disorders related to erythrocyte production. Sequences AAX32305-312
XX CC represent radioactivator isolate sequences obtained from a R10 library
XX SQ Sequence 10 BP; 1 A; 2 C; 4 G; 0 T; 3 U; 0 Other;
XX
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 9 TGGTGGCGA 17
Db :|:|||||
2 UGUGGCGA 10
XX
RESULT 532
AAX79567
ID AAX79567 standard; DNA; 10 BP.
XX
XX AC AAX79567;
XX
XX DT 10-APR-2000 (first entry)
XX
XX DE Human dendritic cell SAGE tag, SEQ ID NO:1995.
XX
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965924-A2.
XX
XX XX 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013800.
XX
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089991P.
XX PR 19-JUN-1998; 98US-0089992P.
XX PR 19-JUN-1998; 98US-0089993P.
XX PR 19-JUN-1998; 98US-0089994P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.

```


other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells. Immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTG 13
 |||||
 Db 1 AGCCTGTG 9

RESULT 534
 AAZ78801/c
 ID AAZ78801 standard; DNA; 10 BP.

AC AAZ78801;

XX 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:1229.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

OS Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

XX 19-JUN-1998; 98US-0089844P.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089878P.

XX 19-JUN-1998; 98US-0089991P.

XX 19-JUN-1998; 98US-0089992P.

XX 19-JUN-1998; 98US-0089993P.

XX 19-JUN-1998; 98US-0089994P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.

PA (ROBE)/ ROBERTS B L.

PA (SHAN)/ SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting

XX cells, useful in gene vaccines against cancer.

XX Claim 1; Page 100; 130pp; English.

XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

XX Query Match 41.1%; Score 7.4; DB 1; Length 10;

XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;

XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
 |||||

Db 10 TTGGGCTG 2

```
RESULT 535
AAZ84279/C
ID AAZ84279 standard; DNA; 10 BP.
XX AC AAZ84279;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #3513.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX DE Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 152; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences).
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 GAGGCTGTT 12
||||| |||
```

```
Db 10 GAGGCAGTT 2
RESULT 536
AAZ81150/C
ID AAZ81150 standard; DNA; 10 BP.
XX AC AAZ81150;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #384.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX DE Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 68; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences).
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```

QY      4 GAGGCTGTT 12
Db      |||||
        10 GAGGCAGTT 2

RESULT 537
AAZ82196
ID      AAZ82196 standard; DNA; 10 BP.
XX
AC      AAZ82196;
XX
DT      07-APR-2000 (first entry)
XX
DE      Metastatic breast tumour cell upregulated transcript tag #1430.
XX
DE      Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW      non-metastatic breast tumour tissue; gene therapy; anticancer;
KW      antimetastatic; vaccine; diagnosis; ss.
XX
OS      Homo sapiens.
XX
PN      WO9965928-A2.
XX
PD      23-DEC-1999.
XX
PF      18-JUN-1999; 99WO-US013647.
XX
PR      19-JUN-1998; 98US-0089853P.
PR      19-JUN-1998; 98US-0089997P.
PR      19-JUN-1998; 98US-0090039P.
PR      19-JUN-1998; 98US-0090040P.
PR      19-JUN-1998; 98US-0090041P.
XX
PA      (GENZ ) GENZYME CORP.
PA      (ROBE/) ROBERTS B L.
PA      (SHAN/) SHANKARA S.
XX
PI      Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.

Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.

Claim 1; Page 97; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      4 GAGGCTGTT 12
Db      |||||
        10 GAGGCTGTT 9

RESULT 538
AAZ81306
ID      AAZ81306 standard; DNA; 10 BP.
XX
AC      AAZ81306;
XX
DT      07-APR-2000 (first entry)
XX
DE      Metastatic breast tumour cell upregulated transcript tag #540.
XX
DE      Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW      non-metastatic breast tumour tissue; gene therapy; anticancer;
KW      antimetastatic; vaccine; diagnosis; ss.
XX
OS      Homo sapiens.
XX
PN      WO9965928-A2.
XX
PD      23-DEC-1999.
XX
PF      18-JUN-1999; 99WO-US013647.
XX
PR      19-JUN-1998; 98US-0089853P.
PR      19-JUN-1998; 98US-0089997P.
PR      19-JUN-1998; 98US-0090039P.
PR      19-JUN-1998; 98US-0090040P.
PR      19-JUN-1998; 98US-0090041P.
XX
PA      (GENZ ) GENZYME CORP.
PA      (ROBE/) ROBERTS B L.
PA      (SHAN/) SHANKARA S.
XX
PI      Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.

Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.

Claim 1; Page 72; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

```

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 AGGCTGTTG 13
 || |||||
 Db 1 AGCCTGTTG 9

RESULT 539
 AAZ83439
 ID AAZ83439 standard; DNA; 10 BP.
 XX
 AC AAZ83439;
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #2673.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 131; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 that are preferentially transcribed in the metastatic breast tumour
 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 to AAZ86677 represent tags corresponding to distinct transcripts that are
 preferentially transcribed in the primary or non-metastatic breast tumour
 tissue (i.e. are downregulated in metastatic breast tumour cells). These
 transcripts can be used for diagnosis, prognosis, monitoring and
 treatment of breast cancer, particularly where metastatic. Diagnosis is
 by standard immunoassays or hybridisation/amplification reactions.
 Compounds that modulate expression of the transcripts are potentially
 useful for treatment of (metastatic) breast cancer, while promoters from
 the transcripts are used to direct expression, in selected cell types, of
 e.g. therapeutic genes (also ribozymes or antisense sequences),
 particularly an antigen-encoding sequence for use in gene or cell-based
 vaccines. Polypeptides encoded by the transcripts are also useful in
 vaccines; for diagnosing breast cancer and for raising specific
 antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 agents. Host cells that produce the polypeptides can be used to expand
 and isolate populations of educated, antigen-specific immune effector
 cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 immunotherapy

SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 GGCTGTTG 14
 |||||
 Db 2 GGCTGTTG 10
 RESULT 540
 AAZ85795/C
 ID AAZ85795 standard; DNA; 10 BP.
 XX
 AC AAZ85795;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5029.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 192; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 that are preferentially transcribed in the metastatic breast tumour
 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 to AAZ86677 represent tags corresponding to distinct transcripts that are
 preferentially transcribed in the primary or non-metastatic breast tumour
 tissue (i.e. are downregulated in metastatic breast tumour cells). These
 transcripts can be used for diagnosis, prognosis, monitoring and
 treatment of breast cancer, particularly where metastatic. Diagnosis is
 by standard immunoassays or hybridisation/amplification reactions.
 Compounds that modulate expression of the transcripts are potentially
 useful for treatment of (metastatic) breast cancer, while promoters from
 the transcripts are used to direct expression, in selected cell types, of
 e.g. therapeutic genes (also ribozymes or antisense sequences),
 particularly an antigen-encoding sequence for use in gene or cell-based
 vaccines. Polypeptides encoded by the transcripts are also useful in
 vaccines; for diagnosing breast cancer and for raising specific
 antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 agents. Host cells that produce the polypeptides can be used to expand
 and isolate populations of educated, antigen-specific immune effector
 cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

```

CC immunotherapy
XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTG 10
Db 10 TTGAGGCAG 2

RESULT 541
AAZ85917/C
ID AAZ85917 standard; DNA; 10 BP.
XX AC AAZ85917;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5151.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX FN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 195; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand

```

```

CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 GTTGCGCAG 18
Db 9 GTTGCCAC 1

RESULT 542
AAZ83130
ID AAZ83130 standard; DNA; 10 BP.
XX AC AAZ83130;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #2364.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX FN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 123; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand

```

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTG 13
| | | | |
Db 1 AAGCTGTG 9

RESULT 543
AAZ81087
ID AAZ81087 standard; DNA; 10 BP.

XX AC AAZ81087;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #321.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN W09965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX Claim 1; Page 66; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGC 15
| | | | |
Db 1 GCTGTGGC 9

RESULT 544
AAZ81916/C
ID AAZ81916 standard; DNA; 10 BP.

XX AC AAZ81916;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #1150.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN W09965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX Claim 1; Page 89; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 AGCGTGTG 13
 | | | | |
 Db 10 ACGTGTG 2
 | | | | |
 RESULT 545
 AAZ82660
 ID AAZ82660 standard; DNA; 10 BP.
 XX
 AC AAZ82660;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #1894.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 XX non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO9965928-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 110; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunosays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 SQ Sequence 10 BP; 2 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 TGTGGCGA 17
 | | | | |
 Db 2 TGTGGAGA 10
 | | | | |
 RESULT 546
 AAZ83470
 ID AAZ83470 standard; DNA; 10 BP.
 XX
 AC AAZ83470;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #2704.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 XX non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO9965928-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 131; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunosays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially

CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 GGCTGTGG 14
 Db 2 GGCTGTGG 10
 |||||
 |||||
 RESULT 547
 ID AA284169 standard; DNA; 10 BP.
 XX
 AC AA284169;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #3403.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 WPI; 2000-106079/09.
 XX
 Isolated polynucleotides differentially expressed between metastatic and
 non-metastatic breast cancer cells, useful for diagnosis, prevention and
 treatment of cancer.
 XX
 Claim 1; Page 150; 219pp; English.
 XX
 AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 TGTGGCGA 17
 Db 9 TGTGGCAA 1
 |||||
 |||||
 RESULT 548
 ID AAA56272 standard; DNA; 10 BP.
 XX
 AC AAA56272;
 XX
 DT 07-SEP-2000 (first entry)
 XX
 DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:166.
 XX
 KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200024892-A1.
 XX
 PD 04-MAY-2000.
 XX
 PR 28-OCT-1999; 99WO-JP005982.
 XX
 PR 28-OCT-1998; 98JP-00307532.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Hashimoto S, Matsushima K, Suzuki T;
 XX
 WPI; 2000-350734/30.
 XX
 Genes most frequently expressed in human monocytes and GM-macrophages and
 M-macrophages studied and with cDNAs characterized, for study of gene
 specificity, disease onset mechanism, drug development and diagnosis.
 XX
 Claim 7; Page 72; 138pp; Japanese.
 XX
 The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody
 CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the

CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AA56107 to AA56586 represent
 CC specifically cloned oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TTGAGGCTG 10
 Db 2 TTGGGGCTG 10
 RESULT 549
 AAA14152
 ID AAA14152 standard; DNA; 10 BP.
 XX
 AC AAA14152;
 XX
 DT 15-SEP-2003 (revised)
 DT 21-JUL-2000 (first entry)
 XX
 DE E. coli K-12 leading strand PCR primer, SEQ ID NO:50.
 XX
 KW Polymorphism detection; over-represented sequence; strand bias;
 KW organism identification; genomic mapping; octamer; leading strand;
 KW Escherichia coli 0157:H7; PCR primer; ss.
 XX
 OS Escherichia coli K12.
 XX
 PN WO200017399-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US021379.
 XX
 PR 18-SEP-1998; 98US-0101011P.
 XX
 PA (UYNE-) UNIV NEBRASKA-LINCOLN.
 XX
 FI Benson AK;
 XX
 DR WPI; 2000-283618/24.
 XX
 PT Detecting DNA polymorphisms, useful e.g. for identifying organisms by
 PT species, strain or serotype, comprises amplification with primers based
 PT on over-represented oligonucleotide sequences.
 XX
 PS Example; Page 28; 49pp; English.
 XX
 CC The invention relates to a novel method for the detection of
 CC polymorphisms in a DNA sequence. Test DNA and a second DNA are amplified
 CC with at least one pair of primers, and the sequence differences between
 CC the amplicons are compared. The primers are based on oligonucleotide
 CC sequences that are over-represented in the genome of the relevant
 CC organism, and which are biased to one strand. The method can be used to
 CC identify an organism by species, serotype or strain, in which case
 CC amplicons are analysed for products, common to all members of the
 CC species, and those specific for strain or serotype, and the results
 CC compared with an existing database. The method can also be used to
 CC identify an individual, by comparison of results for a test DNA with an
 CC existing database. When applied to differential display analysis, pattern
 CC differences in the amplicons are determined, particularly by a
 CC quantitative method such as densitometry, fluorimetry or radiometry. The
 CC method of the invention is used to identify individuals, to classify
 CC organisms by species, strain or serotype, and to identify genes based on

CC differential display. The method can also be used for genomic mapping,
 CC detecting changes in expression patterns, genetic linkage studies,
 CC medical diagnosis, epidemiology, forensics, and agriculture. The method
 CC uses over-represented sequences to prime amplification. These sequences
 CC are distributed over the entire genome, so analysis is not restricted to
 CC particular regions, and a single primer pair can amplify up to 5% of the
 CC complete Escherichia coli genome. The primers are rationally designed, so
 CC non-specific amplification is limited and the method does not require
 CC restriction enzymes or adapters. Sequences AAA14149-AA14154 represent PCR
 CC primers based on over-represented octamer sequences biased to the leading
 CC strand of the E. coli K-12 genome and are fluorescently labelled at the
 CC 5' end. These primers, and lagging strand primers AAA14155-AAA14160 were
 CC used in the exemplifications of the invention to differentiate and
 CC further characterise two strains of E. coli 0157:H7 (strains FR1K 1641
 CC and FR1K 533) and two strains from the ECOR collection (ECOR 20 and ECOR
 CC 50). (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 TGTGGCGA 17
 Db 2 TGCTGGCGA 10
 RESULT 550
 AAH63655
 ID AAH63655 standard; cDNA; 10 BP.
 XX
 AC AAH63655;
 XX
 DT 20-SEP-2001 (first entry)
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 495.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 21-NOV-2000; 2000WO-US031922.
 XX
 PR 24-NOV-1999; 99US-00448480.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS..
 XX
 PI Velculescu VE, Vogelstein B, Kinzler KW;
 XX
 DR WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 PS Claim 11; Page 50; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH6161-
 CC AAH6474 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

```

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GGCTGTTGG 14
        |||||
DB      2 GGCTGTTG 10

RESULT 551
AAH64281
ID AAH64281 standard; cDNA; 10 BP.
XX
AC AAH64281;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1121.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu VB, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 64; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTGAGGCTG 10
        |||||
DB      2 TTGAGGCTG 10

RESULT 552
AAH41710
ID AAH41710 standard; DNA; 10 BP.
XX
AC AAH41710;
XX
DT 28-AUG-2001 (first entry)
XX

```

```

DE Anti-PEP gene construction related oligonucleotide S15.
XX
KW Phosphoenopyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;
KW oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;
KW sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.
XX
OS Synthetic.
XX
PN WO200134812-A1.
XX
PD 17-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-CN000418.
XX
PR 09-NOV-1999; 99CN-00124511.
XX
PA (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.
XX
PI Chen J, Lang C, Huang R, Hu Z, Liu Z;
XX
DR WPI; 2001-335934/35.
XX
PT Altering protein/fatty acid composition of seeds, useful for producing
PT e.g. soya bean or sesame seed with high protein/fatty acid content,
PT comprises introducing antisense gene.
XX
PS Example 8; Page 9; 25pp; Chinese.
XX
CC The present invention describes a method for altering the protein/fatty
CC acid composition of seeds. The method comprises: (1) cloning
CC phosphoenopyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)
CC genes or their fragments; (2) constructing the corresponding antisense
CC gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into
CC the plant cell of a crop. The method is applicable in plant breeding to
CC give oilseed crops with high oil or protein content like soya bean,
CC sunflower, rapeseed, peanut and sesame. The produced crop plants have
CC high yield of oil or protein. The present sequence represents an
CC oligonucleotide which is used in the construction of an anti-PEP gene in
CC an example from the present invention
XX
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GAGGCTGTT 12
        |||||
DB      2 GAGGCTGTT 10

RESULT 553
AAF34448/C
ID AAF34448 standard; DNA; 10 BP.
XX
AC AAF34448;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1187.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.

```



```
XX PR 16-JUN-1999; 99US-00335032.
XX PF (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR
XX XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX XX
XX PS Example; Page 42; 419pp; English.
XX XX
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ
XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 8 CTGTTGGCG 16
Db 10 CTATTGGCG 2
|||||
|||

RESULT 554
AAF41885/c
ID AAF41885 standard; DNA; 10 BP.
XX AC AAF41885;
XX DT
XX DT 23-MAR-2001 (first entry)
XX XX
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8624.
XX XX
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX XX
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX FN
```

```
PD 21-DEC-2000.
XX XX
XX PF 14-JUN-2000; 2000WO-US016223.
XX XX
XX PR 16-JUN-1999; 99US-00335032.
XX XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX XX
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX XX
XX PT WPI; 2001-061874/07.
XX XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX XX
XX PS Example; Page 308; 419pp; English.
XX XX
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ
XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
XX
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 TGAGGCTGT 11
Db 10 TGAAGCTGT 2
|||||
|||

RESULT 555
AAF42672/c
ID AAF42672 standard; DNA; 10 BP.
XX AC AAF42672;
XX XX
XX DT 23-MAR-2001 (first entry)
XX XX
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10811.
XX XX
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX XX
XX OS Saccharomyces cerevisiae.
XX PN
```

XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX DR WPI; 2001-061874/07.
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX PT gene expression (SAGE) tags, useful for studying, monitoring and
 XX PT affecting phases of the cell cycle.
 XX PS Example; Page 336; 419pp; English.
 XX CC The present invention describes an isolated DNA molecule comprising a
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX CC previously assigned open reading frame; or nonannotated ORF) genes
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
 XX CC cycle comprising administering a NORF gene whose expression varies by at
 XX CC least 10% between any two phases of the cell cycle selected from log
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX CC cell; and (b) monitoring expression of a NORF gene whose expression
 XX CC varies as in M1, where a test substance which modifies the expression of
 XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX CC identifying human genes which are involved in cell cycle progression
 XX CC comprising contacting human DNA with a probe which comprises at least 10
 XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
 XX CC class of drugs having a characteristic effect on gene expression in a
 XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
 XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX CC expression is affected by the class of drugs. The NORF genes may be used
 XX CC to study, monitor and affect phases of the cell cycle, the differentially
 XX CC expressed genes may be used as markers of phases of the cell cycle. The
 XX CC methods may be used to identify candidate drugs which affect the cell
 XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX CC represent SAGE tags used in the exemplification of the present invention.
 XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX CC method, in the exemplification of the present invention
 XX SQ Sequence 10 BP; 3 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 AGGCTGTG 13
 |||||
 Db 10 AGGATGTG 2
 RESULT 556
 AAF40816/c
 ID AAF40816 standard; DNA; 10 BP.
 XX AC AAF40816;
 XX DT 23-MAR-2001 (first entry)
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7555.
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX DR WPI; 2001-061874/07.
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX PT gene expression (SAGE) tags, useful for studying, monitoring and
 XX PT affecting phases of the cell cycle.
 XX PS Example; Page 269; 419pp; English.
 XX CC The present invention describes an isolated DNA molecule comprising a
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX CC previously assigned open reading frame; or nonannotated ORF) genes
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
 XX CC cycle comprising administering a NORF gene whose expression varies by at
 XX CC least 10% between any two phases of the cell cycle selected from log
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX CC cell; and (b) monitoring expression of a NORF gene whose expression
 XX CC varies as in M1, where a test substance which modifies the expression of
 XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX CC identifying human genes which are involved in cell cycle progression
 XX CC comprising contacting human DNA with a probe which comprises at least 10
 XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
 XX CC class of drugs having a characteristic effect on gene expression in a
 XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
 XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX CC expression is affected by the class of drugs. The NORF genes may be used
 XX CC to study, monitor and affect phases of the cell cycle, the differentially
 XX CC expressed genes may be used as markers of phases of the cell cycle. The
 XX CC methods may be used to identify candidate drugs which affect the cell
 XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX CC represent SAGE tags used in the exemplification of the present invention.
 XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX CC method, in the exemplification of the present invention
 XX SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGCTGTGG 14
 |||||
 Db 9 GGCTCTGG 1
 RESULT 557
 AAF34965
 ID AAF34965 standard; DNA; 10 BP.
 XX AC AAF34965;
 XX DT 23-MAR-2001 (first entry)
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1704.
 XX KW

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 60; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GAGGCTGTT 12
 |||||
 1 GAGGCTGGT 9
 Db
 RESULT 558
 AAF40673
 ID AAF40673 standard; DNA; 10 BP.
 XX
 AC AAF40673;
 XX
 DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7412.
 DE
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 264; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 AGGCTGTTG 13
 |||||
 2 AGGATGTTG 10
 Db
 RESULT 559
 AAF35576
 ID AAF35576 standard; DNA; 10 BP.
 XX

```

AC AAF35576;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2315.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX OS Saccharomyces cerevisiae.
XX
XX W0200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 82; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 GAGGCTGTT 12
DB 1 GAGGCTGTT 9
|||||
|||||

RESULT 560

```

```

AAF37348/c
ID AAF37348 standard; DNA; 10 BP.
XX
XX AAF37348;
AC
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4087.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX OS Saccharomyces cerevisiae.
XX
XX W0200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 146; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 TGAGGCTGT 11
DB 10 TGAGGATGT 2
|||||
|||||

```



```
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
Db 1 CTTGATGCT 9

      ||||| |||
      ||||| |||

RESULT 563
AAF39653/C
ID AAF39653 standard; DNA; 10 BP.
XX AC AAF39653;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6392.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WP1; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of
gene expression (SAGE) tags, useful for studying, monitoring and
affecting phases of the cell cycle.

Example; Page 228; 419pp; English.

The present invention describes an isolated DNA molecule comprising a
coding sequence of a yeast gene selected from a group of 745 NORF (not
previously assigned open reading frame; or nonannotated ORF) genes
comprising a SAGE (serial analysis of gene expression) tag. Also
described are: (1) a method (M1) of using NORF genes to affect the cell
cycle comprising administering a NORF gene whose expression varies by at
least 10% between any two phases of the cell cycle selected from log
phase, S phase and G2/M; (2) a method (M2) for screening candidate
cell; and (b) monitoring expression of a NORF gene whose expression
varies as in M1, where a test substance which modifies the expression of
the yeast gene is a candidate antifungal drug; (3) a method (M3) for
identifying human genes which are involved in cell cycle progression
comprising contacting human DNA with a probe which comprises at least 10
contiguous nucleotides of a NORF gene whose expression varies as in M1;
and (4) a method (M4) for identifying a candidate drug and
yeast cell comprising contacting a yeast cell with a candidate drug and
monitoring expression in the yeast cell of at least 1 NORF gene whose
expression is affected by the class of drugs. The NORF genes may be used
to study, monitor and affect phases of the cell cycle, the differentially
expressed genes may be used as markers of phases of the cell cycle. The
methods may be used to identify candidate drugs which affect the cell
cycle and for identification of antifungal drugs. AAF33268 to AAF4064
represent SAGE tags used in the exemplification of the present invention.
AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
method, in the exemplification of the present invention
```

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GCTGTGGC 15
 |||||
 Db 9 GCTGTGGC 1

RESULT 565
 AAF36315
 ID AAF36315 standard; DNA; 10 BP.
 XX
 AC AAF36315;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3054.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 FF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 109; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 TGTGGCGA 17
 |||||
 Db 2 TGTGGCGA 10

RESULT 566
 AAF40655/c
 ID AAF40655 standard; DNA; 10 BP.
 XX
 AC AAF40655;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7394.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 FF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 264; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTG 10
||| |||||
Db 9 TTAAGGCTG 1
RESULT 567
AAF33950/c
ID AAF33950 standard; DNA; 10 BP.
XX AAF33950;
AC
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:689.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Claim 1; Page 399; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GCTGTTGGC 15
||| |||||
Db 9 GCTGTTGGC 1
RESULT 568
AAF39162/c
ID AAF39162 standard; DNA; 10 BP.
XX AAF39162;
AC AAF39162;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5901.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 210; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression

comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTG 13
|||||
Db 10 AGGCTGTG 2

RESULT 569
AAF39237/C
ID AAF39237 standard; DNA; 10 BP.

XX AAF39237;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5976.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.

XX Example; Page 213; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression

varies as in M1, where a test substance which modifies the expression of
the yeast gene is a candidate antifungal drug; (3) a method (M3) for
identifying human genes which are involved in cell cycle progression
comprising contacting human DNA with a probe which comprises at least 10
contiguous nucleotides of a NORF gene whose expression varies as in M1;
and (4) a method (M4) for identifying a candidate drug as a member of a
class of drugs having a characteristic effect on gene expression in a
yeast cell comprising contacting a yeast cell with a candidate drug and
monitoring expression in the yeast cell of at least 1 NORF gene whose
expression is affected by the class of drugs. The NORF genes may be used
to study, monitor and affect phases of the cell cycle, the differentially
expressed genes may be used as markers of phases of the cell cycle. The
methods may be used to identify candidate drugs which affect the cell
cycle and for identification of antifungal drugs. AAF33268 to AAF44064
represent SAGE tags used in the exemplification of the present invention. CC
AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
|||||
Db 9 GAGGCTGTT 1

RESULT 570

AAF43110
ID AAF43110 standard; DNA; 10 BP.

XX AAF43110;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11249.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.

XX Example; Page 351; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX cell; and (b) monitoring expression of a NORF gene whose expression

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
 |||||
 Db 1 TGAGGCTGT 9

RESULT 571

AAF36967
 ID AAF36967 standard; DNA; 10 BP.

XX AAF36967;

AC AAF36967;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3706.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 132; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTGT 13
 |||||
 Db 2 AGACTGTGT 10

RESULT 572

AAF39593

ID AAF39593 standard; DNA; 10 BP.

XX AAF39593;

AC AAF39593;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6332.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 226; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTTT 12
 Db 2 GAGGCTTT 10
 |||||
 |||||

RESULT 573
 AAF42943/C
 ID AAF42943 standard; DNA; 10 BP.
 XX AC AAF42943;
 XX DT 23-MAR-2001 (first entry)
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11082.
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO20007214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX PT gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.

PS Example; Page 345; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGTGCGA 17
 Db 9 TGTGTGCGA 1
 |||||
 |||||

RESULT 574
 AAF40433/C
 ID AAF40433 standard; DNA; 10 BP.
 XX AC AAF40433;
 XX DT 23-MAR-2001 (first entry)
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7172.
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO20007214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX PT

```

PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
PS Example; Page 256; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTG 13
Db 9 AGGCTTTTG 1

RESULT 575
AAF42050
ID AAF42050 standard; DNA; 10 BP.
XX
XX AAF42050;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8789.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
FD
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
PI
XX

```

```

DR WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 313; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTT 12
Db 1 GAGGCTGAT 9

RESULT 576
AAF36317
ID AAF36317 standard; DNA; 10 BP.
XX
XX AAF36317;
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3056.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
KW
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX

```

XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 109; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
XX method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 TGTGTGGCGA 17
Db 2 TGTGTGGGGA 10
RESULT 577
AAF43031
ID AAF43031 standard; DNA; 10 BP..
XX AC AAF43031;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11170.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX

PR 16-JUN-1999; 99US-00335032.
XX (UYJO') UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 348; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
XX method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CTGTGTGGCG 16
Db 2 CTGTGTGGGG 10
RESULT 578
AAF43054
ID AAF43054 standard; DNA; 10 BP..
XX AC AAF43054;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11193.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 21-DEC-2000.

```
XX 14-JUN-2000; 2000WO-US016223.
XX
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 349; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
XX Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTTGAGGCT 9
Db 2 CTTGAGGAT 10
|||||||
RESULTS 579
AAF37820
ID AAF37820 standard; DNA; 10 BP.
XX
XX AAF37820;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4559.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX
```

```
PN WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 162; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
XX Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 GGCTGTTGG 14
Db 1 GGCTGTTTG 9
|||||||
RESULTS 580
AAF35067/C
ID AAF35067 standard; DNA; 10 BP.
XX
XX AAF35067;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1806.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
```

```
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 64; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 10 TGATGCTGT 2

RESULT 581
AAF35976/c
ID AAF35976 standard; DNA; 10 BP.
XX AC AAF35976;
XX XX
DT 23-MAR-2001 (first entry)
XX XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2715.
XX XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
```

```
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 97; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGCC 15
Db 9 GCTGTTGCC 1

RESULT 582
AAF39787/c
ID AAF39787 standard; DNA; 10 BP.
XX AC AAF39787;
XX XX
DT 23-MAR-2001 (first entry)
XX XX
```

```
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6526.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
XX 16-JUN-1999; 99US-00335032.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 233; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention.
XX
XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 GTTGGCGAC 18
Db 10 GTTGGCTAC 2
| | | | |
| | | | |
RESULT 583
AAF36067
ID AAF36067 standard; DNA; 10 BP.
XX
XX AAF36067;
```


CC studying expression of the RLBPI isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against RLBPI protein, and for testing the
 CC efficacy of therapeutic agents and compounds for retinal diseases in a
 CC biological system. The gene for RLBPI is located on chromosome 15q26. The
 CC present sequence is an allele specific oligonucleotide (ASO) PCR primer
 CC for amplifying a nucleic acid containing a polymorphic RLBPI sequence,
 CC using the primer extension method
 CC
 SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 TGAAGGCTGT 11
 Db 10 TGTGGCTGT 2
 RESULT 587
 ABK14252/C
 ID ABK14252 standard; DNA; 10 BP.
 XX AC ABK14252;
 XX DT 08-MAY-2002 (first entry)
 XX DE Human RRAS allele specific oligonucleotide (ASO) primer #16.
 XX KW Primer; ss; human; RRAS; Ras; oncogene; SNP; single nucleotide;
 KW polymorphism; viral oncogene; GTPase; cell growth; antisense;
 KW drug development; cancer; allele specific oligonucleotide; ASO;
 KW primer extension.
 XX OS Homo sapiens.
 XX PN WO200188201-A1.
 XX PD 22-NOV-2001.
 XX PF 17-MAY-2001; 2001WO-US016158.
 XX PR 17-MAY-2000; 2000US-0204694P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Chew A, Choi JY, Nandabalan K, Sausker EA;
 XX WPI; 2002-164141/21.
 PT Isolated polynucleotide comprising a related RAS viral (r-ras) oncogene
 PT homolog (RRAS) isogene (comprising defined polymorphism) useful for
 PT providing haplotype information and drug screening.
 XX
 PS Claim 18; Page 12; 60pp; English.
 CC This invention relates to genetic variants of the human related RAS viral
 CC oncogene RRAS. Ras proteins are a member of a superfamily of small
 CC GTPases that are involved in the regulation of cell growth. The invention
 CC also comprises a related RAS viral (r-ras) oncogene homologue (RRAS)
 CC isogene comprising one or more of the polymorphisms shown. The sequences
 CC of the invention may be used to study the function of RRAS or to treat
 CC disorders such as cancer using antisense therapy. The polymorphic
 CC sequence of the invention is useful for providing haplotype information
 CC of an individual. Furthermore, the polymorphic sequence is useful for
 CC studying the biological function of RRAS as well as identifying drugs
 CC targeting the protein for the treatment of disorders related to its
 CC abnormal expression or function. In particular for validating whether
 CC RRAS is a suitable target for drugs to treat cancer, screening for such
 CC drugs and reducing bias in clinical trials. The present sequence
 CC represents an allele specific oligonucleotide primer #16 used to detect
 CC the human related RAS viral oncogene (RRAS) polymorphisms of the
 CC invention using the primer extension technique

CC RESULT 586
 CC ABK24270/C
 CC ID ABK24270 standard; DNA; 10 BP.
 CC AC ABK24270;
 CC DT 09-APR-2002 (first entry)
 CC DE Retinaldehyde-binding protein 1 ASO primer extension primer #43.
 CC KW Human; retinaldehyde-binding protein 1; ss; RLBPI; haplotype; primer;
 CC genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
 CC chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
 CC OS Homo sapiens.
 CC PN WO200192278-A2.
 CC PD 06-DEC-2001.
 CC PF 29-MAY-2001; 2001WO-US017252.
 CC PR 26-MAY-2000; 2000US-0207618P.
 CC PA (GENA-) GENAISSANCE PHARM INC.
 CC PI Choi JY, Kazemi A, Koshy B;
 CC WPI; 2002-122053/16.
 CC New genetic variants having polymorphisms in the retinaldehyde-binding
 CC protein 1 gene, useful for studying the function of and for expressing
 CC RLBPI protein for use in screening drugs for treating diseases related to
 CC RLBPI activity.
 CC
 PS Claim 18; Page 14; 107pp; English.
 CC The invention relates to an isolated polynucleotide, which comprises
 CC genes and haplotypes of the retinaldehyde-binding protein 1 (RLBPI) gene.
 CC The polynucleotide comprises polymorphic sites in the RLBPI gene, which
 CC are referred to as PS1-24 to designate the order in which they are
 CC located in the gene. Also included are methods for haplotyping or
 CC genotyping the RLBPI gene of an individual, a method for predicting a
 CC haplotype pair for the RLBPI gene of an individual, a method for
 CC identifying an association between a trait and at least one haplotype or
 CC haplotype pair of the RLBPI gene, a composition comprising at least one
 CC genotyping oligonucleotide for detecting a polymorphism in the RLBPI gene
 CC at a PS consisting of PS1-PS24, a kit for genotyping the RLBPI gene of an
 CC individual comprising a set of oligonucleotides designed to genotype each
 CC of PS1-PS24 recombinant non-human organisms transformed or transfected
 CC with the isolated polynucleotide, where the organism expresses an RLBPI
 CC protein encoded by the first nucleotide sequence or expresses an RLBPI
 CC polypeptide comprising the polymorphic variant sequence, an isolated
 CC variant of a reference sequence for the RLBPI protein or its fragment, an
 CC anti-RLBPI antibody, a method for screening for drugs targeting the
 CC isolated polypeptide, and a computer system for storing and analyzing
 CC polymorphism data for the RLBPI oncogene gene. The polynucleotide
 CC comprising polymorphisms in the RLBPI gene is useful in studying the
 CC expression and function of RLBPI, and in expressing RLBPI protein for use
 CC in screening candidate drugs to treat diseases related to RLBPI activity
 CC (e.g. autosomal recessive retinitis pigmentosa (arRP)). The methods and
 CC haplotypes are useful in improving the efficiency and output of several
 CC steps in the drug discovery and development process, including target
 CC validation, identifying lead compounds, and early phase clinical trials.
 CC These are also useful for designing clinical trials of candidate drugs
 CC for treating a specific condition or disease, as well as for screening
 CC compounds targeting RLBPI to treat a specific condition or disease
 CC predicted to be associated with RLBPI activity. The kit and method are
 CC useful for determining whether an individual has one of the haplotypes or
 CC haplotype pairs cited above. The transgenic animals are useful for

```

XX SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 CTGTTGGCG 16
   |||||
Db 10 CTGGTGGCG 2

RESULT 588
AAS95514/C
ID AAS95514 standard; DNA; 10 BP.
XX
XX AAS95514;
AC
XX 14-FEB-2002 (first entry)
DT
XX Human HSD3B2 gene allele-specific oligonucleotide PCR primer #4.
DE
XX Human; steroid; dehydrogenase; isomerase; haplotyping; ss; cytostatic;
KW haplotype pair; single nucleotide polymorphism; genotyping; gene therapy;
KW drug screening; congenital adrenal hyperplasia; prostate cancer; HSD3B2;
KW sequencing primer; PCR primer; probe.
XX
XX Homo sapiens.
OS
XX WO200177126-A2.
FN
XX 18-OCT-2001.
PD
XX 10-APR-2001; 2001WO-US011707.
PF
XX 10-APR-2000; 2000US-0195775P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
PI WPI; 2002-041283/05.
XX
DR
XX New haplotypes of the human hydroxy-delta-5-steroid dehydrogenase, 3 beta
PT - and steroid delta-isomerase 2 gene, useful to diagnose and treat
PT congenital adrenal hyperplasia and prostate cancer.
XX
PS Claim 18; Page 13; 60pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human hydroxy-delta-5-steroid dehydrogenase, 3 beta- and
CC steroid delta-isomerase 2 gene (HSD3B2). A method for haplotyping the
CC HSD3B2 gene in an individual comprises identifying the nucleotide at one
CC or more polymorphic sites and determining whether one of the copies of
CC the gene is defined by one of the HSD3B2 haplotypes given in the
CC specification or whether both copies are defined by a haplotype pair.
CC This method is useful in genotyping, whereby all possible haplotype pairs
CC can be assigned to specific genotypes. An association between a trait and
CC a haplotype or haplotype pair of the HSD3B2 gene can be identified by
CC comparing the frequency of the haplotype or haplotype pair in a
CC population exhibiting the trait with the frequency of the haplotype or
CC haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. HSD3B2 and its corresponding DNA are
CC used for studying the expression and function of HSD3B2, for use in
CC screening for candidate drugs to treat diseases related to HSD3B2
CC activity, such as congenital adrenal hyperplasia and prostate cancer. The
CC sequences are also useful for studying the effect of variation on the
CC biological activity of HSD3B2 as well as on the binding affinity of
CC candidate drugs targeting HSD3B2. Sequences AAS95490-AAS95524 represent
CC allele-specific oligonucleotide probes, sequencing primers and PCR
XX primers used to detect HSD3B2 gene polymorphisms

SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TGAGGCTGT 11
   |||||
Db 9 TGAGGCAGT 1

RESULT 589
AAD32507/C
ID AAD32507 standard; DNA; 10 BP.
XX
XX AAD32507;
AC
XX 18-JUN-2002 (first entry)
DT
XX Human OR1G1 gene polymorphism detecting primer #22.
DE
XX Human; olfactory receptor family 1 subfamily G member 1; OR1G1; therapy;
KW polymorphism; drug screening; olfactory sensory deficit; gene therapy;
KW chromosome 17p13.3; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200212561-A2.
FN
XX 14-FEB-2002.
PD
XX 03-AUG-2001; 2001WO-US024478.
PF
XX 03-AUG-2000; 2000US-0222755P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Kazemi A, Messer C, Tanguay DA;
PI WPI; 2002-269097/31.
XX
DR
XX Novel isolated human olfactory receptor, family 1, subfamily G, member 1
PT polynucleotide, for therapeutic purposes, for studying expression and
PT function of the polynucleotide and for expressing receptor protein.
XX
PS Claim 18; Page 14; 96pp; English.
XX
CC The present invention relates to an isolated human olfactory receptor,
CC family 1, subfamily G, member 1, (OR1G1) polynucleotide comprising a
CC sequence which is a polymorphic variant for a reference sequence for the
CC OR1G1 gene or its fragment, or a polymorphic variant of a reference
CC sequence for a OR1G1 cDNA or its fragment. OR1G1 is useful in studying
CC the expression and function of OR1G1 and in expressing OR1G1 protein for
CC use in screening for candidate drugs to treat diseases related to OR1G1
CC activity. OR1G1 is useful for therapeutic purposes. The invention is
CC useful for studying expression of the OR1G1 isogenes in vivo, for in vivo
CC screening and testing of drugs targeted against OR1G1 protein, and for
CC testing the efficacy of therapeutic agents and compounds for olfactory
CC sensory deficits, in a biological system. The invention is useful in gene
CC therapy and is located on the . The present sequence is human OR1G1 gene
CC polymorphism detecting primer
XX
SQ Sequence 10 BP; 3 A; 3 G; 0 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 CTGTTGGCG 16
   |||||
Db 10 CTCTTGGCG 2

```


XX 15-JUL-2002 (first entry)
XX Human PHK22 preferred oligonucleotide primer SEQ ID NO:44.
XX
XX Human; phosphorylase kinase gamma 2 (testis); PHK22; enzyme; SNP;
KW phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW liver cirrhosis; primer; ss.
XX
XX Homo sapiens.
XX WO200194365-A2.
XX 13-DEC-2001.
XX
XX 11-JUN-2001; 2001WO-US018814.
XX
XX 09-JUN-2000; 2000US-0210568P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Choi JY, Koshiy B, Sanchis A, Sausker EA;
XX WPI; 2002-404359/43.
XX
XX New variants of phosphorylase kinase gamma 2 isoforms, useful for
XX improving efficiency and reliability in the development of drugs for
XX treating diseases e.g. liver cirrhosis.
XX
XX Claim 18; Page 14; 76pp; English.
XX
XX The present invention describes an isolated polynucleotide (I) comprising
XX a nucleotide sequence which is a polymorphic variant of a reference
XX sequence for human phosphorylase kinase gamma2 (testis) (PHK22) gene or
XX its fragment, or a polymorphic variant of a reference sequence for a
XX PHK22 cDNA or its fragment. Also described is an isolated polypeptide
XX (II) comprising an amino acid sequence which is a polymorphic variant of
XX a reference sequence for PHK22 protein or its fragment, where the
XX reference sequence comprises a sequence (see AB09290) of 406 amino
XX acids, and the polymorphic variant comprises one or more variant amino
XX acids selected from glutamic acid at a position corresponding to amino
XX acid position 153 and tryptophan at position corresponding to amino acid
XX position 329. (I) has hepatotropic activity and can be used in gene
XX therapy. (II) is useful in screening for drugs targeting (II), by
XX contacting a PHK22 polymorphic variant with a candidate agent and
XX assaying for binding activity. The identified candidate agents targeting
XX PHK22, are useful for treating liver cirrhosis and glycogen storage
XX diseases. The present sequence represents a preferred oligonucleotide
XX primer for the PHK22 gene, which is used in the exemplification of the
XX present invention
XX
XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTTGAGGCT 9
Db 9 CTTGAGGCT 1
RESULT 593
ABQ71544
ID ABQ71544 standard; DNA; 10 BP.
XX
XX AC ABQ71544;
XX
XX 28-AUG-2002 (first entry)
XX
XX Zinc finger protein related oligonucleotide target SEQ ID NO:1278.
XX

KW Zinc finger protein; ZPP; DNA binding protein; zinc finger; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200242459-A2.
XX
XX 30-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX 20-NOV-2000; 2000US-00716637.
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX Liu Q;
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 47; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subsite. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subsite, selecting the F2 zinc finger such that it
XX binds to the S2 target subsite, and selecting the F3 zinc finger such
XX that it binds to the S3 target subsite, thus designing (I) that binds to
XX a target site. (I) is useful for recognition of triplet target subsites
XX having the nucleotide G in the 5'-most position of the subsite. (I) is
XX useful in studying gene function, and for human therapeutics and plant
XX engineering. (I), (II) or (III) is useful in therapeutic methods to
XX modulate the expression of a target region within a subject, in
XX diagnostic methods for sequence specific detection of target nucleic acid
XX in a sample, and in assays to determine the phenotype and function of
XX gene expression. (I) has improved affinity and specificity for their
XX target sequences, as well as enhanced biological activity. ABQ71213 to
XX ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
XX finger peptides which are given in the exemplification of the present
XX invention
XX
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 AGGCTGTGTG 13
Db 2 AGGCTGTGTG 10
RESULT 594
ABA96083
ID ABA96083 standard; DNA; 10 BP.
XX
XX AC ABA96083;
XX
XX 08-APR-2002 (first entry)
XX
XX CYP8B1 primer-extension oligonucleotide primer terminus #8.
XX
XX Primer; CYP8B1; allele-specific oligonucleotide; ASO; cytochrome P450;
KW VIIIB; cardiant; gene therapy; cardiovascular disorder; human; ss.
XX
XX Homo sapiens.

```

XX WO200179224-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 12-APR-2001; 2001WO-US011946.
XX
XX 12-APR-2000; 2000US-0196408P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
PI
XX WPI; 2002-075057/10.
XX
XX Novel polymorphic variants of cytochrome P450 subfamily VIIIB gene useful
PT in studying expression and function of the protein, for screening
PT candidate drugs to treat diseases e.g. cardiovascular disorders.
PT
XX
XX Claim 17; Page 13; 63pp; English.
PS
XX
CC The sequence represents the terminal sequence of a primer for detecting
CC CYP8B1 gene polymorphisms by primer extension. The invention relates to a
CC novel isolated polynucleotide which is a polymorphic variant of a
CC reference sequence for cytochrome P450 subfamily VIIIB (CYP8B1) gene or
CC their fragment. The polynucleotides of the invention have cardiant
CC activity, and may have a use in gene therapy. A polymorphic variant of
CC the CYP8B1 protein is useful for screening drugs targeting CYP8B1. A
CC haplotype or haplotype pair is useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with CYP8B1 activity e.g.,
CC cardiovascular disorders. The invention includes a method for haplotyping
CC CYP8B1 gene in an individual, which can also be used to validate CYP8B1
CC as a candidate target for, and in design of clinical trials of candidate
CC drugs for, treating a specific condition drugs or disease predicted to be
CC associated with CYP8B1 activity. A method is also included for genotyping
CC CYP8B1 gene of an individual which can also be used in developing
CC diagnostic tests and therapeutic treatments. The advantage to this is
CC that without requiring any a prior knowledge of the phenotypic effect of
CC any particular CYP8B1 haplotype or haplotype pair, the invention provides
CC a method to identify lead compounds that are more likely to show efficacy
CC in clinical trials
XX
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
Db 1 TTGAGGATG 9

RESULT 595
ABQ72349/c
ID ABQ72349 standard; DNA; 10 BP.
XX
XX ABQ72349;
AC
XX
XX 02-SEP-2002 (first entry)
DT
XX
XX Human CYP2D6 gene polymorphism detection primer, SEQ ID NO:136.
DE
XX
XX Human; cytochrome P450; subfamily IID polypeptide 6; CYP2D6; enzyme;
KW chromosome 22q13.1; drug metabolism; detoxification; mono-oxygenase;
KW antiarrhythmic; arrhythmia; adrenoceptor antagonist; hypertension;
KW tricyclic antidepressant; procainamide; drug induced lupus syndrome;
KW environmentally linked disease; Parkinson's disease; haplotyping;
KW genotyping; haplotype; genetic variant; single nucleotide polymorphism;
KW SNP; drug screening; drug discovery; primer extension; primer; ss.
XX
XX Homo sapiens.
OS

```

```

XX WO200238589-A2.
PN
XX
XX 16-MAY-2002.
PD
XX
XX 09-NOV-2001; 2001WO-US047396.
XX
XX 09-NOV-2000; 2000US-0247943P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Anastasio AE, Chew A, Choi JY, Denton RR, Nandabalan K;
PI Petersen N, Rounds E;
XX
XX WPI; 2002-519292/55.
XX
XX Novel genetic variants of Cytochrome P450, Subfamily IID, Polypeptide 6
PT isogenes, useful for improving efficiency and reliability in drug
PT development for treating hypertension, arrhythmias and Parkinson's
PT disease.
PT
XX
XX Claim 17; Page 19; 158pp; English.
PS
XX
CC The invention relates to a method for haplotyping the cytochrome P450,
CC subfamily IID, polypeptide 6 (CYP2D6) gene (ABQ72215, ABQ72364) of an
CC individual, and also describes 29 novel polymorphic sites within the
CC human CYP2D6 gene. The CYP2D6 gene is located on chromosome 22q13.1 and
CC contains 9 exons which encode a 497 amino acid protein (AB090563). CYP2D6
CC is a mono-oxygenase involved in the detoxification of many drugs and
CC environmental chemicals. It plays a role in the metabolism of drugs such
CC as antiarrhythmics, adrenoceptor antagonists and tricyclic
CC antidepressants, and is also involved in the formation of a metabolite
CC linked to the drug-induced lupus syndrome observed with procainamide.
CC Variations in CYP2D6 activity or expression may also influence an
CC individual's susceptibility to environmentally-linked diseases, and it
CC has been demonstrated that CYP2D6 activity may be involved in the
CC pathogenesis of Parkinson's disease, with individuals with a less active
CC form of the enzyme tending to have an earlier onset of this condition.
CC CYP2D6 nucleic acid sequences are useful in studying the expression and
CC function of CYP2D6, and in expressing CYP2D6 protein for use in screening
CC drugs for the treatment of CYP2D6-associated diseases (e.g.,
CC hypertension, atrial and ventricular arrhythmias, Parkinson's disease,
CC CYP2D6 nucleic acids and proteins are also useful in studying the effect
CC of polymorphisms on the biological activity of CYP2D6. Polymorphisms in
CC the target region may be determined by the use of allele-specific
CC oligonucleotides (ASOs; ABQ72217-ABQ72303) as probes and primers, and by
CC primer extension using oligonucleotide primers comprising sequences
CC ABQ72304-ABQ72361. The method of the invention is useful for haplotyping
CC the CYP2D6 gene in populations and in individuals, enabling decisions to
CC be made as to whether CYP2D6 is a likely therapeutic target for a disease
CC of interest, and to control for genetically-based bias in the design of
CC drugs that target or are metabolised by CYP2D6. In addition, transgenic
CC animals comprising a human CYP2D6 gene are useful for studying the
CC expression of CYP2D6 isogenes in vivo, for in vivo screening and testing
CC of drugs targeted to or metabolised by CYP2D6, and for testing the
CC efficacy of therapeutic agents and compounds for treating CYP2D6-
CC associated conditions in a biological system. Sequences ABQ72304-
CC ABQ72361 represent sequences that are specifically claimed as components
CC of primers used to detect polymorphisms in the CYP2D6 gene by primer
CC extension
XX
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
Db 10 TTGAGGCTG 2

```

```

RESULT 596
ABV78564
ID ABV78564 standard; cDNA; 10 BP.
XX
XX
AC ABV78564;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human Th2 cell preferentially expressed EST SAGE tag, SEQ ID NO:275.
XX
XX SAGE tag; serial analysis of gene expression; human; Th2 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
XX Homo sapiens.
XX
XX JP2002186482-A.
XX
XX 02-JUL-2002.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-594261/64.
XX
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
PT
XX
XX Claim 19; Page 11; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78561-ABV78610 are SAGE tags
CC representing 50 genes which are more highly expressed in Th2 cells
CC compared with Th1 cells
XX
XX Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TTGAGGCTG 10
Db 2 TTGGGGCTG 10
XX
XX
RESULT 597
ABV78497/c
ID ABV78497 standard; cDNA; 10 BP.
XX
XX ABV78497;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:208.
XX
XX SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW ss.
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX
RESULT 598
ABV84944/c
ID ABV84944 standard; cDNA; 10 BP.
XX
XX ABV84944;
XX
XX 12-DEC-2002 (first entry)
XX
XX Human HCC highly expressed EST SAGE tag #754.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 5 AGGCTGTG 13
Db 10 AGGCTTTG 2
XX
XX

```

```

KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
XX Homo sapiens.
XX
XX JP2002186482-A.
XX
XX 02-JUL-2002.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-594261/64.
XX
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
PT
XX
XX Claim 19; Page 11; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
CC compared with Th2 cells
XX
XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 5 AGGCTGTG 13
Db 10 AGGCTTTG 2
XX
XX
RESULT 598
ABV84944/c
ID ABV84944 standard; cDNA; 10 BP.
XX
XX ABV84944;
XX
XX 12-DEC-2002 (first entry)
XX
XX Human HCC highly expressed EST SAGE tag #754.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX

```

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2002-631294/68.
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
XX Claim 64; Page 31; 139pp; Japanese.
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CMTG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC expressed in hepatocellular carcinoma
XX
SQ Sequence 10 BP; 4 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 TGTGGCGA 17
Db 9 TGTGGAGA 1
RESULT 599
ABK23444/C
ID ABK23444 standard; DNA; 10 BP.
XX
AC ABK23444;
XX
DT 09-APR-2002 (first entry)
XX
DE Transcript tag DNA sequence #33 induced or suppressed by N-myc.
XX
KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN WO200185941-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-NL000361.
XX
PR 11-MAY-2000; 2000EP-00201698.
PR 29-JUN-2000; 2000EP-00202284.
XX
XX (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX Versteeg R, Caron HN;
XX WPI; 2002-066603/09.
XX
XX A new nucleic acid library of myc-dependent downstream genes capable of
PT supporting a neoplastic characteristic of cancer is useful to find new

PT therapies and diagnoses for cancer.
XX
PS Disclosure; Page 49; 69pp; English.
XX
CC The present invention relates to a nucleic acid library comprising myc-
CC dependent downstream genes or their functional fragments essentially
CC capable of supporting a neoplastic character of cancer such as growth,
CC invasion or spread. These myc target or tag sequences are identified by
CC SAGE (serial analysis of gene expression). The library is useful to find
CC new diagnoses and treatments for cancer. The invention is also useful to
CC enhance production of recombinant proteins in a production system with
CC high expression of endogenous or transfected myc oncogenes. ABK23412-
CC ABK23828 represent transcript tag DNA sequences that are activated or
CC repressed by N-myc in human neuroblastoma
XX
SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGGCTGT 11
Db 9 TGAGGATGT 1
RESULT 600
ABL52030
ID ABL52030 standard; DNA; 10 BP.
XX
AC ABL52030;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:78.
XX
KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
KW haplotyping; genotyping; respiratory inflammatory disease;
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200222652-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US042217.
XX
PR 15-SEP-2000; 2000US-0232895P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
XX Anastasio AE, Han J, Klem SE, Sausker EA;
XX WPI; 2002-393942/42.
XX
XX Novel genetic variants of soluble carrier family 18 (vesicular
PT monoamine), member 2 gene useful for screening drugs to treat diseases
PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.
XX
PS Claim 19; Page 15; 183pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) having a
CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
CC member 2 (SLC18A2) isogene selected from 49 isoforms with regions of a
CC sequence (SS) of 40023 bp (see ABL51954), and defined by a corresponding
CC set of polymorphisms whose locations and identities are given in the
CC specification; or a sequence (S2) complementary to (S1). (I) has
CC antiinflammatory and neuroleptic activities, and can be used in gene
CC therapy. Methods from the present invention can be used for haplotyping
CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known

CC as the vesicular monoamine transporter (VMAT2). (1) is useful in studying
 CC the expression and function of SLC18A2, and in expressing the SLC18A2
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to SLC18A2 activity and in studying the effect of the variation
 CC on the biological activity of SLC18A2 as well as on the binding affinity
 CC of candidate drugs targeting SLC18A2 for the treatment of respiratory
 CC inflammatory diseases such as neuropsychiatric disorders involving
 CC monoaminergic brain systems. The present sequence represents a preferred
 CC oligonucleotide primer for human SLC18A2, which is given in the present
 CC invention

XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGA 17
 |||||
 Db 1 TGTGGCGA 9

RESULT 601

AAS19861
 ID AAS19861 standard; DNA; 10 BP.

XX AC AAS19861;

XX DT 08-MAY-2002 (first entry)

XX DE Oligonucleotide #41 to detect human RANGAP1 gene polymorphisms.

XX KW Human; single nucleotide polymorphism; SNP; RANGAP1;
 KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;
 KW genotyping; cancer; irregular cell cycle associated disorder; primer; ss.

XX OS Homo sapiens.

XX PN WO200179240-A2.

XX PD 25-OCT-2001.

XX PF 17-APR-2001; 2001WO-US012455.

XX PR 17-APR-2000; 2000US-0198072P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Chew A, Choi JY, Koshy B;

XX WPI; 2002-075068/10.

XX Genotyping human Ran GTPase activating protein 1 gene of individual for
 PT determining haplotype of individual, involves determining identity of
 FT nucleotide pair at specific polymorphic sites for two copies of the gene.

XX Claim 17; Page 16; 148pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
 CC genotyping the RANGAP1 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC treatment of diseases associated with RANGAP1 activity, such as cancer
 CC and other disorders associated with an irregular cell cycle. AAS19821-
 CC AAS19898 represent primer-extension oligonucleotides for detecting human
 CC RANGAP1 gene polymorphisms

XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
 |||||
 Db 1 TAGAGGCTG 9

RESULT 602
 ABK70762/c
 ID ABK70762 standard; DNA; 10 BP.

XX AC ABK70762;

XX DT 15-JUL-2002 (first entry)

XX DE Primer-extension oligonucleotide #19 to detect human SCYA8 polymorphisms.

XX KW Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
 KW small inducible cytokine subfamily A member 8; SCYA8; anti-HIV;
 KW haplotyping; genotyping; inflammatory disease; HIV infection;
 KW human immunodeficiency virus; primer; ss.

XX OS Homo sapiens.

XX PN WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US029332.

XX PR 15-SEP-2000; 2000US-0232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX WPI; 2002-371973/40.

XX New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
 PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
 FT efficiency and reliability in drug development for treating diseases.

XX Claim 18; Page 14; 84pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
 CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
 CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
 CC gene. The methods of the invention make use of allele-specific
 CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
 CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
 CC polynucleotides and screened compounds are useful for the treatment of
 CC diseases associated with SCYA8 activity, such as inflammatory diseases
 CC and human immunodeficiency virus (HIV) infection. ABK70744-ABK70767
 CC represent primer-extension oligonucleotides for detecting human SCYA8
 CC gene polymorphisms

XX Sequence 10 BP; 4 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGA 17
 |||||
 Db 9 TGTGGCGA 1

RESULT 603

AAL40878

ID AAL40878 standard; DNA; 10 BP.

XX

AC AAL40878;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Zinc finger protein #14target DNA SEQ ID No 91.
 XX
 KW Non-canonical zinc finger binding protein; ZFP; gene therapy; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200257293-A2.
 XX
 PD 25-JUL-2002.
 XX
 PP 22-JAN-2002; 2002WO-US001893.
 XX
 PR 22-JAN-2001; 2001US-0263445P.
 PR 11-MAY-2001; 2001US-0290716P.
 XX
 PA (SANG-) SANGAMO BIOSCIENCES INC.
 XX
 PI Rebar E, Jamieson A;
 XX
 DR WPI; 2002-566791/60.
 XX
 XX Non-canonical zinc finger binding protein for modulating gene expression
 XX comprises non-canonical zinc finger components that bind to a target
 PT sequence.
 XX
 PS Example 7; Page 51; 63pp; English.
 XX
 CC The invention relates to an isolated, non-canonical (e.g., non-C2H2) zinc
 CC finger binding protein (ZFP) comprising one or more non-canonical zinc
 CC finger components that bind to a target sequence. A fusion polypeptide of
 CC the invention is useful for modulating expression of a gene. The non-
 CC canonical ZFP and its encoding polynucleotide, and a fusion protein
 CC comprising the non-canonical ZFP and its encoding polynucleotide can be
 CC used to treat disease. The non-canonical ZFP can be used in diagnostic
 CC assays and to link phenotype to expression of particular genes. The
 CC polynucleotide encoding the non-canonical ZFP can be used to treat
 CC disorders by gene therapy. This polynucleotide sequence represents zinc
 CC finger binding protein related target DNA of the invention
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTTGAGGCT 9
 DB 2 CTTGTGGCT 10
 RESULT 604
 ABS64281
 ID ABS64281 standard; DNA; 10 BP.
 XX
 AC ABS64281;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Tachykinin receptor gene TACR2, primer extension oligo #35.
 XX
 KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
 KW tachykinin receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200263046-A1.
 XX
 PD 15-AUG-2002.
 XX

PF 09-NOV-2001; 2001WO-US047394.
 XX
 PR 09-NOV-2000; 2000US-0247649P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Cappola G, Chew A, Gilson CR, Koshy B;
 XX
 DR WPI; 2002-636600/68.
 XX
 XX New genetic variants having polymorphisms in the Tachykinin receptor
 PT (TACR2) protein, useful for studying the function of TACR2, and for
 PT treating disorders associated with abnormal expression or function of
 PT TACR2 isogene.
 XX
 PS Claim 16; Page 15; 139pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a polymeric
 CC variant of a reference sequence for the Tachykinin receptor (TACR2)
 CC protein. Also described is a method for: (1) haplotyping or genotyping
 CC the TACR2 gene of an individual; (2) predicting a haplotype pair for the
 CC TACR2 gene of an individual; (3) identifying an association between a
 CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and
 CC (4) isolated oligonucleotide for detecting a single nucleotide
 CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene
 CC are useful in studying the expression and biological function of TACR2,
 CC and in identifying drugs targeting TACR2 protein for treating disorders
 CC associated with abnormal expression or function of TACR2, e.g. asthma or
 CC breast cancer. Polynucleotides comprising a polymorphic gene variant or
 CC fragment may be used for therapeutic purposes, where a patient could
 CC benefit from expression or increased expression of a particular TACR2
 CC protein isoform, or an expression vector encoding the isoform may be
 CC administered to the patient. Haplotype information is useful in improving
 CC the efficiency and output of several steps in drug discovery and
 CC development process, including target validation, identifying lead
 CC compounds, and early phase clinical trials. Information on polymorphisms
 CC may be applied in studying biological functions of TACR2 as well as in
 CC identifying drugs targeting this protein for the treatment of disorders
 CC related to its abnormal expression or function. ABS64163-ABS64302
 CC represent human TACR2 gene allele-specific oligonucleotide probes and
 CC primers used to detect haplotypes of the TACR2 gene of the invention
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTTGAGGCT 9
 DB 1 CTTGAGGCT 9
 RESULT 605
 AAS95472/c
 ID AAS95472 standard; DNA; 10 BP.
 XX
 AC AAS95472;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Interleukin 5 (IL5) allele-specific oligonucleotide #30.
 XX
 KW Human; allele-specific oligonucleotide; ASO; interleukin 5; IL5;
 KW antiinflammatory; antiasthmatic; haplotyping; inflammatory disorder;
 KW asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200177132-A2.
 XX
 PD 18-OCT-2001.
 XX

CC plant. The altered phenotype is high in nutritional value, yield, stress
 CC tolerance, pathogen resistance, resistance to agrochemicals, production
 CC of pharmaceutical compounds or production of industrial chemicals. The
 CC present sequence is a nucleotide sequence of the gamma tocopherol
 CC methyltransferase gene target site

XX
 SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
 |||||
 Db 2 CTTGTGGCT 10

RESULT 608

ACC57793
 ID ACC57793 standard; DNA; 10 BP.

XX
 AC ACC57793;

DT 28-JUL-2003 (first entry)

XX
 DE DNA template.

XX
 KW DNA template; nucleic acid detection; ss.

XX
 OS Synthetic.

XX
 PN W02003020984-A2.

XX
 PD 13-MAR-2003.

XX
 PF 29-AUG-2002; 2002WO-US027563.

XX
 PR 29-AUG-2001; 2001US-0315798P.

PR 01-APR-2002; 2002US-00113030.

XX
 PA (AMSH) AMERSHAM BIOSCIENCES CORP.

XX
 PI Nelson J, Fuller C, Sood A, Kumar S;

XX
 WPI; 2003-371723/35.

XX
 PT Detecting presence of nucleic acid, by conducting nucleic acid polymerase
 PT reaction resulting in production of labeled polyphosphate, permitting
 PT polyphosphate to react with phosphatase to produce a detectable species.

XX
 PS Example 5; Page 51; 52pp; English.

XX The present sequence is a DNA template used in examples from the
 CC invention describing nucleic acid detection using polymerase
 CC incorporation of gamma-phosphate-labelled ddGTP or ddATP. A claimed
 CC method of detecting the presence of a nucleic acid sequence comprises
 CC conducting a nucleic acid polymerase reaction. This involves the reaction
 CC of a nucleotide which is non-reactive to phosphatase and one terminal-
 CC phosphate-labelled nucleotide. The reaction results in the production of
 CC labelled polyphosphate, which reacts with a phosphatase to produce a
 CC detectable species. The method is useful for detecting the presence of a
 CC nucleic acid sequence such as DNA, RNA, a natural or synthetic
 CC oligonucleotide, a chromosome or part of a chromosome

XX
 SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
 |||||
 Db 2 AGGCTGCTG 10

RESULT 609
 ABZ75761
 ID ABZ75761 standard; DNA; 10 BP.

XX
 AC ABZ75761;

DT 15-MAY-2003 (first entry)

XX
 DE C. purpureum RAPD1 fragment isolating PCR primer OPB15.

XX
 KW Fungus; herbicide; sprouting inhibitor; PCR; primer; ss.

XX
 OS Chondrostereum purpureum.

XX
 PN W02003001903-A1.

XX
 PD 09-JAN-2003.

XX
 PF 27-JUN-2002; 2002WO-CA000986.

XX
 PR 28-JUN-2001; 2001CA-02351825.

XX
 PA (MYCO-) MYCO FORESTIS CORP.

XX
 PI Gosselin L, Dubois-Calero N, Major N;

XX
 WPI; 2003-239153/23.

XX
 PT Novel purified culture of Chondrostereum purpureum fungus, useful for
 PT biologically controlling weedy deciduous trees and for inhibiting
 PT sprouting and regrowth of freshly cut stems of weedy deciduous trees.

XX
 PS Disclosure; Page 9; 33pp; English.

XX The invention relates to a purified culture of Chondrostereum purpureum
 CC fungus deposited under deposit number 090502-01 or 090502-02 at the
 CC International Depository Authority of Canada (IDAC). The culture or a
 CC composition comprising the culture and an environmentally acceptable
 CC carrier, are useful for biologically controlling weedy deciduous trees,
 CC by colonizing the trees with an effective amount of the culture or the
 CC composition, or by cutting a stem of a weed tree to provide a stump, and
 CC applying the culture or the composition on the stump. They are also
 CC useful for inhibiting sprouting and regrowth of freshly cut stems of
 CC weedy deciduous trees. Sequences ABZ75754-765 represent PCR primers for
 CC isolating RAPD fragments from C. purpureum DNA

XX
 SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
 |||||
 Db 2 GAGGGTCTT 10

RESULT 610
 ACC41745
 ID ACC41745 standard; DNA; 10 BP.

XX
 AC ACC41745;

XX
 DT 21-MAY-2003 (first entry)

XX
 DE Zinc finger protein DNA-binding domain target sequence SEQ ID NO:292.

XX
 KW Zinc finger domain; zinc finger; zinc finger binding domain; probe;
 KW chimeric nucleic acid; library; PCR primer; ss.

XX
 OS Synthetic.


```
Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
   |||||
Db 2 GAGGCTGTT 10

RESULT 613
ADA63307
ID ADA63307 standard; DNA; 10 BP.
AC
XX ADA63307;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #329.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
XX US2003068675-A1.
XX
PD 10-APR-2003.
XX
XX 20-NOV-2001; 2001US-00990186.
XX
XX 24-MAR-1999; 99US-0126238P.
XX
PR 24-MAR-1999; 99US-0126239P.
XX
PR 30-JUL-1999; 99US-0146595P.
XX
PR 30-JUL-1999; 99US-0146615P.
XX
PR 23-MAR-2000; 2000US-00535008.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
XX Liu Q;
PI
XX
XX WPI; 2003-567233/53.
XX
DR Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
XX Disclosure; Page 18; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
SQ

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
   |||||
Db 2 AGGCTGTTG 10

RESULT 614
ADB67173/C
ID ADB67173 standard; DNA; 10 BP.
XX
AC ADB67173;

XX 04-DEC-2003 (first entry)
DT
DE PNA related binding oligonucleotide SEQ ID NO:33.
XX
KW staged assembly; nanostructure; peptide nucleic acid; PNA;
KW structural reinforcement; aerogel; paper; plastic; cement;
KW tensile strength; identification marker; anti-counterfeiting marker;
KW enzyme support; catalyst support; assembly scaffold; nanowire;
KW nanocircuit; molecular sieve; molecular filter; biosensor; ss.
XX
OS Synthetic.
XX
XX WO2003072829-A1.
XX
XX
PD 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005390.
XX
XX 21-FEB-2002; 2002US-00080608.
XX
XX (NANO-) NANOFRAMES INC.
XX
XX Hyman PL, Goldberg EB;
XX
XX WPI; 2003-721788/68.
XX
XX Staged assembly of nanostructures, useful e.g. in biosensors or as
XX catalyst supports, using assembly units derived from peptide nucleic
XX acids.
XX
XX Disclosure; Page 19; 118pp; English.
XX
CC The present invention describes a method (M1) for the staged assembly of
CC a nanostructure using peptide nucleic acids (PNAs). M1 comprises: (a)
CC contacting a nanostructure intermediate (NSI) having at least one unbound
CC joining element (JE) with an assembly unit (AU) that comprises several
CC different JE where: (i) none of these JE can interact with itself or
CC other JE; and (ii) only one JE in AU and a single unbound JE in NSI are
CC complementary, so that AU becomes non-covalently linked to NSI to produce
CC a new NSI for use in subsequent cycles; (b) removing unbound AU; and (c)
CC cyclic repetition of (a) and (b) to form a nanostructure. The new feature
CC is that the complementary JE in at least one cycle are PNAs. Also
CC described are nanostructures formed from many AU, comprising different
CC JE, where at least one AU includes PNA. M1 is useful for producing
CC nanostructures with a very wide range of potential applications, e.g.
CC structural reinforcements (for aerogels, paper, plastics or cement,
CC particularly as long fibres to improve tensile strength); identification
CC (anti-counterfeiting) markers; enzyme or catalyst supports; assembly
CC scaffolds; for construction of nanowires or nanocircuits; size markers
CC for electron microscopy; molecular sieves and filters; substrates for
CC optical and other surface coatings; scaffolds for solubilising enzymes or
CC for trapping, protecting and delivering specific molecules; in high-
CC density computer memories; as artificial zeolite for absorbing ions from
CC water and for construction of new materials, including use in biosensors.
CC PNAs are more homogeneous than inorganic nanoparticles generally used to
CC form nanostructures, so will produce structures with predictable geometry
CC and stoichiometry. The present sequence represents a PNA related binding
CC oligonucleotide, which is used in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
SQ

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
   |||||
Db 10 CTGAGGCT 2

RESULT 615
```

```

AAZ18956/c
ID AAZ18956 standard; DNA; 11 BP.
XX
XX
AC AAZ18956;
XX
XX
DT 22-OCT-1999 (first entry)
XX
XX
DE Murine MRL SAGE tag 1233218.
XX
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX
OS Mus sp.
XX
XX
PN WO9941364-A2.
XX
XX
PD 19-AUG-1999.
XX
XX
PF 12-FEB-1999; 99WO-US002962.
XX
XX
PR 13-FEB-1998; 98US-0074737P.
XX
PR 26-AUG-1998; 98US-0097937P.
XX
PR 28-SEP-1998; 98US-0102051P.
XX
XX
(WIST-) WISTAR INST.
XX
PA Heber-Katz E;
XX
PI WPI; 1999-494533/41.
XX
XX
PT New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
XX
PS Claim 13; Page 73; 136pp; English.
XX
XX
CC This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
XX
SQ Sequence 11 BP; 4 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
Db 11 GTTGGTGAC 3
|||||
RESULT 616
AAZ18727/c
ID AAZ18727 standard; DNA; 11 BP.
XX
XX
AC AAZ18727;
XX
XX
DT 22-OCT-1999 (first entry)
XX
XX
DE Murine MRL SAGE tag 1233218.
XX
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX
OS Mus sp.
XX
XX
PN WO9941364-A2.
XX
XX
PD 19-AUG-1999.
XX
XX
PF 12-FEB-1999; 99WO-US002962.
XX
XX
PR 13-FEB-1998; 98US-0074737P.
XX
PR 26-AUG-1998; 98US-0097937P.
XX
PR 28-SEP-1998; 98US-0102051P.
XX
XX
(WIST-) WISTAR INST.
XX
PA Heber-Katz E;
XX
PI WPI; 1999-494533/41.
XX
XX
PT New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
XX
PS Claim 13; Page 73; 136pp; English.
XX
XX
CC This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
XX
SQ Sequence 11 BP; 4 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
Db 11 GTTGGTGAC 3
|||||
RESULT 616
AAZ18727/c
ID AAZ18727 standard; DNA; 11 BP.
XX
XX
AC AAZ18727;
XX
XX
DT 22-OCT-1999 (first entry)
XX
XX
DE Murine MRL SAGE tag 1233218.
XX
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX
OS Mus sp.
XX
XX
PN WO9941364-A2.
XX
XX
PD 19-AUG-1999.
XX
XX
PF 12-FEB-1999; 99WO-US002962.
XX
XX
PR 13-FEB-1998; 98US-0074737P.
XX
PR 26-AUG-1998; 98US-0097937P.
XX
PR 28-SEP-1998; 98US-0102051P.
XX
XX
(WIST-) WISTAR INST.
XX
PA Heber-Katz E;
XX
PI WPI; 1999-494533/41.
XX
XX
PT New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
XX
PS Claim 13; Page 73; 136pp; English.
XX
XX
CC This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
XX
SQ Sequence 11 BP; 4 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
Db 11 GTTGGTGAC 3
|||||
RESULT 617
AAZ82053/c
ID AAZ82053 standard; DNA; 11 BP.
XX
XX
AC AAZ82053;
XX
XX
DT 13-SEP-1999 (first entry)
XX
XX
DE DNA probe sequence DNA003-11.
XX
XX
KW Linear Beacon; polymer; nucleobase sequence; hybridisation; signal;
KW energy transfer; organism detection; pharmaceutical; beta-thalassemia;
KW nucleic acid detection; sickle cell anemia; Factor-V Leiden; cancer;

```


RESULT 619
AAAS2523/c
ID AAAS2523 standard; DNA; 11 BP.
XX
AC AAAS2523;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human MN gene intron 6 splice acceptor sequence.
XX
KW MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW abnormal expression; neoplastic disease; cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
FN W0200024913-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024879.
XX
PR 23-OCT-1998; 98US-00177776.
XX
PR 23-OCT-1998; 98US-00178115.
XX
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
XX
PI Zavada J, Pastorekova S, Pastorek J;
XX
DR WPI; 2000-350752/30.
XX
PT A molecule which specifically binds to a site on MN protein (oncoprotein)
PT and prevents adhesion of vertebrate cells to the protein, useful for
PT treating preneoplastic or neoplastic diseases such as cancer.
XX
PS Disclosure; Page 26; 154pp; English.
XX
CC The invention relates to the inhibition of cell adhesion mediated by the
CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC protein). The MN protein is a tumour-associated adhesion molecule which
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC Abnormal expression of the MN protein is associated with tumorigenicity.
CC The invention encompasses molecules (e.g., proteins and peptides) which
CC which specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site
CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domains of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAB03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (AAAS2473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents a fragment of the human MN
CC gene (AAAS2462) specified in the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGAGGCTGT 11
| | | | |
DB 11 TGAGCCTGT 3
| | | | |
RESULT 620
AAF77709
ID AAF77709 standard; DNA; 11 BP.
XX
AC AAF77709;
XX
DT 23-MAY-2001 (first entry)
XX
DE KTF-1 binding sequence.
XX
KW Keratinocyte transcription proximal element; KTF-1;
KW keratinocyte nuclear factor; KER1; keratinocyte-specific expression; ds.
XX
OS Xenopus sp.
XX
FN US6183984-B1.
XX
PD 06-FEB-2001.
XX
PF 29-APR-1992; 92US-00875790.
XX
PR 12-NOV-1991; 91US-00791664.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Fuchs EV;
XX
DR WPI; 2001-256100/26.
XX

New DNAs having keratinocyte gene regulatory distal and proximal elements
for the human K14 gene useful for controlling gene expression,
particularly to sequences for promoting keratinocyte-specific gene
expression.
Example 1; Col 25; 36pp; English.
The present invention relates to the human keratinocyte gene (K14)
transcription proximal element (see AAF75889). The proximal element binds
to keratinocyte nuclear factor (KER1), to control keratinocyte-specific
expression. The proximal element, when located upstream from and proximal
to a transcription initiation site of a selected structural gene, may
confer a keratinocyte-specific, and often epidermal abundant, expression
capability to such a gene. To confer keratinocyte specificity, the
proximal element must be combined with a distal element and a TATA box.
The present sequence is the Xenopus embryo nuclear factor, KTF-1 binding
sequence. This sequence is similar to the KER1 binding site
Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTGAGGCT 9
| | | | |
DB 3 CCTGAGGCT 11
| | | | |
RESULT 621
ABQ87081/c
ID ABQ87081 standard; cDNA; 11 BP.
XX
AC ABQ87081;
XX

DT 10-SEP-2002 (first entry)
XX Human skin stress/ageing related EST SEQ ID NO 836.
DE Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253773-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015178.
XX 03-JAN-2001; 2001DE-01000121.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX Claim 8; Page 72; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX Sequence 11 BP; 3 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGAGGCTGT 11
Db 9 TGAGGATGT 1
RESULT 622
ABQ86561/c
ID ABQ86561 standard; cDNA; 11 BP.
XX AC ABQ86561;
XX 10-SEP-2002 (first entry)
XX Human skin stress/ageing related EST SEQ ID NO 316.
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253773-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015178.
XX 03-JAN-2001; 2001DE-01000121.
XX

PA (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX Claim 8; Page 49; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTTGAGGCT 9
Db 11 CTTGAGGAT 3
RESULT 623
ABQ87626
ID ABQ87626 standard; cDNA; 11 BP.
XX AC ABQ87626;
XX 10-SEP-2002 (first entry)
XX Human skin stress/ageing related EST SEQ ID NO 1381.
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253773-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015178.
XX 03-JAN-2001; 2001DE-01000121.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX Claim 8; Page 96; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from

CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention

XX SQ Sequence 11 BP; 0 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 GGCTGTTGG 14
 |||||
 Db 2 GGCTGTTG 10

RESULT 624

ABV62854/c
 ID ABV62854 standard; cDNA; 11 BP.

XX AC ABV62854;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 640.

XX KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 43; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma of sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 3 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCTGTTGCC 15
 |||||
 Db 11 GCTGTTGCC 3

RESULT 625

ABV69436
 ID ABV69436 standard; cDNA; 11 BP.

XX AC ABV69436;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 7222.

XX KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 226; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma of sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 0 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TTGAGGCTG 10
 |||||
 Db 2 TTGAGGCTG 10

RESULT 626

ABV64542
 ID ABV64542 standard; cDNA; 11 BP.

XX AC ABV64542;

XX DT 21-OCT-2002 (first entry)

```
XX Human skin EST 2328.
DE
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX
XX (HENK ) HENKEL KGAA.
PA
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
PT
XX
XX Disclosure; Page 89; 1345pp; German.
PS
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 GGCTGTTGG 14
Qy |||||
Db 1 GGCTTTGG 9
XX
XX RESULT 627
XX ABV66285/C
XX ID ABV66285 standard; cDNA; 11 BP.
XX
XX AC ABV66285;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 4071.
XX
XX Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX
```

```
PF 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK ) HENKEL KGAA.
PA
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
PT
XX
XX Disclosure; Page 138; 1345pp; German.
PS
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5 AGGCTGTGTG 13
Qy |||||
Db 9 AGGCTGTGG 1
XX
XX RESULT 628
XX ABV67862
XX ID ABV67862 standard; cDNA; 11 BP.
XX
XX AC ABV67862;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 5648.
XX
XX Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX
XX (HENK ) HENKEL KGAA.
PA
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
DR
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
PT
XX
```



```

RESULT 631
ABV62726/c
ID ABV62726 standard; cDNA; 11 BP.
XX AC
XX ABV62726;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 512.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX PF WPI; 2002-590638/63.
XX PR In vitro identification of skin-expressed genes, useful for determining
XX PR homeostasis and identifying cosmetic or pharmaceutical agents against
XX PR e.g. skin cancer.
XX PS Disclosure; Page 102; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX Qy 6 GGCTGTGG 14
XX Db 10 GGCTGTGG 2
XX RESULT 632
ABV65010/c
ID ABV65010 standard; cDNA; 11 BP.
XX AC
XX ABV65010;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 2796.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX PF WPI; 2002-590638/63.
XX PR In vitro identification of skin-expressed genes, useful for determining
XX PR homeostasis and identifying cosmetic or pharmaceutical agents against
XX PR e.g. skin cancer.
XX PS Disclosure; Page 39; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 7 C; 2 G; 0 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX Qy 6 GGCTGTGG 14
XX Db 11 GGCTGTGG 3
XX RESULT 633
ABV71892/c
ID ABV71892 standard; cDNA; 11 BP.
XX AC
XX ABV71892;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 9678.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.

```

XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 313; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GAGGCTGTT 12
 Db 11 GAGGCCGTT 3
 RESULT 634
 ABV67256/c
 ID ABV67256 standard; cDNA; 11 BP.
 XX AC ABV67256;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 5042.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 164; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CTTGAGGCT 9
 Db 11 CTTGAGGAT 3
 RESULT 635
 ABV65152/c
 ID ABV65152 standard; cDNA; 11 BP.
 XX AC ABV65152;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 2938.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 106; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

```

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 TTGAGGCTG 10
Db  11 TTCAGGCTG 3

RESULT 636
ABV66544
ID  ABV66544 standard; cDNA; 11 BP.
XX
AC  ABV66544;
XX
XX  21-OCT-2002 (first entry)
XX
XX  Human skin EST 4330.
XX
XX  Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX  immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX  psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX  Homo sapiens.
XX
XX  WO200253774-A2.
XX
XX  11-JUL-2002.
XX
XX  20-DEC-2001; 2001WO-EP015179.
XX
XX  03-JAN-2001; 2001DE-01000127.
XX
XX  (HENK ) HENKEL KGAA.
XX
XX  Petersohn D, Conradt M, Hofmann K;
XX
XX  WPI; 2002-590638/63.
XX
XX  In vitro identification of skin-expressed genes, useful for determining
XX  homeostasis and identifying cosmetic or pharmaceutical agents against
XX  e.g. skin cancer.
XX
XX  Claim 24; Page 253; 1345pp; German.
XX
XX  The invention relates to in vitro identification (M1) of genes expressed
XX  in the skin of humans or animals by subjecting a mixture of genetically
XX  encoded factors from skin, to serial analysis of gene expression (SAGE)
XX  so as to identify skin-expressed genes and quantify their expression.
XX  (M1) is useful for identifying genes involved in skin homeostasis; to
XX  determine skin homeostasis and to test agent (A) that maintains or
XX  promotes skin homeostasis or that can be used for treating skin
XX  disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX  ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX  rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX  skin. The present sequence is that of a human expressed sequence tag
XX  (EST) of the invention
XX
XX  Disclosure; Page 144; 1345pp; German.
XX
XX  The invention relates to in vitro identification (M1) of genes expressed
XX  in the skin of humans or animals by subjecting a mixture of genetically
XX  encoded factors from skin, to serial analysis of gene expression (SAGE)
XX  so as to identify skin-expressed genes and quantify their expression.
XX  (M1) is useful for identifying genes involved in skin homeostasis; to
XX  determine skin homeostasis and to test agent (A) that maintains or
XX  promotes skin homeostasis or that can be used for treating skin
XX  disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX  ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX  rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX  skin. The present sequence is that of a human expressed sequence tag
XX  (EST) of the invention
XX
XX  Sequence 11 BP; 1 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  6 GGCTGTGG 14
Db  2 GGCTGTGG 10

RESULT 637
ABV70147/C
ID  ABV70147 standard; cDNA; 11 BP.
XX
XX
AC  ABV70147;
XX
XX  21-OCT-2002 (first entry)
XX
XX  Human skin EST 4993.
XX
XX  Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX  immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX  psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX  Homo sapiens.
XX
XX  WO200253774-A2.
XX

```



```

XX PD 11-JUL-2002.
XX XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENK ) HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX
XX DR WPI; 2002-590638/63.
XX XX
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX XX
XX PS Disclosure; Page 162; 1345pp; German.
XX CC
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Oy 3 TGAGGCTGT 11
Db 9 TGAGGAGT 1
|||||
|||||

RESULT 639
ABV72073
ID ABV72073 standard; cDNA; 11 BP.
XX
XX AC ABV72073;
XX XX
XX DT 21-OCT-2002 (first entry)
XX XX
XX DE Human skin EST 9859.
XX XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200253774-A2.
XX XX
XX PD 11-JUL-2002.
XX XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENK ) HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX
XX DR WPI; 2002-590638/63.
XX XX
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX XX
XX PS Disclosure; Page 54; 1345pp; German.
XX CC
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin

```


XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 109; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 9 TGTGGCGA 17
XX |||||
XX 11 TGTGGAGA 3
XX
XX RESULT 644
XX ABV68120/C
XX ID ABV68120 standard; cDNA; 11 BP.
XX AC ABV68120;
XX 21-OCT-2002 (first entry)
XX Human skin EST 5906.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.

PR 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 189; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 CTTGAGGCT 9
XX |||||
XX 11 CGTGAGGCT 3
XX
XX RESULT 645
XX ABV68138/C
XX ID ABV68138 standard; cDNA; 11 BP.
XX AC ABV68138;
XX 21-OCT-2002 (first entry)
XX Human skin EST 5924.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 189; 1345pp; German.

XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX CC

SQ Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
 Db 11 TTCAGGCTG 3
 || |||||

RESULT 646
 ABV66358
 ID ABV66358 standard; cDNA; 11 BP.
 AC ABV66358;
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 4144.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Disclosure; Page 140; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
 Db 2 CCTGAGGCT 10
 || |||||

RESULT 647
 ABL91912/C
 ID ABL91912 standard; cDNA; 11 BP.
 XX ABL91912;
 AC ABL91912;
 DT 30-MAY-2002 (first entry)
 XX Human Pan-Endothelial Marker SEQ ID NO 10.
 DE
 XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; ss.
 XX Homo sapiens.
 OS
 XX WO200210217-A2.
 PN 07-FEB-2002.
 PD
 XX 01-AUG-2001; 2001WO-US024031.
 PF
 XX 02-AUG-2000; 2000US-0222599P.
 PR 11-AUG-2000; 2000US-0224360P.
 PR 11-APR-2001; 2001US-0282850P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX St Croix B, Kinzler KW, Vogelstein B;
 PI WPI; 2002-291856/33.
 DR
 XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.
 XX
 XX Example 4; Page 324; 331pp; English.
 PS
 XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
 CC are disclosed, as are marker oligonucleotide sequences: tumour
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 CC (PEM) ABL91903-ABL91995. The present sequence is that of an
 CC oligonucleotide marker useful to the invention
 XX

SQ Sequence 11 BP; 4 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2129.
 DE Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 XX
 KW Homo sapiens.
 OS Synthetic.
 OS
 XX W0200242459-A2.
 PN 30-MAY-2002.
 XX
 XX 20-NOV-2001; 2001WO-US043438.
 XX
 XX 20-NOV-2000; 2000US-00716637.
 XX
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 PI Liu Q;
 XX WPI; 2002-500284/53.
 DR
 XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 PT
 XX Example 1; Page 56; 81pp; English.
 PS
 XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GAGCGTG 10
 |||||
 Db 1 GAGCGTG 7
 RESULT 651
 ABQ71412
 ID ABQ71412 standard; DNA; 9 BP.
 XX
 XX ABQ71412;
 AC
 XX 28-AUG-2002 (first entry)
 DT
 XX Zinc finger protein related oligonucleotide target SEQ ID NO:531.
 DE
 XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 KW

XX Homo sapiens.
 OS Synthetic.
 XX W0200242459-A2.
 PN 30-MAY-2002.
 XX
 XX 20-NOV-2001; 2001WO-US043438.
 XX
 XX 20-NOV-2000; 2000US-00716637.
 XX
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 PI Liu Q;
 XX WPI; 2002-500284/53.
 DR
 XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.
 PT
 XX Example 1; Page 42; 81pp; English.
 PS
 XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 9 BP; 0 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 CTGTTGG 14
 |||||
 Db 2 CTGTTGG 8
 RESULT 652
 ABQ71830
 ID ABQ71830 standard; DNA; 9 BP.
 XX
 XX ABQ71830;
 AC
 XX 28-AUG-2002 (first entry)
 DT
 XX Zinc finger protein related oligonucleotide target SEQ ID NO:2128.
 DE
 XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX

```
PN WO200242459-A2.
XX
XX
PD 30-MAY-2002.
XX
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
XX
PR 20-NOV-2000; 2000US-00716637.
XX
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX
PI Liu Q;
XX
XX
DR WPI; 2002-500284/53.
XX
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX
PS Example 1; Page 56; 8lpp; English.
XX
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
DB 2 AGGCTGT 8

RESULT 653
ABQ71828
ID ABQ71828 standard; DNA; 9 BP.
XX
XX
AC ABQ71828;
XX
XX
DT 28-AUG-2002 (first entry)
XX
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2126.
XX
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX
OS Homo sapiens.
XX
XX
OS Synthetic.
XX
XX
PN WO200242459-A2.
XX
XX
PD 30-MAY-2002.
XX
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
XX
PR 20-NOV-2000; 2000US-00716637.
XX
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX
PI Liu Q;
XX
XX
DR WPI; 2002-500284/53.
XX
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX
PS Example 1; Page 56; 8lpp; English.
XX
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
DB 2 AGGCTGT 8

RESULT 654
ADA64155
ID ADA64155 standard; DNA; 9 BP.
XX
XX
AC ADA64155;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX
DE Zinc finger target sequence DNA #613.
XX
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
XX
OS Synthetic.
XX
XX
OS US2003068675-A1.
XX
XX
PD 10-APR-2003.
XX
XX
PF 20-NOV-2001; 2001US-00990186.
XX
XX
PR 24-MAR-1999; 99US-0126238P.
```



```

Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8

RESULT 657
ADA62560
ID ADA62560 standard; DNA; 9 BP.
XX
AC ADA62560;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #197.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
FN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
OS
XX
FN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 22; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
Db      1 GAGGCTG 7

RESULT 659
AAQ97103/C
ID AAQ97103 standard; DNA; 10 BP.
XX
AC AAQ97103;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 LTR nucleotide deletion 85.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
FN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX

```

```

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
SQ
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGGC 8
Db 7 TTGAGGC 1

RESULT 660
AAQ97099/c
ID AAQ97099 standard; DNA; 10 BP.
XX
AC AAQ97099;
XX
XX 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 81.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
XX
XX 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX
XX 21-FEB-1994; 94AU-00004002.
XX
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
SQ
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGGC 8
Db 7 TTGAGGC 1

RESULT 660
AAQ97099/c
ID AAQ97099 standard; DNA; 10 BP.
XX
AC AAQ97099;
XX
XX 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 81.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
XX
XX 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX
XX 21-FEB-1994; 94AU-00004002.
XX
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
SQ
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGGCT 9
Db 10 TGAGGCT 4

RESULT 661
AAQ99832/c
ID AAQ99832 standard; cDNA; 10 BP.
XX
AC AAQ99832;
XX
XX 06-MAR-1996 (first entry)
DT
DE Eucalyptus grandis coppicing vigour marker primer Y3.
XX
XX Eucalyptus; urophylla; grandis; coppicing vigour marker;
XX RAPD genetic marker; random amplified polymorphic DNA analysis;
XX woody perennial plant; family selection; pedigree; mapping; primer; ss.
XX
XX Synthetic.
XX
XX WO9519697-A1.
XX
XX 27-JUL-1995.
XX
XX 19-JAN-1995; 95WO-US0000677.
XX
XX 21-JAN-1994; 94US-00184567.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Onalley DM, Sederoff RR, Grattapaglia D;
XX WPI; 1995-269212/35.
XX
XX Determn. of heritable oligogenic traits in woody plants by genomic
XX mapping of multiple markers in a two generation plant family - used to
XX select plants with desired characteristics for breeding.
XX
XX Example 6; Page 58; 103pp; English.
XX
XX RAPD analysis was used to determine whether certain quantitative traits
XX were heritable oligogenic traits in Eucalyptus trees. Sets of
XX commercially available random 10-mer primers were used to amplify
XX fragments from the genomic DNA of E.urophylla, E.grandis and E.progeny
XX obtained by crossing the two species. Subsequent mapping analysis showed
XX that the primers in AAQ99829-Q99833 are all useful for amplifying markers
XX of coppicing vigour from E.grandis
XX
XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
SQ
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
Db 7 AGGCTGT 1

```

```

RESULT 662
AAT29349/C
ID AAT29349 standard; DNA; 10 BP.
XX AC
XX AAT29349;
XX
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX OS
XX Synthetic.
XX
XX WO9531574-A1.
XX
XX 23-NOV-1995.
XX
XX 12-MAY-1995; 95WO-US006032.
XX
XX 16-MAY-1994; 94US-00242887.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
XX
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
CC from them, which target mammalian G-protein coupled receptor coding
CC sequences, together comprise a PCR primer kit. The kit is used in a new
CC method for the characterisation of nucleic acid sequences obtd. from
CC mammalian biological samples, which comprises PCR amplification and
CC indexing of the prods. w.r.t the primer pair that hybridised to its
CC delineating subsequences. The method may be used in the identification,
CC cloning and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 7 GCTGTTG 13
XX Db 8 GCTGTTG 2
XX
XX RESULT 663
AAT29273/C
ID AAT29273 standard; DNA; 10 BP.
XX AC
XX AAT29273;
XX
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
XX
XX
XX Shimizu N, Mizuno Y;
XX

```

```

KW disease diagnosis; ss.
XX Synthetic.
XX
XX WO9531574-A1.
XX
XX 23-NOV-1995.
XX
XX 12-MAY-1995; 95WO-US006032.
XX
XX 16-MAY-1994; 94US-00242887.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
XX
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
CC from them, which target mammalian G-protein coupled receptor coding
CC sequences, together comprise a PCR primer kit. The kit is used in a new
CC method for the characterisation of nucleic acid sequences obtd. from
CC mammalian biological samples, which comprises PCR amplification and
CC indexing of the prods. w.r.t the primer pair that hybridised to its
CC delineating subsequences. The method may be used in the identification,
CC cloning and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 7 GCTGTTG 13
XX Db 7 GCTGTTG 1
XX
XX RESULT 664
AAX99938/C
ID AAX99938 standard; DNA; 10 BP.
XX AC
XX AAX99938;
XX
XX 21-OCT-1999 (first entry)
DT
XX Human parkin gene intron 7 fragment.
XX
XX Parkinson's disease related gene; parkin gene; variant; gene therapy;
KW intron; ss.
XX
XX Homo sapiens.
XX
XX WO9940191-A1.
XX
XX 12-AUG-1999.
XX
XX 09-FEB-1999; 99WO-JP000545.
XX
XX 09-FEB-1998; 98JP-00027531.
XX
XX (SHIM/) SHIMIZU N.
XX (MIZU/) MIZUNO Y.
XX
XX Shimizu N, Mizuno Y;
XX

```

```

DR WPI; 1999-494295/41.
XX
PT Gene implicated in the pathology of Parkinson's disease, used for
PT treatment of the disease.
XX
XX Claim 11; Page 100; 114pp; English.
XX
CC This sequence represents a fragment of an intron from the gene of the
CC invention. The gene has been designated the parkin gene, and variants of
CC it are implicated in the pathology of Parkinson's disease, and found in
CC parkinson's disease patients. The sequences may be used for the
CC diagnosis, treatment (including gene therapy) and investigation of
CC Parkinson's disease
XX
XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8 CTGTTGG 14
XX 10 CTGTTGG 4
XX
XX
XX RESULT 665
XX AAX86216/C
XX ID AAX86216 standard; DNA; 10 BP.
XX AC AAX86216;
XX
XX 22-SEP-1999 (first entry)
XX
XX SAGE tag used to identify transcripts which are enhanced by p53.
XX
XX p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
XX neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.
XX
XX Homo sapiens.
XX
XX WO9914356-A2.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019300.
XX
XX 17-SEP-1997; 97US-0059153P.
XX 30-MAR-1998; 98US-0079817P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Polyak K;
XX WPI; 1999-443793/37.
XX
XX Use of p53 transcription tags to determine p53 status in, e.g. cancer
XX diagnosis.
XX
XX Claim 1; Page 26; 73pp; English.
XX
XX The specification describes the use of p53 transcription tags for
XX developing products to determine p53 status, to diagnose cancer and to
XX evaluate cytotoxicity or carcinogenicity of a test agent. A method for
XX diagnosing cancer or determining p53 status in a sample suspected for
XX being neoplastic comprises comparing the level of transcription of an RNA
XX transcript in a first sample (s1) of a first tissue (t1) to the level of
XX transcription of the transcript in a second sample (s2) of a second
XX tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal
XX human tissue (of the same type) and the transcript is identified by a tag
XX ; and categorizing s1 as neoplastic or as having a mutant p53 when
XX transcription is found to be the same or lower in the first, than in s2.
XX The methods and products can be used to determine p53 status, to diagnose
XX cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.
XX AAX86201-33 represent SAGE tags used to identify transcripts which are
XX enhanced by p53
XX
XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 AGGCTGT 11
XX |||||

```

```

CC AAX86201-33 represent SAGE tags used to identify transcripts which are
CC enhanced by p53
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 9 TGTGGC 15
XX 10 TGTGGC 4
XX
XX
XX RESULT 666
XX AAX86213
XX ID AAX86213 standard; DNA; 10 BP.
XX AC AAX86213;
XX
XX 22-SEP-1999 (first entry)
XX
XX SAGE tag used to identify transcripts which are enhanced by p53.
XX
XX p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
XX neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.
XX
XX Homo sapiens.
XX
XX WO9914356-A2.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019300.
XX
XX 17-SEP-1997; 97US-0059153P.
XX 30-MAR-1998; 98US-0079817P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Polyak K;
XX WPI; 1999-443793/37.
XX
XX Use of p53 transcription tags to determine p53 status in, e.g. cancer
XX diagnosis.
XX
XX Claim 1; Page 26; 73pp; English.
XX
XX The specification describes the use of p53 transcription tags for
XX developing products to determine p53 status, to diagnose cancer and to
XX evaluate cytotoxicity or carcinogenicity of a test agent. A method for
XX diagnosing cancer or determining p53 status in a sample suspected for
XX being neoplastic comprises comparing the level of transcription of an RNA
XX transcript in a first sample (s1) of a first tissue (t1) to the level of
XX transcription of the transcript in a second sample (s2) of a second
XX tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal
XX human tissue (of the same type) and the transcript is identified by a tag
XX ; and categorizing s1 as neoplastic or as having a mutant p53 when
XX transcription is found to be the same or lower in the first, than in s2.
XX The methods and products can be used to determine p53 status, to diagnose
XX cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.
XX AAX86201-33 represent SAGE tags used to identify transcripts which are
XX enhanced by p53
XX
XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 AGGCTGT 11
XX |||||

```

```

Db          1 AGGCTGT 7

RESULT 667
AAZ59805/c
ID AAZ59805 standard; DNA; 10 BP.
XX
AC AAZ59805;
XX
DT 28-JUL-1999 (first entry)
XX
DE Primer Y3 for amplifying E. grandis coppicing vigour markers.
XX
KW Genetic marker; genetic locus; resistance; fusiform rust disease;
KW tree family; Pinus; E. grandis; coppicing vigour marker; PCR primer; ss.
XX
OS Synthetic.
XX
FN US5908978-A.
XX
PD 01-JUN-1999.
XX
PF 18-OCT-1995; 95US-00545253.
XX
PR 21-JAN-1994; 94US-00184567.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Grattapaglia D, O'malley DM, Amerson HV, Sederoff RR, Wilcox P;
PI Kuhlman EG;
XX
DR WPI; 1999-347038/29.
XX
PT Identifying resistance to fusiform rust disease in trees of the genus
PT Pinus.
XX
PS Example 6; Col 37; 69pp; English.
XX
CC The specification describes a method of identifying a genetic marker
CC associated with a genetic locus conferring resistance to fusiform rust
CC disease in a family of trees of the genus Pinus. The method comprises
CC obtaining a sexually mature Pinus parent tree exhibiting resistance to
CC fusiform rust disease, obtaining a plurality of progeny trees of the
CC parent by self or cross-pollinations, assessing multiple progeny trees
CC for a number of genetic markers, identifying genetic markers segregating
CC in a Mendelian ratio and showing linkage with other genetic markers,
CC measuring resistance to fusiform rust disease in multiple progeny trees
CC and correlating the presence of resistance to fusiform rust disease with
CC at least one marker identified in the previous step. The method is useful
CC for determining the genetic basis of resistance to fusiform rust disease
CC and for producing trees of the Pinus genus that are resistant to the
CC disease. The present primer was to amplify E. grandis coppicing vigour
CC markers, in the course of invention
XX
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 7 AGGCTGT 1

RESULT 668
AAZ22662
ID AAZ22662 standard; DNA; 10 BP.
XX
AC AAZ22662;
XX
DT 04-JAN-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1843.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CDL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
FN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.

```

T7 primer for amplification of fungal genomic DNA.

commercial; assay; test; fungal pathogen; crop protection; cucurbit;
primer; PCR; RAPD analysis; isolate; food crop; ss.

Synthetic.

EP950719-A2.
20-OCT-1999.

10-MAR-1999; 99EP-00104751.
16-MAR-1998; 98US-0078103P.
22-FEB-1999; 99US-00255432.

(UYCL-) UNIV CLEMSON.

Keinath AP, Somai BM, Dean RA;
WPI; 1999-582557/50.

Detecting a pathogenic fungus in cucumbers, pumpkins and gourds using
recombinant techniques.

Example 3; Page 8; 19pp; English.

This is a commercial oligonucleotide primer for the PCR-based RAPD
analysis of fungal isolates of *Didymella bryoniae* and *Phoma species*. The
new method may be used to distinguish *D. bryoniae* from non-pathogenic
Phoma species fungal infections in Cucurbits (i.e. cucumbers, pumpkins,
watermelons, gourds, cantaloupes, squashes and related plants). The new
method of detection of *D. bryoniae* and *Phoma species* infections allows
rapid diagnosis even before symptoms are visible as compared to prior art
methods which involved growing pure cultures of the pathogens from the
infected plants and identifying them under the light microscope. The
method leads to the early treatment of the infected plants with
fungicides resulting in an increased chance of saving the infected food
crops

Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 4 AGGCTGT 10

RESULT 669
AAZ79415/c
ID AAZ79415 standard; DNA; 10 BP.

AC AAZ79415;
XX
DT 10-APR-2000 (first entry)

Human dendritic cell SAGE tag, SEQ ID NO:1843.

SAGE tag; serial analysis of gene expression; antigen-presenting cell;
APC; monocyte-derived dendritic cell; differential gene expression;
immunostimulatory cofactor; costimulatory factor; CDL;
cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.
WO9965924-A2.
23-DEC-1999.
18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089911P.
PR 19-JUN-1998; 98US-0089921P.
PR 19-JUN-1998; 98US-0089933P.
PR 19-JUN-1998; 98US-0089944P.
PR 19-JUN-1998; 98US-0089977P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
FA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
FT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 117; 130pp; English.
PS
XX Sequences AAZ7573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the

CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTTG 13
Db 8 GCTGTTG 2
RESULT 670
AAZ79495
ID AAZ79495 standard; DNA; 10 BP.
XX
AC AAZ79495;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1923.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089911P.
PR 19-JUN-1998; 98US-0089921P.
PR 19-JUN-1998; 98US-0089933P.
PR 19-JUN-1998; 98US-0089944P.
PR 19-JUN-1998; 98US-0089977P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
FA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
FT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 117; 130pp; English.
PS
XX Sequences AAZ7573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the

XX WPI; 2000-106077/09.
 DR Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX Claim 1; Page 119; 130pp; English.
 PS Sequences AA27573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
 SQ Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GAGGCTG 10
 Db |||||
 2 GAGGCTG 8
 RESULT 671
 AAZ79121
 ID AAZ79121 standard; DNA; 10 BP.
 XX AC AAZ79121;
 XX DT 10-APR-2000 (first entry)
 XX DE Human dendritic cell SAGE tag, SEQ ID NO:1549.
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 OS Homo sapiens.
 XX WO9965924-A2.
 XX PD 23-DEC-1999.
 XX

PF 18-JUN-1999; 99WO-US013800.
 XX 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 PT Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 Claim 1; Page 109; 130pp; English.
 CC Sequences AA27573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells

CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
| | | | |
Db 3 AGGCTGT 9

RESULT 672

AAZ79694/C
ID AAZ79694 standard; DNA; 10 BP.

XX AC AAZ79694;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:2122.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTU;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN W09965924-A2.

XX XX 23-DEC-1999.

XX XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.

FA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX

PI Roberts BL, Shankara S;

XX WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 125; 130pp; English.

XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC secretion of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells

XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7

| | | | |

Db 9 CTTGAGG 3

RESULT 673

AAZ78251

ID AAZ78251 standard; DNA; 10 BP.

XX AC AAZ78251;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:679.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTU;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN W09965924-A2.

XX XX 23-DEC-1999.

PD

XX PF 18-JUN-1999; 99WO-US013800.
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089891P.
XX PR 19-JUN-1998; 98US-0089923P.
XX PR 19-JUN-1998; 98US-0089939P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089977P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PF WPI; 2000-106077/09.
XX DR
XX CC Isolated polynucleotides differentially expressed in antigen-presenting
XX CC cells, useful in gene vaccines against cancer.
XX CC Claim 1; Page 84; 130pp; English.
XX CC Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX CC expression) tags used to identify mRNA transcripts encoding
XX CC immunostimulatory cofactor proteins which are preferentially or
XX CC differentially expressed in monocyte-derived dendritic cells compared
XX CC with monocytes. Some of the transcripts correspond to known genes or ESTs
XX CC (expressed sequence tags) which were previously unknown to be
XX CC preferentially or differentially expressed in dendritic cells, while
XX CC other transcripts correspond to novel genes. Antigen-presenting cell
XX CC (APC)-associated costimulatory factors play an important role in the
XX CC activation of the cytotoxic immune response, particularly against tumour
XX CC cells. Tumour antigen presentation via the MHC (major histocompatibility
XX CC complex) and subsequent recognition by T-cell receptors is alone
XX CC insufficient to activate a robust cytotoxic immune response that can lyse
XX CC the tumour cells. Immunostimulatory cofactors also being required for
XX CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX CC sequences identified using the SAGE tags have several potential uses.
XX CC They may be used in vaccines to induce an immune response, particularly
XX CC against a tumour antigen; to modulate the genotype of an APC; to screen
XX CC for agents that modulate expression of differentially expressed genes in
XX CC an APC; and as hybridisation probes/amplification primers for the
XX CC diagnosis, prognosis and monitoring of diseases related to abnormal
XX CC expression of these genes. Detection of the dendritic cell differentially
XX CC expressed genes, or of their encoded proteins, can be used to identify
XX CC cells as belonging to the monocyte lineage. Cells containing these genes
XX CC can be used in active immunotherapy (or to stimulate production of a
XX CC population of antigen-specific effector cells) and vectors containing
XX CC them are used in gene therapy. Co-administration of tumour antigens and

CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 CTGTGG 14
Db 2 CTGTGG 8
RESULT 674
AAZ82381/C
ID AAZ82381 standard; DNA; 10 BP.
XX AC AAZ82381;
XX AC AAZ82381;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #1615.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089977P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PF WPI; 2000-106079/09.
XX DR
XX CC Isolated polynucleotides differentially expressed between metastatic and
XX CC non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX CC treatment of cancer.
XX CC Claim 1; Page 101; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGC 8
 |||||
 Db 9 TTGAGGC 3

RESULT 675

AAZ86113/C
 ID AAZ86113 standard; DNA; 10 BP.

XX AC AAZ86113;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell downregulated transcript tag #5347.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX FN WO9965928-A2.

XX XX 23-DEC-1999.

XX XX 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 200; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
 |||||
 Db 8 TGAGGCT 2

RESULT 676

AAZ82142/C

ID AAZ82142 standard; DNA; 10 BP.

XX AC AAZ82142;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #1376.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX FN WO9965928-A2.

XX XX 23-DEC-1999.

XX XX 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 95; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 AGGCTGT 11
 Db 10 AGGCTGT 4

RESULT 677
 AAZ84467/C
 ID AAZ84467 standard; DNA; 10 BP.

AC AAZ84467;
 XX
 XX 07-APR-2000 (first entry)
 DT
 DE Metastatic breast tumour cell downregulated transcript tag #3701.
 XX
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.

OS
 XX WO9965928-A2.
 XX
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 157; 219pp; English.

PS
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTGAGG 7
 Db 10 CTTGAGG 4

RESULT 678
 AAZ83486
 ID AAZ83486 standard; DNA; 10 BP.

AC AAZ83486;
 XX
 XX 07-APR-2000 (first entry)
 DT
 DE Metastatic breast tumour cell upregulated transcript tag #2720.
 XX
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 XX Homo sapiens.

OS
 XX WO9965928-A2.
 XX
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013647.
 PF
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX

PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 DR
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 XX Claim 1; Page 132; 219pp; English.

PS
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences).
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCTGTT 12
 |||||
 Db 8 GGCTGTT 2

RESULT 681
 AA284940/C
 ID AA284940 standard; DNA; 10 BP.

AC AA284940;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4174.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0030039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 170; 219pp; English.

XX

CC AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences).
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 7 GAGGCTG 1

RESULT 682
 AA284022
 ID AA284022 standard; DNA; 10 BP.

XX AC AA284022;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #3256.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX

```

PS Claim 1; Page 146; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGG 7
Db 3 CTTGAGG 9
|||||
|
RESULT 683
AAZ86522
ID AAZ86522 standard; DNA; 10 BP.
AC AAZ86522;
XX
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell downregulated transcript tag #5756.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX

```

```

PT treatment of cancer.
XX
XX Claim 1; Page 210; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTG 13
Db 2 GCTGTTG 8
|||||
|
RESULT 684
AAZ85103/C
ID AAZ85103 standard; DNA; 10 BP.
XX
XX AAZ85103;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4337.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX

```

PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

PS Claim 1; Page 175; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
 |||||
 Db 8 CTTGAGG 2

RESULT 685

AAZ85221
 ID AA285221 standard; DNA; 10 BP.

AC AA285221;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4455.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX

DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX Claim 1; Page 178; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCTGTT 12
 |||||
 Db 4 GGCTGTT 10

RESULT 686

AAZ86089/c

ID AA286089 standard; DNA; 10 BP.

XX AA286089;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5323.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX

```

PI Roberts BL, Shankara S;
XX
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 200; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 CTGTGG 14
XX Db 9 CTGTGG 3
XX
XX RESULT 687
XX AAZ83028
XX ID AAZ83028 standard; DNA; 10 BP.
XX
XX AC AAZ83028;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell upregulated transcript tag #2262.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX ROBE/) ROBERTS B L.

```

```

PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 120; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 TTGAGGC 8
XX Db 4 TTGAGGC 10
XX
XX RESULT 688
XX AAZ84058
XX ID AAZ84058 standard; DNA; 10 BP.
XX
XX AC AAZ84058;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #3292.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX ROBE/) ROBERTS B L.

```



```

PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 147; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 3 GAGGCTG 9
|||||
|

RESULT 689
AAZ82188/c
ID AAZ82188 standard; DNA; 10 BP.
XX
AC AAZ82188;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1422.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 96; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTG 13
Db 9 GCTGTTG 3
|||||
|

RESULT 690
AAZ82729/c
ID AAZ82729 standard; DNA; 10 BP.
XX
AC AAZ82729;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1963.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.

```

```

PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 112; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
Db 8 TGAGGCT 2

RESULT 691
AAZ82373/c
ID AAZ82373 standard; DNA; 10 BP.
XX
AC AAZ82373;
XX
DT 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #1607.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX

```

```

PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 101; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
Db 10 TGAGGCT 4

RESULT 692
AAZ85270
ID AAZ85270 standard; DNA; 10 BP.
XX
AC AAZ85270;
XX
DT 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4504.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX

```

```

PF 18-JUN-1999; 99WO-US013647.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 179; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences).
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy.
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AGGCTGT 11
Db 4 AGGCTGT 10
|||||
RESULT 693
AAZ85752/C
ID AAZ85752 standard; DNA; 10 BP.
XX AAZ85752;
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell downregulated transcript tag #4986.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX W09965928-A2.
XX

PD 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 191; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences).
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy.
XX Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTGAGGC 8
Db 8 TTGAGGC 2
|||||
RESULT 694
AAZ82359/C
ID AAZ82359 standard; DNA; 10 BP.
XX AAZ82359;
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell upregulated transcript tag #1593.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX

```

```

PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR
XX 19-JUN-1998; 98US-0089997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR
XX 19-JUN-1998; 98US-0090040P.
PR
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 101; 219pp; English.
XX
XX AZ80767 to AA283941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
CC to AA286677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences).
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGC 15
Db 10 TGTGGC 4
RESULT 695
AAZ84231/C
XX AAZ84231 standard; DNA; 10 BP.
XX
XX AC AAZ84231;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #3465.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR
XX 19-JUN-1998; 98US-0089997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR
XX 19-JUN-1998; 98US-0090040P.
PR
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 151; 219pp; English.
XX
XX AZ80767 to AA283941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
CC to AA286677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences).
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTG 13
Db 8 GCTGTTG 2
RESULT 696
AAZ85767/C
XX AAZ85767 standard; DNA; 10 BP.
XX
XX AC AAZ85767;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #5001.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;

```

```

KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
OS WO9965928-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 192; 219pp; English.
XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
XX to AA286677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGG 7
Db 9 CTTGAGG 3
RESULT 697
AAZ81283
ID AAZ81283 standard; DNA; 10 BP.
XX AC AAZ81283;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #517.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO9965928-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 72; 219pp; English.
XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
XX to AA286677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AGGCTGT 11
Db 1 AGGCTGT 7
RESULT 698
AAZ82557/c
ID AAZ82557 standard; DNA; 10 BP.
XX AC AAZ82557;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #517.
XX

```

```

DE Metastatic breast tumour cell upregulated transcript tag #1791.
XX
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag: primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN W09965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 106; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 TGAGGCT 9
XX |||||
XX 9 TGAGGCT 3
XX
XX Db
XX
XX RESULT 699
XX AAZ84862/C
XX ID AAZ84862 standard; DNA; 10 BP.
XX
XX AC AAZ84862;
XX

```

```

DT 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4096.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag: primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX W09965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 167; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 7 GCTGTTG 13
XX |||||
XX 9 GCTGTTG 3
XX
XX Db
XX
XX RESULT 700
XX AAZ85638/C
XX ID AAZ85638 standard; DNA; 10 BP.
XX
XX AC AAZ85638;
XX

```

```

AC AAZ85638;
XX
XX 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4872.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 189; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGGCTG 10
DB 9 GAGGCTG 3
RESULT 701
AAZ82011

```

```

ID AAZ82011 standard; DNA; 10 BP.
XX
XX AC AAZ82011;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #1245.
DE
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 92; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CTGTGTGG 14
DB 4 CTGTGTGG 10

```

```

RESULT 702
AAZ83742/C
ID  AAZ83742 standard; DNA; 10 BP.
XX  AC
XX  AAZ83742;
XX  DT
XX  07-APR-2000 (first entry)
XX  DE
XX  Metastatic breast tumour cell upregulated transcript tag #2976.
XX  DE
XX  Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX  KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX  KW antimetastatic; vaccine; diagnosis; ss.
XX  OS Homo sapiens.
XX  XX
XX  PN WO9965928-A2.
XX  XX
XX  PD 23-DEC-1999.
XX  PF 18-JUN-1999; 99WO-US013647.
XX  PR 19-JUN-1998; 98US-0089853P.
XX  PR 19-JUN-1998; 98US-0089997P.
XX  PR 19-JUN-1998; 98US-0090039P.
XX  PR 19-JUN-1998; 98US-0090040P.
XX  PR 19-JUN-1998; 98US-0090041P.
XX  XX
XX  (GENZ ) GENZYME CORP.
XX  PA (ROBE/) ROBERTS B L.
XX  PA (SHAN/) SHANKARA S.
XX  XX
XX  PI Roberts BL, Shankara S;
XX  DR WPI; 2000-106079/09.
XX  DR
XX  Isolated polynucleotides differentially expressed between metastatic and
XX  PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX  PT treatment of cancer.
XX  PS Claim 1; Page 138; 219pp; English.
XX  XX
XX  AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX  CC that are preferentially transcribed in the metastatic breast tumour
XX  CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX  CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX  CC preferentially transcribed in the primary or non-metastatic breast tumour
XX  CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX  CC transcripts can be used for diagnosis, prognosis, monitoring and
XX  CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX  CC by standard immunoassays or hybridisation/amplification reactions.
XX  CC Compounds that modulate expression of the transcripts are potentially
XX  CC useful for treatment of (metastatic) breast cancer, while promoters from
XX  CC the transcripts are used to direct expression, in selected cell types, of
XX  CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX  CC particularly an antigen-encoding sequence for use in gene or cell-based
XX  CC vaccines; for diagnosing breast cancer and for raising specific
XX  CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX  CC agents. Host cells that produce the polypeptides can be used to expand
XX  CC and isolate populations of educated, antigen-specific immune effector
XX  CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX  CC immunotherapy
XX  CC
XX  SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
XX  Query Match 38.9%; Score 7; DB 1; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 3 TGAGGCT 9
XX  Db 10 TGAGGCT 4

```

```

RESULT 703
AAZ83255
ID  AAZ83255 standard; DNA; 10 BP.
XX  AC
XX  AAZ83255;
XX  DT
XX  07-APR-2000 (first entry)
XX  DE
XX  Metastatic breast tumour cell upregulated transcript tag #2489.
XX  DE
XX  Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX  KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX  KW antimetastatic; vaccine; diagnosis; ss.
XX  OS Homo sapiens.
XX  XX
XX  PN WO9965928-A2.
XX  XX
XX  PD 23-DEC-1999.
XX  PF 18-JUN-1999; 99WO-US013647.
XX  PR 19-JUN-1998; 98US-0089853P.
XX  PR 19-JUN-1998; 98US-0089997P.
XX  PR 19-JUN-1998; 98US-0090039P.
XX  PR 19-JUN-1998; 98US-0090040P.
XX  PR 19-JUN-1998; 98US-0090041P.
XX  XX
XX  (GENZ ) GENZYME CORP.
XX  PA (ROBE/) ROBERTS B L.
XX  PA (SHAN/) SHANKARA S.
XX  XX
XX  PI Roberts BL, Shankara S;
XX  DR WPI; 2000-106079/09.
XX  DR
XX  Isolated polynucleotides differentially expressed between metastatic and
XX  PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX  PT treatment of cancer.
XX  PS Claim 1; Page 126; 219pp; English.
XX  XX
XX  AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX  CC that are preferentially transcribed in the metastatic breast tumour
XX  CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX  CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX  CC preferentially transcribed in the primary or non-metastatic breast tumour
XX  CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX  CC transcripts can be used for diagnosis, prognosis, monitoring and
XX  CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX  CC by standard immunoassays or hybridisation/amplification reactions.
XX  CC Compounds that modulate expression of the transcripts are potentially
XX  CC useful for treatment of (metastatic) breast cancer, while promoters from
XX  CC the transcripts are used to direct expression, in selected cell types, of
XX  CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX  CC particularly an antigen-encoding sequence for use in gene or cell-based
XX  CC vaccines; for diagnosing breast cancer and for raising specific
XX  CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX  CC agents. Host cells that produce the polypeptides can be used to expand
XX  CC and isolate populations of educated, antigen-specific immune effector
XX  CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX  CC immunotherapy
XX  CC
XX  SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX  Query Match 38.9%; Score 7; DB 1; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 5 AGGCTGT 11

```



```

Db          |||||
            4 AGGCTGT 10

RESULT 704
AAZ85439/C
ID AAZ85439 standard; DNA; 10 BP.
XX
XX AC AAZ85439;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4673.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX anti-metastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX PS Claim 1; Page 184; 219pp; English.
XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          |||||
            4 AGGCTGT 10

RESULT 705
AAZ85480
ID AAZ85480 standard; DNA; 10 BP.
XX
XX AC AAZ85480;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4714.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX anti-metastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX PA (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX PS Claim 1; Page 185; 219pp; English.
XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX
XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
Db 1 GAGGCTG 7
|||||

RESULT 706
AAZ85719/c
ID AAZ85719 standard; DNA; 10 BP.
XX AC
AC AAZ85719;
DT 07-APR-2000 (first entry)
XX Metastatic breast tumour cell downregulated transcript tag #4953.
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
KW
XX Homo sapiens.
OS
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
PI
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 190; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
Db 9 CTTGAGG 3
|||||

RESULT 707
AAC74122
ID AAC74122 standard; cDNA; 10 BP.
XX AC
AC AAC74122;
XX
XX 02-FEB-2001 (first entry)
DT Human monocyte and dendritic cell expressed gene oligonucleotide #209.
XX
DE Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
KW
XX Homo sapiens.
OS
XX WO200060074-A1.
XX
XX 12-OCT-2000.
XX
XX 30-MAR-2000; 2000WO-JP002019.
XX
XX 01-APR-1999; 99JP-00095481.
XX
XX (MISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Hashimoto S, Matsushima K, Suzuki T;
XX WPI; 2000-619172/59.
XX
XX Groups of genes expressed in human dendritic cells at a greater or lesser
PT extent than in monocytes for investigation and diagnosis of autoimmune
PT disease and tumors.
XX
XX Claim 19; Page 15; 95pp; Japanese.
XX
XX The present invention describes a group of genes consisting of 100 genes
CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group of
CC genes are characterised in that cDNAs of these genes respectively have
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'
CC located most closely to the poly-A region. The sequences can be used for
CC the investigation of the role and mechanism of the involvement of
CC dendritic cells in the immune system and for the study and diagnosis of
CC diseases in which dendritic cells play a significant role, e.g. cancers
CC and autoimmune diseases
XX
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTG 13
Db 1 GCTGTG 7
|||||

RESULT 708
AAA56554

CC dendritic cells (antigen-presenting cells, or APCs), may be operably
 CC linked to a sequence encoding an immunostimulatory molecule and a
 CC sequence encoding an antigen. Such a construct could be transduced into
 CC APCs and would be useful for inducing an immune response by educating
 CC immune effector cells in vivo, or in cancer immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
 Db 3 CTTGAGG 9
 |||||

RESULT 710
 AAZ79781
 ID AAZ79781 standard; DNA; 10 BP.
 XX
 AC AAZ79781;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human breast preferentially expressed gene SAGE tag, SEQ ID NO:72.
 XX
 KW SAGE tag; serial analysis of gene expression; diagnosis;
 KW differential gene expression; characterisation; targetted expression;
 KW tumour; cancer; immunotherapy; sa.
 XX
 OS Homo sapiens.
 XX
 XX WO9966303-A2.
 XX
 PD 23-DEC-1999.
 XX
 XX 17-JUN-1999; 99WO-US013820.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX

PI Roberts BL, Shankara S;
 XX WPI; 2000-106132/09.
 DR
 XX New polynucleotide useful in cancer immunotherapy.
 PT
 XX Claim 1; Page 55; 97pp; English.
 XX
 CC Sequences AAZ79710-279916 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts which are
 CC differentially expressed in a variety of normal or malignant cell types.
 CC Some of the transcripts correspond to known genes or ESTs (expressed
 CC sequence tags) which were previously unknown to be preferentially or
 CC differentially expressed in that particular cell type, while other
 CC transcripts correspond to novel genes. The invention also provides a
 CC nucleotide comprising a promoter sequence derived from one of the
 CC differentially expressed genes, which may optionally be operably linked
 CC to a foreign nucleotide sequence, and gene delivery vehicles and host
 CC cells comprising the polynucleotides of the invention. A nucleotide
 CC comprising sequences AAZ79710-279916 may be used in diagnostic procedures
 CC to characterise a cell of a specific tissue type and to determine whether
 CC it is normal or malignant. They may be used to screen for agents that
 CC modulate expression of differentially expressed genes compound. The
 CC promoter/foreign gene construct of the invention may be used for
 CC targeted expression of the foreign gene in a particular cell type. For
 CC example, a promoter derived from a gene preferentially expressed in
 CC dendritic cells (antigen-presenting cells, or APCs), may be operably
 CC linked to a sequence encoding an immunostimulatory molecule and a
 CC sequence encoding an antigen. Such a construct could be transduced into
 CC APCs and would be useful for inducing an immune response by educating
 CC immune effector cells in vivo, or in cancer immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGAC 18
 Db 2 TGGCGAC 8
 |||||

RESULT 711
 AAD15400
 ID AAD15400 standard; DNA; 10 BP.
 XX
 AC AAD15400;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Tag #1 used in SAGE analysis of NOV7 in various cells and tissues.
 XX
 KW Human; NOVX; cancer; stroke; diabetes; antisense therapy; cirrhosis;
 KW Cushing's syndrome; heart failure; vascular disease; gene therapy; SAGE;
 KW serial analysis of gene expression; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200161008-A2.
 PN
 XX 23-AUG-2001.
 PD
 XX 15-FEB-2001; 2001WO-US004779.
 PF
 XX 15-FEB-2000; 2000US-0182637P.
 PR 04-OCT-2000; 2000US-0237862P.
 PR 13-OCT-2000; 2000US-0240316P.
 PR 14-FEB-2001; 2001US-00783436.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Vernet CAM, Shinkets RA, Rastelli L, Burgess CE, Taupier RJ;
 PI

AAH63571 standard; cDNA; 10 BP.
AAH63571;
20-SEP-2001 (first entry)
Human ubiquitously expressed transcriptome sequence SEQ ID NO: 411.
Human; transcriptome; gene expression pattern; cancer; drug screening;
cancer diagnosis; cell specific gene expression; ss.
Homo sapiens.
WO200138577-A2.
31-MAY-2001.
21-NOV-2000; 2000WO-US031922.
24-NOV-1999; 99US-00448480.
(UYJO) UNIV JOHNS HOPKINS.
Velculescu VE, Vogelstein B, Kinzler KW;
WPI; 2001-367706/38.
New isolated polynucleotides, useful for identifying specific cell type,
such as cancer cell, comprises transcriptomes expressed in particular
cell types.
Claim 13; Page 48; 94pp; English.
The present invention describes a method of identifying the type of cell
in a sample, involving determining which of the sequences AAH63161-
AAH64724 is expressed by the cell. The transcriptomes described in the
invention are cell-type specific, cancer specific or ubiquitously
expressed in humans. They can also be used to screen for drugs, reduce
cancer specific gene expression, standardise expression and restore the
function of a diseased cell or tissue. The present sequence is one of the
transcriptomes described in the exemplification of the invention
Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 2 GAGGCTG 8
RESULT 715
AAH64720/C
ID AAH64720 standard; cDNA; 10 BP.
AAH64720;
20-SEP-2001 (first entry)
Human highly expressed transcriptome sequence SEQ ID NO: 1558.
Human; transcriptome; gene expression pattern; cancer; drug screening;
cancer diagnosis; cell specific gene expression; ss.
Homo sapiens.
WO200138577-A2.
31-MAY-2001.
21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX Disclosure; Page 77; 94pp; English.
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCT 9
Db 9 TGAGGCT 3
RESULT 716
AAH64185
ID AAH64185 standard; cDNA; 10 BP.
XX AAH64185;
XX 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1025.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX Claim 13; Page 62; 94pp; English.
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCT 9
Db 9 TGAGGCT 3
RESULT 716
AAH64185
ID AAH64185 standard; cDNA; 10 BP.
XX AAH64185;
XX 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1025.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX Claim 13; Page 62; 94pp; English.
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the

CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcripts described in the exemplification of the invention

XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Oy 7 GCTGTG 13

Db 1 GCTGTG 7

RESULT 717

AAH64422/C
ID AAH64422 standard; cDNA; 10 BP.

XX AC AAH64422;

DT 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1262.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcripts expressed in particular
XX cell types.

XX Claim 13; Page 68; 94pp; English.

XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcripts described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcripts described in the exemplification of the invention

XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Oy 3 TGAGGCT 9

Db 9 TGAGGCT 3

RESULT 718

AAH63338

ID AAH63338 standard; cDNA; 10 BP.

XX AC AAH63338;

DT 20-SEP-2001 (first entry)

XX Human melanocyte specific transcriptome sequence SEQ ID NO: 178.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcripts expressed in particular
XX cell types.

XX Claim 13; Page 43; 94pp; English.

XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcripts described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcripts described in the exemplification of the invention

XX Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Oy 6 GGCTGTT 12

Db 4 GGCTGTT 10

RESULT 719

AAH63570

ID AAH63570 standard; cDNA; 10 BP.

XX AC AAH63570;

DT 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 410.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

```
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 13; Page 48; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific. Cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGGCTG 10
DB 2 GAGGCTG 8
|||||||
|||||||

RESULT 720
AAH64072/c
ID AAH64072 standard; cDNA; 10 BP.
AC AAH64072;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 912.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 13; Page 60; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
CC 21-NOV-2000; 2000WO-US031922.
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
CC
CC Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTTG 13
DB 9 GCTGTTG 3
|||||||
|||||||

RESULT 721
AAH20543/c
ID AAH20543 standard; DNA; 10 BP.
XX
XX AAH20543;
AC AAH20543;
XX
XX 09-AUG-2001 (first entry)
XX
XX Human MTR1 intron7/exon8 junction.
XX
XX MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
XX transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
XX 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
XX intracellular calcium ion regulation; hormone; growth factor; apoptosis;
XX cell growth; cell death; cell differentiation; urogenital disease;
XX polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
XX rhabdomyosarcoma; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX intron 1..5
XX /*tag= a
XX /number= 7
XX exon 6..10
XX /*tag= b
XX /number= 8
XX
XX WO200132693-A2.
XX
XX 10-MAY-2001.
XX
XX 06-NOV-2000; 2000WO-DE003876.
XX
XX 04-NOV-1999; 99DE-01053167.
XX
XX (UYGU-) UNIV GUTENBERG JOHANNES.
XX
XX Prawitt D, Pelletier J, Zabel B;
XX
XX WPI; 2001-316417/33.
XX
XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies.
XX
XX Example 2; Fig 2; 46pp; German.
XX
XX This invention describes a novel DNA sequence (I) encoding the MTR1
XX protein that: (i) has at least one biological activity of a TRP
XX (transient receptor potential) family protein; (ii) is connected with
XX etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
XX with tumors involving 11p15.5 abnormalities. The products of the
XX invention have anticancer and developmental activity. MTR1 is involved in
XX regulation of intracellular calcium ion levels, which are essential for
XX cellular responses to hormones and/or growth factors; also in apoptosis
XX
```


CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers, for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents human MTR1 gene intron7/exon8 junction region described in the
 CC method of the invention

SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
 |||||
 Db 8 AGGCTGT 2

RESULT 722

AAH20726
 ID AAD20726 standard; DNA; 10 BP.

AC AAD20726;

DT 03-JAN-2002 (first entry)

DE Primer #18 used to detect human GPIBA gene polymorphism.

XX Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;
 XX Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;
 KW Alzheimer's disease; polymorphism; human immunodeficiency virus; primer;
 KW ss.

OS Homo sapiens.

XX WO200175065-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010671.

XX 03-APR-2000; 2000US-0194341P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Choi JY, Klien SF, Koshiy B, Parks KE;

XX WPI; 2001-626427/72.

XX New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are
 PT useful for diagnosis and drug discovery for treating Bernard Soulier
 PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's
 PT disease.

PS Claim 18; Page 14; 66pp; English.

XX The invention relates to methods for haplotyping glycoprotein Ib
 CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method
 CC involves determining if the individual has one of the GPIBA haplotypes or
 CC haplotype pairs. The methods of the invention are useful for disease
 CC diagnosis and in the discovery and development of drugs for treating
 CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,
 CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The

CC present sequence is a primer used for detecting human GPIBA gene
 CC polymorphisms

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10

|||||
 Db 4 GAGGCTG 10

RESULT 723

AAH32828
 ID AAH32828 standard; cDNA; 10 BP.

XX AAH32828;

DT 13-AUG-2001 (first entry)

DE LPS activated human monocyte expression gene cDNA tag SEQ:201.

XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.

OS Homo sapiens.

XX JP2001069993-A.

XX 21-MAR-2001.

XX 28-APR-2000; 2000JP-00131079.

XX 08-JUL-1999; 99JP-00195103.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2001-304369/32.

XX LPS activated human monocyte expression gene group.

XX Claim 19; Page 36; 52pp; Japanese.

XX The present invention describes an lipopolysaccharide (LPS) activated
 CC human monocyte expression gene group consisting of the high-ranking 50
 CC genes of the highest expression among the genes expressed by human
 CC monocyte stimulated by LPS in which the cDNA of each gene has the base
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
 CC CATG-3' nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AAB98009, which are given in the exemplification of the present invention

SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13

|||||
 Db 1 GCTGTTG 7

RESULT 724

AAH32662/C
 ID AAH32662 standard; cDNA; 10 BP.

XX

```
AC AAH32662;
XX
XX DT 13-AUG-2001 (first entry)
XX
XX DE LPS activated human monocyte expression gene cDNA tag SEQ:35.
XX
XX KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
XX expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX OS Homo sapiens.
XX
XX XX JP2001069993-A.
XX
XX XX 21-MAR-2001.
XX
XX FF 28-APR-2000; 2000JP-00131079.
XX
XX XX 08-JUL-1999; 99JP-00195103.
XX
XX XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2001-304369/32.
XX
XX FT LPS activated human monocyte expression gene group.
XX
XX PS Claim 1; Page 16; 52pp; Japanese.
XX
XX CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CC The present invention describes an lipopolysaccharide (LPS) activated
XX human monocyte expression gene group consisting of the high-ranking 50
XX genes of the highest expression among the genes expressed by human
XX monocyte stimulated by LPS in which the cDNA of each gene has the base
XX sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
XX CATG-3' nearest to the polyA region. The gene group is useful for the
XX development of new means for the diagnosis and the treatment of various
XX human diseases in which human monocyte plays an important role. AAH32628
XX to AAH32943 represent specifically claimed LPS activated human monocyte
XX expression gene cDNA tags from the present invention. AAH32944 represents
XX an LPS activated human monocyte expression gene cDNA sequence encoding
XX AAB98009, which are given in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 GGCTGTT 12
XX Db 8 GGCTGTT 2
XX
XX RESULT 725
XX ID AAH32879 standard; cDNA; 10 BP.
XX
XX AC AAH32879;
XX
XX XX 13-AUG-2001 (first entry)
XX
XX DE LPS activated human monocyte expression gene cDNA tag SEQ:252.
XX
XX KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
XX expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX OS Homo sapiens.
XX
XX XX JP2001069993-A.
XX
XX XX 21-MAR-2001.
XX
XX FF 28-APR-2000; 2000JP-00131079.
XX
XX XX 08-JUL-1999; 99JP-00195103.
```

```
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2001-304369/32.
XX
XX FT LPS activated human monocyte expression gene group.
XX
XX PS Claim 19; Page 42; 52pp; Japanese.
XX
XX CC The present invention describes an lipopolysaccharide (LPS) activated
XX human monocyte expression gene group consisting of the high-ranking 50
XX genes of the highest expression among the genes expressed by human
XX monocyte stimulated by LPS in which the cDNA of each gene has the base
XX sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
XX CATG-3' nearest to the polyA region. The gene group is useful for the
XX development of new means for the diagnosis and the treatment of various
XX human diseases in which human monocyte plays an important role. AAH32628
XX to AAH32943 represent specifically claimed LPS activated human monocyte
XX expression gene cDNA tags from the present invention. AAH32944 represents
XX an LPS activated human monocyte expression gene cDNA sequence encoding
XX AAB98009, which are given in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 5 AGGCTGT 11
XX Db 4 AGGCTGT 10
XX
XX RESULT 726
XX AAH32805/C
XX ID AAH32805 standard; cDNA; 10 BP.
XX
XX AC AAH32805;
XX
XX DT 13-AUG-2001 (first entry)
XX
XX DE LPS activated human monocyte expression gene cDNA tag SEQ:178.
XX
XX KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
XX expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
XX OS Homo sapiens.
XX
XX XX JP2001069993-A.
XX
XX PD 21-MAR-2001.
XX
XX XX 28-APR-2000; 2000JP-00131079.
XX
XX XX 08-JUL-1999; 99JP-00195103.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2001-304369/32.
XX
XX FT LPS activated human monocyte expression gene group.
XX
XX PS Claim 10; Page 33; 52pp; Japanese.
XX
XX CC The present invention describes an lipopolysaccharide (LPS) activated
XX human monocyte expression gene group consisting of the high-ranking 50
XX genes of the highest expression among the genes expressed by human
XX monocyte stimulated by LPS in which the cDNA of each gene has the base
XX sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
XX CATG-3' nearest to the polyA region. The gene group is useful for the
XX development of new means for the diagnosis and the treatment of various
XX human diseases in which human monocyte plays an important role. AAH32628
XX to AAH32943 represent specifically claimed LPS activated human monocyte
```

CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AAB98009, which are given in the exemplification of the present invention
 SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCTGTT 12
 |||||
 Db 8 GGCTGTT 2

RESULT 727

ABA06211/c
 ID ABA06211 standard; cDNA; 10 BP.

XX AC ABA06211;

XX DT 10-JAN-2002 (first entry)

XX DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 188.

XX KW Human; hepatocyte; gene expression; hepatopathy; ss.

XX OS Homo sapiens.

XX PN JP2001211883-A.

XX PD 07-AUG-2001.

XX PF 31-JAN-2000; 2000JP-00023170.

XX PR 31-JAN-2000; 2000JP-00023170.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2001-629566/73.

XX FT Human normal hepatocyte expression gene group.

XX PS Claim 1; Page 9; 26pp; Japanese.

XX CC The invention relates to a human normal hepatocyte expression gene group
 CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
 CC gene comprises one of 200 fully defined nucleotide sequences as given in
 CC the specification. The gene group and the cDNAs corresponding to each of
 CC the genes in the group are useful in the diagnosis and treatment of human
 CC hepatopathy. The present sequence is a cDNA corresponding to a gene
 CC expressed by normal human hepatocytes

XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
 |||||
 Db 7 AGGCTGT 1

RESULT 728

ABA06100/c
 ID ABA06100 standard; cDNA; 10 BP.

XX AC ABA06100;

XX DT 10-JAN-2002 (first entry)

XX DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 77.

XX KW Human; hepatocyte; gene expression; hepatopathy; ss.

XX OS Homo sapiens.

XX PN JP2001211883-A.

XX PD 07-AUG-2001.

XX PF 31-JAN-2000; 2000JP-00023170.

XX PR 31-JAN-2000; 2000JP-00023170.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2001-629566/73.

XX FT Human normal hepatocyte expression gene group.

XX PS Claim 1; Page 7; 26pp; Japanese.

XX CC The invention relates to a human normal hepatocyte expression gene group
 CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
 CC gene comprises one of 200 fully defined nucleotide sequences as given in
 CC the specification. The gene group and the cDNAs corresponding to each of
 CC the genes in the group are useful in the diagnosis and treatment of human
 CC hepatopathy. The present sequence is a cDNA corresponding to a gene
 CC expressed by normal human hepatocytes

XX SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11

|||||

Db 10 AGGCTGT 4

RESULT 729

AAF74038

ID AAF74038 standard; DNA; 10 BP.

XX AC AAF74038;

XX DT 30-APR-2001 (first entry)

XX DE Human SLC6A4 allele-specific oligonucleotide primer #158.

XX KW Solute carrier family 6 neurotransmitter transporter; seotonin 4; SLC6A4;

XX KW genotyping; allele specific oligonucleotide; ss.

XX OS Homo sapiens.

XX PN WO200109161-A1.

XX PD 08-FEB-2001.

XX PF 31-JUL-2000; 2000WO-US020638.

XX PR 29-JUL-1999; 99US-0146290P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;

XX DR WPI; 2001-123317/13.

XX PT New isolated polynucleotide comprising a polymorphic variant for the
 PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
 PT gene for identifying drugs for treating disorders related to expression
 PT of the protein.

XX Disclosure; Page 23; 152pp; English.

XX The present invention relates to a polymorphic variant of a reference

XX sequence for the solute carrier family 6 neurotransmitter transporter,

XX serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence

XX complementary to the first sequence. The invention is used in producing a

XX recombinant organism that can be used to express SLC6A4 for protein

XX structure analysis and binding studies. A composition comprising a

XX genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4

XX gene

XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

XX

XX Query Match 38.9%; Score 7; DB 1; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGGC 8

Db 3 TTGAGGC 9

RESULT 730

AAF35143

ID AAF35143 standard; DNA; 10 BP.

XX AC AAF35143;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1882.

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;

XX nor previously assigned open reading frame; nonannotated ORF; SAGE;

XX serial analysis of gene expression; antifungal; tag; identification;

XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Veiculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

XX gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

XX Example; Page 67; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

XX coding sequence of a yeast gene selected from a group of 745 NORF (not

XX previously assigned open reading frame; or nonannotated ORF) genes

XX comprising a SAGE (serial analysis of gene expression) tag. Also

XX described are: (1) a method (M1) of using NORF genes to affect the cell

XX cycle comprising administering a NORF gene whose expression varies by at

XX least 10% between any two phases of the cell cycle selected from log

XX phase, S phase and G2/M; (2) a method (M2) for screening candidate

XX antifungal drugs comprising: (a) contacting a test substance with a yeast

XX cell; and (b) monitoring expression of a NORF gene whose expression

XX identifies human genes which are involved in cell cycle progression

XX comprising contacting human DNA with a probe which comprises at least 10

XX contiguous nucleotides of a NORF gene whose expression varies as in M1;

XX and (4) a method (M4) for identifying a candidate drug as a member of a

XX class of drugs having a characteristic effect on gene expression in a

XX yeast cell comprising contacting a yeast cell with a candidate drug and

XX monitoring expression in the yeast cell of at least 1 NORF gene whose

XX expression is affected by the class of drugs. The NORF genes may be used

XX to study, monitor and affect phases of the cell cycle, the differentially

XX expressed genes may be used as markers of phases of the cell cycle. The

XX methods may be used to identify candidate drugs which affect the cell

XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064

XX represent SAGE tags used in the exemplification of the present invention.

XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

XX method, in the exemplification of the present invention

XX

XX Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

XX

XX Query Match 38.9%; Score 7; DB 1; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCTGTT 12

Db 4 GGCTGTT 10

RESULT 731

AAF37041

ID AAF37041 standard; DNA; 10 BP.

XX AC AAF37041;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3780.

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;

XX nor previously assigned open reading frame; nonannotated ORF; SAGE;

XX serial analysis of gene expression; antifungal; tag; identification;

XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Veiculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

XX gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

XX Example; Page 135; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

XX coding sequence of a yeast gene selected from a group of 745 NORF (not

XX previously assigned open reading frame; or nonannotated ORF) genes

XX comprising a SAGE (serial analysis of gene expression) tag. Also

XX described are: (1) a method (M1) of using NORF genes to affect the cell

XX cycle comprising administering a NORF gene whose expression varies by at

XX least 10% between any two phases of the cell cycle selected from log

XX phase, S phase and G2/M; (2) a method (M2) for screening candidate

XX antifungal drugs comprising: (a) contacting a test substance with a yeast

XX cell; and (b) monitoring expression of a NORF gene whose expression

XX identifies human genes which are involved in cell cycle progression

varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTGGCGA 17
| | | | |
Db 3 TTGGCGA 9

RESULT 732
AAF41905/c
ID AAF41905 standard; DNA; 10 BP.
XX AAF41905;
XX 23-MAR-2001 (first entry)
DT XX
DE XX
YEAST NORF gene SAGE tag oligonucleotide SEQ ID NO:8644.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UJJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 308; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGG 14
| | | | |
Db 10 CTGTGG 4

RESULT 733
AAF39747
ID AAF39747 standard; DNA; 10 BP.
XX AAF39747;
XX 23-MAR-2001 (first entry)
DT XX
DE XX
YEAST NORF gene SAGE tag oligonucleotide SEQ ID NO:6486.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UJJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 231; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
| | | | |
Db 4 CTTGAGG 10

RESULT 734
AAF40492
ID AAF40492 standard; DNA; 10 BP.
XX
AC AAF40492;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7231.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UWJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 258; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7
| | | | |
Db 4 CTTGAGG 10

RESULT 735
AAF43211
ID AAF43211 standard; DNA; 10 BP.
XX
AC AAF43211;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11350.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UWJO) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX

```

PS Example; Page 355; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTG 13
Db 2 GCTGTG 8
RESULT 736
AAF42714
ID AAF42714 standard; DNA; 10 BP.
AC AAF42714;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10853.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of

```

```

PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 337; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGG 7
Db 4 CTTGAGG 10
RESULT 737
AAF43979
ID AAF43979 standard; DNA; 10 BP.
AC AAF43979;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12118.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX

```

```

DR WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 382; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TTGGCGA 17
DB 2 TTGGCGA 8
RESULT 738
AAF34385/C
ID AAF34385 standard; DNA; 10 BP.
XX
XX AAF34385;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1124.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX

```

```

XX Velculescu V, Vogelstein B, Kinzler K;
PI
XX WPI; 2001-061874/07.
DR
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 40; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TTGGCGAC 18
DB 7 TTGGCGAC 1
RESULT 739
AAF39293
ID AAF39293 standard; DNA; 10 BP.
XX
XX AAF39293;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6032.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX
XX

```



```
PR 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Veiculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 215; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC comprising nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGG 14
Db 3 CTGTTGG 9
RESULT 740
AAF42400
ID AAF42400 standard; DNA; 10 BP.
XX
XX AAF42400;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9139.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
PD
```

```
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Veiculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 326; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC comprising nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTTGG 14
Db 4 CTGTTGG 10
RESULT 741
AAF43251
ID AAF43251 standard; DNA; 10 BP.
XX
XX AAF43251;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11390.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX
```

```
PN WO200077214-A2.
XX
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 356; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 TGGCGAC 18
XX Db 1 TGGCGAC 7
XX
XX RESULT 742
XX AAF34637/C
XX ID AAF34637 standard; DNA; 10 BP.
XX
XX AC AAF34637;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1376.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
```

```
XX OS Saccharomyces cerevisiae.
XX
XX PN WO200077214-A2.
XX
XX PD 21-DEC-2000.
XX
XX PF 14-JUN-2000; 2000WO-US016223.
XX
XX PP 16-JUN-1999; 99US-00335032.
XX
XX PR (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PA Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX PS Example; Page 49; 419pp; English.
XX
XX SS The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TTGAGGC 8
XX Db 8 TTGAGGC 2
XX
XX RESULT 743
XX AAF39100
XX ID AAF39100 standard; DNA; 10 BP.
XX
XX AC AAF39100;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5939.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX
```

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS
 XX WO200077214-A2.
 FN
 XX 21-DEC-2000.
 PD
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI
 XX WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 FS Example; Page 208; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 TTGAGGC 8
 DB 3 TTGAGGC 9
 RESULT 744
 ID AAF42420/c
 XX AAF42420 standard; DNA; 10 BP.
 AC AAF42420;
 XX
 XX 23-MAR-2001 (first entry)
 DT
 XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9159.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 PD
 XX 21-DEC-2000.
 PF
 XX 14-JUN-2000; 2000WO-US016223.
 PR
 XX 16-JUN-1999; 99US-00335032.
 PA
 XX (UYJO) UNIV JOHNS HOPKINS.
 PI
 XX Velculescu V, Vogelstein B, Kinzler K;
 DR
 XX WPI; 2001-061874/07.
 PT
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 FS Example; Page 327; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 TTGAGGC 8
 DB 7 TTGAGGC 1
 RESULT 745
 ID AAF43780
 XX AAF43780 standard; DNA; 10 BP.
 AC AAF43780;
 XX

XX 23-MAR-2001 (first entry)
DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11919.
XX
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX PF
XX 16-JUN-1999; 99US-00335032.
XX PR
XX (UYJO) UNIV JOHNS HOPKINS.
XX PA
XX Veiculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 375; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TTGGCGA 17
Db 1 TTGGCGA 7

RESULT 746
AAF35242/c

ID AAF35242 standard; DNA; 10 BP.
XX
AC AAF35242;
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1981.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX PF
XX 16-JUN-1999; 99US-00335032.
XX PR
XX (UYJO) UNIV JOHNS HOPKINS.
XX PA
XX Veiculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 70; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGC 15
Db 10 TGTGGC 4

```

RESULT 747
AAF41021/c
ID AAF41021 standard; DNA; 10 BP.
XX
XX
AC AAF41021;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7760.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 277; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTTGAGG 7

```

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 2 GAGGCTG 8
|||||
2 GAGGCTG 8

RESULT 749
AAF34894/C
ID AAF34894 standard; DNA; 10 BP.
XX
AC AAF34894;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1633.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 58; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 TGGCGAC 18
Db 10 TGGCGAC 4
|||||
10 TGGCGAC 4

RESULT 750
AAF35393
ID AAF35393 standard; DNA; 10 BP.
XX
AC AAF35393;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2132.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 76; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
```

CC method, in the exemplification of the present invention
XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
Db 1 TGAGGCT 7

RESULT 751

AAF41531
ID AAF41531 standard; DNA; 10 BP.

XX AAF41531;

AC AAF41531;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8270.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 295; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGG 14

Db 1 CTGTGG 7

RESULT 752

AAF43549

ID AAF43549 standard; DNA; 10 BP.

XX AAF43549;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11688.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 367; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell

CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGC 8
 |||||
 Db 4 TTGAGGC 10

RESULT 753
 AAF37385/C
 ID AAF37385 standard; DNA; 10 BP.

XX AC AAF37385;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4124.

XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX KW Saccharomyces cerevisiae.

XX OS WO200077214-A2.

XX PN 21-DEC-2000.

XX PD 14-JUN-2000; 2000WO-US016223.

XX PF 16-JUN-1999; 99US-00335032.

XX PR (UYJO) UNIV JOHNS HOPKINS.

XX PA Velulescu V, Vogelstein B, Kinzler K;

XX PI WPI; 2001-061874/07.

XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.

XX PT Example; Page 147; 419pp; English.

XX PS The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGG 14
 |||||
 Db 7 CTGTTGG 1

RESULT 754
 AAF40582/C
 ID AAF40582 standard; DNA; 10 BP.

XX AC AAF40582;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7321.

XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX KW Saccharomyces cerevisiae.

XX OS WO200077214-A2.

XX PN 21-DEC-2000.

XX PD 14-JUN-2000; 2000WO-US016223.

XX PF 16-JUN-1999; 99US-00335032.

XX PR (UYJO) UNIV JOHNS HOPKINS.

XX PA Velulescu V, Vogelstein B, Kinzler K;

XX PI WPI; 2001-061874/07.

XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.

XX PT Example; Page 261; 419pp; English.

XX PS The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGG 7
Db 9 CTTGAGG 3
|||||

RESULT 755
AAAF3159/c
ID AAF43159 standard; DNA; 10 BP.
XX
AC AAF43159;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11298.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 353; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGC 15
Db 8 TGTGGC 2
|||||

RESULT 756
ABK24251
ID ABK24251 standard; DNA; 10 BP.
XX
AC ABK24251;

DT 09-APR-2002 (first entry)
XX
DE Retinaldehyde-binding protein 1 ASO primer extension primer #24.
XX

Human; retinaldehyde-binding protein 1; ss; RLBPI; haplotype; primer;
genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.

XX Homo sapiens.

XX WO200192278-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US017252.

XX 26-MAY-2000; 2000US-0207618P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Kazemi A, Koshy B;

XX WPI; 2002-122053/16.

XX New genetic variants having polymorphisms in the retinaldehyde-binding
XX protein 1 gene, useful for studying the function of and for expressing
XX RLBPI protein for use in screening drugs for treating diseases related to
XX RLBPI activity.

XX Claim 18; Page 14; 107pp; English.

XX The invention relates to an isolated polynucleotide, which comprises
XX genes and haplotypes of the retinaldehyde-binding protein 1 (RLBPI) gene.
XX The polynucleotide comprises polymorphic sites in the RLBPI gene, which
XX are referred to as PS1-24 to designate the order in which they are
XX located in the gene. Also included are methods for haplotyping or
XX genotyping the RLBPI gene of an individual, a method for predicting a
XX haplotype pair for the RLBPI gene of an individual, a method for
XX identifying an association between a trait and at least one haplotype or

haplotype pair of the RLBP1 gene, a composition comprising at least one genotyping oligonucleotide for detecting a polymorphism in the RLBP1 gene at a PS consisting of PS1-PS24, a kit for genotyping the RLBP1 gene of an individual comprising a set of oligonucleotides designed to genotype each of PS1-PS24 recombinant non-human organisms transformed or transfected with the isolated polynucleotide, where the organism expresses a RLBP1 protein encoded by the first nucleotide sequence or expresses an RLBP1 polypeptide comprising an amino acid sequence that is a polymorphic variant of a reference sequence for the RLBP1 protein or its fragment, an anti-RLBP1 antibody, a method for screening for drugs targeting the isolated polypeptide, and a computer system for storing and analyzing polymorphism data for the RLBP1 oncogene gene. The polynucleotide comprising polymorphisms in the RLBP1 gene is useful in studying the expression and function of RLBP1, and in expressing RLBP1 protein for use in screening candidate drugs to treat diseases related to RLBP1 activity (e.g. autosomal recessive retinitis pigmentosa (arRP)). The methods and haplotypes are useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. These are also useful for designing clinical trials of candidate drugs for treating a specific condition or disease, as well as for screening compounds targeting RLBP1 to treat a specific condition or disease predicted to be associated with RLBP1 activity. The kit and method are useful for determining whether an individual has one of the haplotypes or haplotype pairs cited above. The transgenic animals are useful for studying expression of the RLBP1 isogenes in vivo, for in vivo screening and testing of drugs targeted against RLBP1 protein, and for testing the efficacy of therapeutic agents and compounds for retinal diseases in a biological system. The gene for RLBP1 is located on chromosome 15q26. The present sequence is an allele specific oligonucleotide (ASO) PCR primer for amplifying a nucleic acid containing a polymorphic RLBP sequence, using the primer extension method

Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
| | | | |
Db 1 GAGGCTG 7

RESULT 757
AAS99280/c
ID AAS99280 standard; DNA; 10 BP.

AC AAS99280;

DT 12-MAR-2002 (first entry)

DE Human F12 gene allele-specific oligonucleotide PCR primer #7.

Human; coagulation factor XII; F12; haplotyping; haplotype pair; ss;
single nucleotide polymorphism; genotyping; gene therapy; drug screening;
coronary artery disease; liver disease; spontaneous abortion; cardiac;
Alzheimer's disease; blood coagulation; hepatotropic; neuroprotective;
nootropic; coagulant; antiabortive; sequencing primer; PCR primer; probe;
primer tail.

OS Homo sapiens.

PN WO200179228-A2.

PD 25-OCT-2001.

PF 13-APR-2001; 2001WO-US012257.

PR 14-APR-2000; 2000US-0197837P.

PA (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Chew A, Choi JY, Nandabalan K;
PI WPI; 2002-075061/10.

XX Novel isolated human coagulation factor XII polynucleotide, F12 useful
PT for treatment of e.g. coronary artery disease, comprises a sequence which
PT is a polymorphic variant of a reference sequence for F12 gene or its
PT fragment.

XX Claim 18; Page 14; 72pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human coagulation factor XII (F12) polypeptide. A method for
CC haplotyping the F12 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the F12 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the F12 gene can be identified
CC by comparing the frequency of the haplotype or haplotype pair in a
CC population exhibiting the trait with the frequency of the haplotype or
CC haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. F12 and its corresponding DNA are used
CC for studying the expression and function of F12, for use in screening for
CC candidate drugs to treat disorders related to F12 activity such as
CC coronary artery disease, liver disease, spontaneous abortion, Alzheimer's
CC disease and other diseases associated with defects in blood coagulation.
CC The sequences are also useful for studying the effect of variation on the
CC biological activity of F12 as well as on the binding affinity of
CC candidate drugs targeting F12. Sequences AAS99229-AAS99305 represent
CC probes, primers and primer tails used to detect F12 gene polymorphisms

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
| | | | |
Db 9 TGAGGCT 3

RESULT 758

ABL52179

ID ABL52179 standard; DNA; 10 BP.

AC ABL52179;

DT 12-JUL-2002 (first entry)

DE Human PER1 preferred oligonucleotide primer SEQ ID NO:104.

Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
single nucleotide polymorphism; SNP; gene; primer; ss.

OS Homo sapiens.

PN WO200222650-A2.

PD 21-MAR-2002.

PF 13-SEP-2001; 2001WO-US028780.

PR 13-SEP-2000; 2000US-0232468P.

PA (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Klieh SE, Koshy B;

XX WPI; 2002-393941/42.
 XX Novel isolated human period Drosophila homolog 1 polynucleotide, useful
 XX for therapeutic purposes, for studying the expression and function of the
 XX polynucleotide, and for expressing the homolog.
 XX Claim 19; Page 15; 162pp; English.
 XX The present invention describes an isolated human period (Drosophila)
 XX homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
 XX polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
 XX or its fragment, or a polymorphic variant of a reference sequence
 XX (ABL52078) for a PER1 cDNA or its fragment. The present invention also
 XX describes methods for genotyping and haplotyping the PER1 gene of an
 XX individual. (I) is useful in studying the expression and function of
 XX PER1, and in expressing PER1 protein for use in screening for candidate
 XX drugs to treat diseases related to PER1 activity. (I) is useful for
 XX therapeutic purposes. A recombinant non-human organism transformed or
 XX transfected with (I) can be used for studying expression of the PER1
 XX isogenes in vivo, for in vivo screening and testing of drugs targeted
 XX against PER1 protein, and for testing the efficacy of therapeutic agents
 XX and compounds for disorders associated with circadian rhythm regulation.
 XX The present sequence represents a preferred oligonucleotide primer for
 XX human PER1, which is used in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 38.9%; Score 7; DB 1; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 9 TGTGGGC 15
 XX | | | | |
 XX 1 TGTGGC 7
 XX
 XX RESULT 759
 XX ABL52208
 XX ID ABL52208 standard; DNA; 10 BP.
 XX
 XX AC ABL52208;
 XX
 XX 12-JUL-2002 (first entry)
 XX
 XX Human PER1 preferred oligonucleotide primer SEQ ID NO:133.
 XX
 XX Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
 XX polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
 XX single nucleotide polymorphism; SNP; gene; primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200222650-A2.
 XX
 XX 21-MAR-2002.
 XX
 XX 13-SEP-2001; 2001WO-US028780.
 XX
 XX 13-SEP-2000; 2000US-0232468P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Duda A, Kliehm SE, Koshy B;
 XX WPI; 2002-393941/42.
 XX
 XX Novel isolated human period Drosophila homolog 1 polynucleotide, useful
 XX for therapeutic purposes, for studying the expression and function of the
 XX polynucleotide, and for expressing the homolog.
 XX Claim 19; Page 16; 162pp; English.

CC The present invention describes an isolated human period (Drosophila)
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
 CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
 CC or its fragment, or a polymorphic variant of a reference sequence
 CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
 CC describes methods for genotyping and haplotyping the PER1 gene of an
 CC individual. (I) is useful in studying the expression and function of
 CC PER1, and in expressing PER1 protein for use in screening for candidate
 CC drugs to treat diseases related to PER1 activity. (I) is useful for
 CC therapeutic purposes. A recombinant non-human organism transformed or
 CC transfected with (I) can be used for studying expression of the PER1
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted
 CC against PER1 protein, and for testing the efficacy of therapeutic agents
 CC and compounds for disorders associated with circadian rhythm regulation.
 CC The present sequence represents a preferred oligonucleotide primer for
 CC human PER1, which is used in the exemplification of the present invention
 CC
 CC Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 CC
 CC Query Match 38.9%; Score 7; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 11 TTGGCGA 17
 CC | | | | |
 CC 2 TTGGCGA 8
 CC
 CC RESULT 760
 CC AAL39607/C
 CC ID AAL39607 standard; DNA; 10 BP.
 CC
 CC AC AAL39607;
 CC
 CC 05-SEP-2002 (first entry)
 CC
 CC SSTR4 gene polymorphism detecting primer SEQ ID No 54.
 CC
 CC Gene therapy; SSTR4 isogene expression modulator; hormone secretion;
 CC somatostatin receptor 4; SSTR4; single nucleotide polymorphism; cancer;
 CC gene therapy; SSTR4 isoform; PCR; primer; ss.
 CC
 CC Homo sapiens.
 CC
 CC WO200226766-A2.
 CC
 CC 04-APR-2002.
 CC
 CC 27-SEP-2001; 2001WO-US030410.
 CC
 CC 27-SEP-2000; 2000US-0235826P.
 CC
 CC (GENA-) GENAISSANCE PHARM INC.
 CC
 CC Bieglecki KM, Choi JY, Kliehm SE, Koshy B;
 CC WPI; 2002-405043/43.
 CC
 CC New isolated polynucleotide, polymorphic variant of somatostatin receptor
 CC 4 gene, useful for expressing somatostatin receptor 4 protein isoform
 CC used in drug screening techniques.
 CC
 CC Claim 16; Page 14; 83pp; English.
 CC
 CC The invention is an isolated polynucleotide having a somatostatin
 CC receptor 4 (SSTR4) isogene that is one of 13 somatostatin genes as given
 CC in the specification, where each somatostatin gene has specific regions
 CC of a fully defined sequence of 9190 nucleotides as given in the
 CC specification, and is defined by polymorphisms at positions 3922, 4723,
 CC 4754, 4783, 4835, 4874, 4921, 4948, 4986, 5216, 5329 or 5411. The
 CC isolated polypeptide is useful for screening drugs which involves
 CC contacting the polypeptide with a candidate agent and assaying for
 CC binding activity. The isolated polynucleotide is useful for studying

CC expression and function of SSTR4 and expressing SSTR4 protein for use in
 CC screening for candidate drugs to treat diseases related to SSTR4
 CC activity. The polymorphism and haplotype data is useful for validating
 CC whether SSTR4 is a suitable target for drugs of cancer and disorders
 CC related to defects in hormone secretion, screening for such drugs and
 CC reducing bias in clinical trials of such drugs. The polynucleotide is
 CC also useful in gene therapy. The isolated polypeptide is useful in
 CC studying the effect of variation on the biological activity of SSTR4 as
 CC well as on the binding affinity of candidate drugs targeting SSTR4 for
 CC treatment of cancer and disorders related to defects in hormone
 CC secretion. The isolated polypeptide is useful in a variety of drug
 CC screening assays to identify agents that bind specifically to all known
 CC SSTR4 isoforms, and for measuring the binding affinities of one or more
 CC candidate drugs targeting the SSTR4 protein. Predicting a haplotype pair
 CC for SSTR4 gene of an individual is useful for identifying an association
 CC between susceptibility to a disease, staging of a disease, or response to
 CC a drug. This polynucleotide sequence represents a preferred primer for
 CC detecting SSTR4 gene polymorphisms relating to the invention
 XX
 XX Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTGGCG 16
 |||||
 Db 8 GTTGGCG 2

RESULT 761
 ABL01179/c
 ID ABL01179 standard; DNA; 10 BP.
 XX
 AC ABL01179;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 XX Human AKR1B1 gene polymorphism detection primer SEQ ID NO:76.

XX Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
 KW AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
 KW allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
 XX
 XX Homo sapiens.

XX WO200179223-A2.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US011944.

XX 12-APR-2000; 2000US-0196315P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Nandabalan K, Rounds E, Sanchis A;

XX WPI; 2002-075056/10.

XX Novel polymorphic variants of aldo-keto reductase family 1, member b1
 PT gene useful in studying expression and function of the protein, useful
 PT for screening drugs to treat diseases e.g. diabetes.

XX Claim 18; Page 15; 103pp; English.

XX The present invention describes an isolated polynucleotide (I) comprising
 CC a sequence which is a polymorphic variant (PV) of a reference sequence
 CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
 CC fragment, having the 22214 base pair sequence given in ABL01105. AKR1B1
 CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
 CC used in the treatment of diabetes. The human AKR1B1 gene is located on
 CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific

CC oligonucleotide (ASO) probes used in the detection of polymorphisms in
 CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
 CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
 CC ABL01221 represent preferred primers used in the detection of
 CC polymorphisms in the human AKR1B1 gene
 XX
 XX Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTGGCGA 17
 |||||
 Db 10 TTGGCGA 4

RESULT 762
 ABL42680/c
 ID ABL42680 standard; cDNA; 10 BP.

XX ABL42680;

XX 12-APR-2002 (first entry)

XX Human maturation/activation dendritic cell expression gene tag #54.

XX Human; maturation/activation dendritic cell expression gene; tag;

XX maturation; activation; dendritic cell; ss.

XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.

XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.

XX Claim 1; Page 10; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention

XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
 |||||
 Db 9 TGAGGCT 3

RESULT 763
 ABL42762
 ID ABL42762 standard; cDNA; 10 BP.

XX ABL42762;
XX AC
XX DT
XX DE
XX DE Human maturation/activation dendritic cell expression gene tag #136.
XX KW Human; maturation/activation dendritic cell expression gene; tag;
XX KW maturation; activation; dendritic cell; ss.
XX OS Homo sapiens.
XX PN JP2001327293-A.
XX PD 27-NOV-2001.
XX PF 22-MAY-2000; 2000JP-00150562.
XX PR 22-MAY-2000; 2000JP-00150562.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-127070/17.
XX PT Human maturation/activation dendritic cell expression gene group.
XX PS Claim 10; Page 13; 41pp; Japanese.
XX CC The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. ABL42627 to ABL42926 represent specifically claimed human maturation/activation DC expression gene tags from the present invention
XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CTGTGG 14
Db 2 CTGTGG 8
RESULT 764
ABL99032
ID ABL99032 standard; cDNA; 10 BP.
XX AC ABL99032;
XX DT 25-JUN-2002 (first entry)
XX DE Mouse neuronal regeneration related SAGE EST 27.
XX KW Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
XX KW learning disorder; serial analysis of gene expression; SAGE;
XX KW gene expression; hippocampus; expressed sequence tag; EST; ss.
XX OS Mus sp.
XX PN DE10048893-A1.
XX PD 11-APR-2002.
XX PF 02-OCT-2000; 2000DE-01048893.
XX PR 02-OCT-2000; 2000DE-01048893.

XX (LION-) LION BIOSCIENCE AG.
XX WPI; 2002-341428/38.
XX PT New nucleic acids involved in neuronal regeneration, useful in screening for modulators of regeneration or synaptic efficiency, and potential therapeutic agents.
XX PS Example 4; Page 8; 38pp; German.
XX CC The invention relates to nucleic acids (ABL98957-ABL99004) involved in regenerative neuronal processes and encoded proteins (ABB79405-ABB79409) used to screen for compounds and potential therapeutic agents that modulate nerve cell regeneration and/or synaptic efficiency. They may also be used for treatment or diagnosis of defective or pathological memory and learning conditions. The present sequence is that of an EST isolated from serial analysis of gene expression (SAGE) experiments comparing gene expression in the hippocampus of GFAP/l1 transgenic mice versus a wildtype control. The resultant EST were used to isolate the nucleic acids of the invention
XX SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGAGG 7
Db 3 CTTGAGG 9
RESULT 765
ABK92584/C
ID ABK92584 standard; DNA; 10 BP.
XX AC ABK92584;
XX DT 20-AUG-2002 (first entry)
XX DE Primer-extension oligonucleotide #9 to detect human CHRM4 polymorphisms.
XX KW Human; single nucleotide polymorphism; SNP; CHRM4; haplotyping;
XX KW chromosome 1p12-p11.2; cholinergic receptor muscarinic 4; genotyping;
XX KW Alzheimer's disease; neurological disorder; primer; ss.
XX OS Homo sapiens.
XX PN WO200236609-A2.
XX PD 10-MAY-2002.
XX PF 31-OCT-2001; 2001WO-US045709.
XX PR 31-OCT-2000; 2000US-0244627P.
XX PA (GENA-) GENAISANCE PHARM INC.
XX PA (PETE/) PETERSON N.
XX PA (ROUN/) ROUNDS E.
XX PI Denton RR, Duda A, Gilson CR, Kazemi A, Nandabalan K, Tirrell C;
XX WPI; 2002-489997/52.
XX PT Novel genetic variants of cholinergic receptor muscarinic 4 useful in studying expression and function of protein, and for screening drugs to treat diseases e.g. Alzheimer's disease and other neurological disorders.
XX PS Claim 16; Page 14; 63pp; English.
XX CC The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human cholinergic receptor, muscarinic 4 (CHRM4) gene

CC located on chromosome 11p12-p11.2, and methods for haplotyping and/or
 CC genotyping the CHRM4 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the CHRM4 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC the treatment of diseases associated with CHRM4 activity, such as
 CC Alzheimer's disease and other neurological disorders. ABK92576-ABK92587
 CC represent primer-extension oligonucleotides for detecting human CHRM4
 CC gene polymorphisms
 XX
 SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
 |||||
 Db 8 GCTGTTG 2

RESULT 766
 ABK96378/c
 ID ABK96378 standard; DNA; 10 BP.

AC ABK96378;

DT 24-SEP-2002 (first entry)

XX Human SA homologue, SAH, primer extension primer 3' terminus #10.

XX Human; ss; primer; rat hypertension-associated homologue; SAH;
 KW hypertension; chromosome 16p13.11; hypertensive; SNP; PCR;
 KW single nucleotide polymorphism; haplotype; genotype; isogene;
 KW primer extension.

XX Homo sapiens.

XX WO200244201-A2.

XX 06-JUN-2002.

XX 03-DEC-2001; 2001WO-US047011.

XX 01-DEC-2000; 2000US-0250441P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bieglecki KM, Chew A, Russo DP;

XX WPI; 2002-519582/55.

XX Novel genetic variants of SA (Rat Hypertension-associated) Homolog
 PT isogenes, useful for improving efficiency and reliability in drug
 PT development for treating hypertension.

XX Claim 17; Page 15; 98pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
 CC first nucleotide sequence (NSI) comprising SAH (SA, Rat Hypertension-
 CC associated Homologue isogene (II) selected from isogenes 1-15 and 17-20
 CC given in the specification, where each isogene comprises the regions of
 CC NSI and is further defined by the corresponding sequence of single
 CC nucleotide polymorphisms or a second nucleotide sequence (NS2)
 CC complementary to NSI. Alternatively, (I) comprises a coding sequence for
 CC SAH isogenes or fragments. Also included are methods of predicting the
 CC haplotype/genotype of the SAH gene of an individual, identifying an
 CC association between a trait and at least one haplotype or haplotype pair
 CC of SAH genes, an isolated oligonucleotide for detecting a polymorphism in
 CC the SAH gene, a recombinant non-human organism transformed or transfected
 CC with the SAH polynucleotide, an isolated polypeptide comprising an amino
 CC acid sequence which is a polymorphic variant of the SAH protein, a
 CC monoclonal antibody specific for SAH, a computer system for storing and

CC analysing polymorphism data for the SAH gene and a genome anthology for
 CC the SAH gene. The SAH proteins and haplotype/genotype methods are useful
 CC in screening for drugs targeting SAH that are useful for treating
 CC hypertension and for drug discovery, development and target validation.
 CC The antibody is useful in diagnostic, prognostic and therapeutic methods.
 CC The polynucleotides are useful in studying the expression and function of
 CC SAH, in expressing SAH protein for use in screening for candidate drugs
 CC and in studying the effect of the variation on the biological activity of
 CC SAH as well as on the binding affinity of candidate drugs targeting SAH.
 CC The gene for SAH is located on chromosome 16p13.11. The present sequence
 CC is the 3' terminus of an allele specific primer for detecting SAH nucleic
 CC acids bearing a polymorphism using the technique of primer extension
 XX

SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
 |||||
 Db 10 GCTGTTG 4

RESULT 767

ABQ71632

ID ABQ71632 standard; DNA; 10 BP.

AC ABQ71632;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:1624.

XX Zinc finger protein; 2FP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 50; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to

CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||
DB 4 GAGGCTG 10

RESULT 768

ABQ71579
ID ABQ71579 standard; DNA; 10 BP.

XX AC ABQ71579;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:1313.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 48; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their

CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||
DB 4 GAGGCTG 10

RESULT 769

ABQ71633
ID ABQ71633 standard; DNA; 10 BP.

XX AC ABQ71633;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:1625.

XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 50; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

```
XX SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
Db |||||
4 GAGGCTG 10

RESULT 770
ABQ71574
ID ABQ71574 standard; DNA; 10 BP.
XX AC
XX ABQ71574;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:1308.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO200242459-A2.
XX PD 30-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX WPI; 2002-500284/53.
XX
New zinc finger protein that binds to target site, useful in studying
gene function and for human therapeutics and plant engineering, comprises
first, second and third zinc fingers, ordered from N- to C-terminus.
Example 1; Page 48; 81pp; English.
XX
The present invention describes a zinc finger protein (I) that binds to a
target site, comprising a first (F1), a second (F2), and a third (F3)
zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
target site comprises, in 3'-5' direction, a first (S1), a second (S2),
and a third (S3) target subsite. Also described are: (1) a polypeptide
(II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
(3) designing (M) (I) involves selecting the F1 zinc finger such that it
binds to the S1 target subsite, selecting the F2 zinc finger such that it
binds to the S2 target subsite, and selecting the F3 zinc finger such
that it binds to the S3 target subsite, thus designing (I) that binds to
a target site. (I) is useful for recognition of triplet target subsites
having the nucleotide G in the 5'-most position of the subsite. (I) is
useful in studying gene function, and for human therapeutics and plant
engineering. (I), (II) or (III) is useful in therapeutic methods to
modulate the expression of a target region within a subject, in
diagnostic methods for sequence specific detection of target nucleic acid
in a sample, and in assays to determine the phenotype and function of
gene expression. (I) has improved affinity and specificity for their
target sequences, as well as enhanced biological activity. ABQ71213 to
ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
finger peptides which are given in the exemplification of the present
invention
XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
```

```
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
Db |||||
4 GAGGCTG 10

RESULT 771
ABQ71545
ID ABQ71545 standard; DNA; 10 BP.
XX AC
XX ABQ71545;
XX DT 28-AUG-2002 (first entry)
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:1279.
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO200242459-A2.
XX PD 30-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US043438.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX PI Liu Q;
XX WPI; 2002-500284/53.
XX
New zinc finger protein that binds to target site, useful in studying
gene function and for human therapeutics and plant engineering, comprises
first, second and third zinc fingers, ordered from N- to C-terminus.
Example 1; Page 47; 81pp; English.
XX
The present invention describes a zinc finger protein (I) that binds to a
target site, comprising a first (F1), a second (F2), and a third (F3)
zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
target site comprises, in 3'-5' direction, a first (S1), a second (S2),
and a third (S3) target subsite. Also described are: (1) a polypeptide
(II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
(3) designing (M) (I) involves selecting the F1 zinc finger such that it
binds to the S1 target subsite, selecting the F2 zinc finger such that it
binds to the S2 target subsite, and selecting the F3 zinc finger such
that it binds to the S3 target subsite, thus designing (I) that binds to
a target site. (I) is useful for recognition of triplet target subsites
having the nucleotide G in the 5'-most position of the subsite. (I) is
useful in studying gene function, and for human therapeutics and plant
engineering. (I), (II) or (III) is useful in therapeutic methods to
modulate the expression of a target region within a subject, in
diagnostic methods for sequence specific detection of target nucleic acid
in a sample, and in assays to determine the phenotype and function of
gene expression. (I) has improved affinity and specificity for their
target sequences, as well as enhanced biological activity. ABQ71213 to
ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
finger peptides which are given in the exemplification of the present
invention
XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
```


XX Human homeo box D3 (HOXD3) gene polymorphism detecting primer #15.
 XX Human, homeo box D3; HOXD3; polymorphism; developmental disorder;
 KW haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy;
 KW drug screening; cytostatic; primer; ss.
 XX Homo sapiens.
 XX WO200190127-A2.
 XX 29-NOV-2001.
 XX 24-MAY-2001; 2001WO-US016982.
 XX 25-MAY-2000; 2000US-0207076P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Duda A, Kazemi A, Koshiy B, Kumar AM;
 XX WPI; 2002-075363/10.
 XX New genetic variants of Homeo Box D3 for studying expression and function
 PT of the protein, and for screening drugs to treat diseases e.g.
 PT developmental disorders and tumors.
 XX Claim 18; Page 13; 66pp; English.
 XX The invention relates to genetic variants of the homeo box D3 (HOXD3)
 CC gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes (HTS)
 CC or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful for
 CC improving the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC HOXD3 activity, e.g., developmental disorders and tumors. HOXD3 isogene
 CC is useful in studying the expression and function of HOXD3 and in
 CC expressing HOXD3 protein for use in screening for candidate drugs to
 CC treat diseases related to HOXD3 activity and in studying the effect of
 CC the variation on the biological activity of HOXD3 as well as on the
 CC binding affinity of candidate drugs targeting HOXD3 for the treatment of
 CC developmental disorders and tumors. An antibody against HOXD3 is useful
 CC in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A recombinant non-human organism is useful in studying
 CC expression of the HOXD3 isogenes in vivo. Allele-specific
 CC oligonucleotides (ASO) are useful as probes and primers and for assaying
 CC a polymorphism in the target region. The present sequence is a primer
 CC used for detecting human HOXD3 gene polymorphisms
 XX
 SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 GTTGGCG 16
 Db 10 GTTGGCG 4
 RESULT 775
 ABV84961/C
 ID ABV84961 standard; cDNA; 10 BP.
 XX
 AC ABV84961;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human complement component C4A SAGE tag #771.
 XX
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.
 XX

OS Homo sapiens.
 XX JP2002209591-A.
 XX 30-JUL-2002.
 XX 19-JAN-2001; 2001JP-00012328.
 XX 19-JAN-2001; 2001JP-00012328.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-631294/68.
 XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 XX Claim 64; Page 31; 139pp; Japanese.
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
 CC expressed in hepatocellular carcinoma
 XX
 SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 AGGCTGT 11
 Db 10 AGGCTGT 4
 RESULT 776
 ABV84988/C
 ID ABV84988 standard; cDNA; 10 BP.
 XX
 AC ABV84988;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human multiple HCC highly expressed genes SAGE tag #798.
 XX
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; ss.
 XX
 OS Homo sapiens.
 XX JP2002209591-A.
 XX 30-JUL-2002.
 XX 19-JAN-2001; 2001JP-00012328.
 XX 19-JAN-2001; 2001JP-00012328.

```

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-631294/68.
XX PT Human chronic hepatitis C tissue expression exasperating gene group
XX PT comprises 100 high-ranking genes.
XX PS Claim 64; Page 31; 139pp; Japanese.
XX CC The invention relates to SAGE (serial analysis of gene expression) tags
XX CC representing groups of genes which are differentially expressed in human
XX CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX CC polyA region of cDNAs derived from a variety of genes. These tags serve
XX CC to uniquely identify each transcript and can thus be used to analyse the
XX CC pattern of gene expression in particular cell types. The invention also
XX CC relates to proteins encoded by the genes expressed in chronic hepatitis C
XX CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX CC the expression of groups of genes that are overexpressed in chronic
XX CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX CC treatment of these diseases. Such genes, inhibitors of their expression
XX CC or activity, and antibodies against the gene products may be used in the
XX CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
XX CC expressed in hepatocellular carcinoma
XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 7 AGGCTGT 1

RESULT 777
AAD43438/C
ID AAD43438 standard; DNA; 10 BP.
XX AC AAD43438;
XX DT 14-NOV-2002 (first entry)
XX DE Human CYP3A5 gene polymorphism detecting primer #24.
XX KW Human; cytochrome P450; subfamily IIIA; polypeptide 5 isogene; CYP3A5;
XX KW drug screening; polymorphism; haplotype; drug metabolising disorder;
XX KW gene therapy; primer; ss.
XX OS Homo sapiens.
XX PN WO200246209-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US047218.
XX PR 08-DEC-2000; 2000US-0254367P.
XX PR 03-MAY-2001; 2001US-0288470P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Anaestasio AE, Han J, Kliep SE, Rounds E;
XX WPI; 2002-636448/68.
XX PT Novel isolated polynucleotide which is a polymorphic variant of

cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5) gene useful for
expressing CYP3A5 protein isoform used in drug screening techniques.
Claim 17; Page 16; 127pp; English.
The invention relates to isolated polynucleotide having cytochrome P450,
subfamily IIIA, polypeptide 5 isogene (CYP3A5). The invention is useful
for screening drugs. The invention is useful for studying expression and
function of CYP3A5 and expressing CYP3A5 protein for use in screening for
candidate drugs to treat diseases related to CYP3A5 activity. The
polymorphism and haplotype data is useful for validating whether CYP3A5
is a suitable target for drugs to treat drug metabolising disorders,
screening for such drugs and reducing bias in clinical trials of such
drugs. The invention is also useful for therapeutic purposes. The
invention is useful in studying the effect of variation on the biological
activity of CYP3A5 as well as on the binding affinity of candidate drugs
to CYP3A5, or for studying the enzymatic properties of such CYP3A5
variants using these candidate drugs as substrate. The invention is
useful in gene therapy. The present sequence is human CYP3A5 gene
polymorphism detecting primer
Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGG 14
Db 8 CTGTTGG 2

RESULT 778
AAS95571/C
ID AAS95571 standard; DNA; 10 BP.
XX AC AAS95571;
XX DT 14-FEB-2002 (first entry)
XX DE Human IL8RB gene allele-specific oligonucleotide PCR primer #14.
XX KW Human; interleukin 8 receptor beta; IL8RB; ss; antiinflammatory; probe;
XX KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;
XX KW gene therapy; drug screening; chronic obstructive pulmonary disease;
XX KW inflammatory disease; sequencing primer; PCR primer.
XX OS Homo sapiens.
XX PN WO200179221-A2.
XX PD 25-OCT-2001.
XX PF 12-APR-2001; 2001WO-US011942.
XX PR 12-APR-2000; 2000US-0196734P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
XX WPI; 2002-055250/07.
XX PT New polymorphic variants comprising interleukin-8 receptor beta (IL8RB)
XX PT isogene, useful in expressing IL8RB protein for use in screening for
XX PT candidate drugs to treat diseases related to IL8RB activity, e.g.
XX PT inflammatory disorders.
XX PS Claim 18; Page 14; 74pp; English.
XX CC The invention relates to single nucleotide polymorphisms in the human
XX CC interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the
XX CC IL8RB gene in an individual comprises identifying the nucleotide at one

```

CC or more polymorphic sites and determining whether one of the copies of
 CC the gene is defined by one of the IL8RB haplotypes given in the
 CC specification or whether both copies are defined by a haplotype pair.
 CC This method is useful in genotyping, whereby all possible haplotype pairs
 CC can be assigned to specific genotypes. An association between a trait and
 CC a haplotype or haplotype pair of the IL8RB gene can be identified by
 CC comparing the frequency of the haplotype or haplotype pair in a
 CC population exhibiting the trait with the frequency of the haplotype or
 CC haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. IL8RB and its corresponding DNA are used
 CC for studying the expression and function of IL8RB, for use in screening
 CC for candidate drugs to treat diseases related to IL8RB activity, such as
 CC chronic obstructive pulmonary disease and other inflammatory disorders.
 CC The sequences are also useful for studying the effect of variation on the
 CC biological activity of IL8RB as well as on the binding affinity of
 CC candidate drugs targeting IL8RB. Sequences AAS95525-AAS95579 represent
 CC allele-specific oligonucleotide probes, sequencing primers and PCR
 CC primers used to detect IL8RB gene polymorphisms

XX
 SQ Sequence 10 BP; 6 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGC 15

Db 8 TGTGGC 2

RESULT 779

ABK16678

ID ABK16678 standard; DNA; 10 BP.

AC ABK16678;

DT 14-MAR-2002 (first entry)

XX Human AGTRL1 gene allele-specific oligonucleotide PCR primer #14.

XX Human; angiotensin receptor-like 1; AGTRL1; haplotyping; haplotype pair;
 KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
 KW hypertension; ss; probe; sequencing primer; PCR primer.

XX Homo sapiens.

XX WO200190123-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016906.

XX 23-MAY-2000; 2000US-0206264P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Kliem SE, Messer C, Tanguay DA;

XX WPI; 2002-097637/13.

XX New isolated polymorphic variant of human angiotensin receptor-like 1
 PT (AGTRL1) gene useful for expressing AGTRL1 protein isoform to screen
 PT drugs to treat AGTRL1 activity-related disease.

XX Claim 18; Page 13; 71pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human angiotensin receptor-like 1 (AGTRL1) polypeptide. A
 CC method for haplotyping the AGTRL1 gene in an individual comprises
 CC identifying the nucleotide at one or more polymorphic sites and
 CC determining whether one of the copies of the gene is defined by one of
 CC the AGTRL1 haplotypes given in the specification or whether both copies

CC are defined by a haplotype pair. This method is useful in genotyping,
 CC whereby all possible haplotype pairs can be assigned to specific
 CC genotypes. An association between a trait and a haplotype or haplotype
 CC pair of the AGTRL1 gene can be identified by comparing the frequency of
 CC the haplotype or haplotype pair in a population exhibiting the trait with
 CC the frequency of the haplotype or haplotype pair in a reference
 CC population, where a higher haplotype frequency in the trait population
 CC indicates the trait is associated with the haplotype or haplotype pair.
 CC AGTRL1 and its corresponding DNA are used for studying the expression and
 CC function of AGTRL1, for use in screening for candidate drugs to treat
 CC diseases related to AGTRL1 activity, such as hypertension. The sequences
 CC are also useful for studying the effect of variation on the biological
 CC activity of AGTRL1 as well as on the binding affinity of candidate drugs
 CC targeting AGTRL1. Sequences ABK16638-ABK16682 represent allele-specific
 CC oligonucleotide probes, sequencing primers and PCR primers used to detect
 CC AGTRL1 gene polymorphisms

XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13

Db 3 GCTGTTG 9

RESULT 780

ABK11494/c

ID ABK11494 standard; DNA; 10 BP.

XX ABK11494;

DT 05-JUN-2002 (first entry)

XX Oligonucleotide primer #6, to detect human ADRB3 gene polymorphisms.

XX Human; beta-3-adrenergic; receptor; ADRB3; primer; anorectic; ss;

KW anti-diabetic; gene therapy; morbid obesity; insulin resistance;

KW non-insulin-dependent diabetes mellitus; haplotyping; SNP;

XX single nucleotide polymorphism.

XX Homo sapiens.

XX WO200208425-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023223.

XX 21-JUL-2000; 2000US-0220088P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Finkel K, Koshy B;

XX WPI; 2002-241571/29.

XX Novel genetic variants of beta-3-adrenergic receptor gene useful in
 PT studying expression and function of the protein, and for screening drugs
 PT to treat diseases e.g. obesity, non-insulin dependent diabetes mellitus.

XX Claim 19; Page 15; 91pp; English.

XX The present invention relates to a new polypeptide comprising a sequence
 CC which is a polymorphic variant of a reference sequence for ADRB3 (beta-3-
 CC adrenergic receptor) protein. The reference sequence comprises a sequence
 CC of 408 amino acids as given in the specification, or its fragment, and
 CC the polymorphic variant comprises one or more variant amino acids. The
 CC polymorphic variants are useful in studying the expression and function
 CC of ADRB3, in expressing ADRB3 protein for use in screening for candidate
 CC drugs to treat diseases related to ADRB3 activity, in studying the effect

CC of the variation on the biological activity of ADRB3, and the binding
 CC affinity of candidate drugs targeting ADRB3 for the treatment of
 CC disorders such as morbid obesity, insulin resistance and an early onset
 CC of non-insulin-dependent diabetes mellitus. Haplotyping methods are
 CC useful in validating ADRB3 as a candidate target for treating a specific
 CC condition or disease predicted to be associated with ADRB3 activity, or
 CC in the design of clinical trials of candidate drugs for treating a
 CC specific condition or disease associated with ADRB3 activity. The present
 CC nucleic acid sequence represents one of a collection of oligonucleotide
 CC primers (ABK11489- ABK11512) that were used in the methods of the
 CC invention to detect polymorphisms in the human ADRB3 gene
 XX
 SQ Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
 |||||
 Db 7 GAGGCTG 1

RESULT 781

AAL43012
 ID AAL43012 standard; DNA; 10 BP.

XX AC AAL43012;

XX DT 08-AUG-2002 (first entry)

XX DE Human cerberus 1 (CER1) gene primer-extension oligonucleotide 17.

XX KW Human; PCR; ss; allele-specific; SNP; single nucleotide polymorphism;
 KW cerberus 1 homologue; cysteine knot superfamily; CER1; drug screening;
 KW developmental disorder; polymorphic site; CER1 haplotyping; primer.

XX OS Homo sapiens.

XX PN WO200232929-A2.

XX PD 25-APR-2002.

XX PF 19-OCT-2001; 2001WO-US046100.

XX PR 19-OCT-2000; 2000US-0241634P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kazemi A, Shah N;

XX PS WPI; 2002-435527/46.

XX PT Novel genetic variants of Cerberus 1 (Xenopus laevis) Homolog (Cysteine
 PT Knot Superfamily) (CER1) isogenes, useful for improving efficiency and
 PT reliability in drug development for treating developmental disorders.

XX PS Claim 16; Page 14; 75pp; English.

XX The invention relates to the identification of 13 novel polymorphic sites
 CC in the human cerberus 1 (Xenopus laevis) homologue (cysteine knot
 CC superfamily) (CER1) gene. The invention also comprises the amino acid and
 CC coding sequence of CER1. The CER1 protein is useful for screening drugs
 CC that target CER1 - for the treatment of developmental disorders. The CER1
 CC coding sequence is useful in studying the expression of CER1 isogenes,
 CC for screening and testing of drugs targeted against CER1 protein, and in
 CC testing the efficacy of therapeutic agents for treating developmental
 CC disorders. The 13 novel polymorphic sites identified in the invention are
 CC useful for haplotyping the CER1 gene of an individual. The present DNA
 CC sequence represents a human CER1 gene primer-extension oligonucleotide

XX SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
 |||||
 Db 2 AGGCTGT 8

RESULT 782

AAD43794
 ID AAD43794 standard; DNA; 10 BP.

XX AC AAD43794;

XX DT 14-NOV-2002 (first entry)

XX DE Human AGR2 gene polymorphism detecting primer #6.

XX KW Human; angiotensin receptor 2; forensic application; drug response;
 KW AGR2; congenital abnormality of kidney and urinary tract; CAKUT;
 KW cardiovascular disorder; premature ovarian failure; gene therapy; POF;
 KW polymorphism; primer; ss.

XX OS Homo sapiens.

XX PN WO200263045-A1.

XX PD 15-AUG-2002.

XX PF 02-FEB-2001; 2001WO-US003620.

XX PR 02-FEB-2001; 2001WO-US003620.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Chew A, Choi JY, Koshy B, Stephens JC;

XX PS WPI; 2002-636599/68.

XX PT Novel genetic variants of angiotensin receptor 2 isogenes, useful in
 PT therapeutic purposes and in screening for drugs targeting the angiotensin
 PT receptor protein.

XX PS Claim 18; Page 21; 69pp; English.

XX The invention relates to genetic variants of human angiotensin receptor 2
 CC (AGTR2) isogenes and methods for detecting variants of AGTR2 gene.
 CC Polynucleotides of the invention are useful in studying the expression
 CC and biological function of AGTR2 and in developing drugs targeting AGTR2
 CC protein. Methods of the invention are useful for studying population
 CC diversity, anthropological lineage, the significance of diversity and
 CC lineage at the phenotypic level, paternity testing, forensic applications
 CC and for identifying associations between AGTR2 genetic variations and a
 CC trait such as levels of drug response or susceptibility to disease. It is
 CC useful in developing diagnostic tests and therapeutic treatments for
 CC cardiovascular disorders, congenital abnormalities of kidney and urinary
 CC tract (CAKUT) and premature ovarian failure (POF). The invention is
 CC useful in gene therapy. The present sequence is a primer used to detect
 CC human AGR2 gene polymorphisms

XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGG 14
 |||||
 Db 1 CTGTTGG 7

RESULT 783

ABS64260
ID ABS64260 standard; DNA; 10 BP.
AC AAK98601;
XX
XX
DT 15-NOV-2002 (first entry)
XX
DE Tachykinin receptor gene TACR2, primer extension oligo #14.
XX
XX Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
KW tachykinin receptor.
XX
OS Homo sapiens.
XX
XX WO200263046-A1.
PN
XX
PD 15-AUG-2002.
XX
XX 09-NOV-2001; 2001WO-US047394.
XX
XX 09-NOV-2000; 2000US-0247649P.
PF
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Cappola G, Chew A, Gilson CR, Koshy B;
XX
XX WPI; 2002-636600/68.
DR
XX
XX New genetic variants having polymorphisms in the Tachykinin receptor
PT (TACR2) protein, useful for studying the function of TACR2, and for
PT treating disorders associated with abnormal expression or function of
PT TACR2 isogene.
XX
XX
PS Claim 16; Page 15; 139pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a polymorphic
CC variant of a reference sequence for the Tachykinin receptor (TACR2)
CC protein. Also described is a method for: (1) haplotyping or genotyping
CC the TACR2 gene of an individual; (2) predicting a haplotype pair for the
CC TACR2 gene of an individual; (3) identifying an association between a
CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and
CC (4) isolated oligonucleotide for detecting a single nucleotide
CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene
CC are useful in studying the expression and biological function of TACR2,
CC and in identifying drugs targeting TACR2 protein for treating disorders
CC associated with abnormal expression or function of TACR2, e.g. asthma or
CC breast cancer. Polynucleotides comprising a polymorphic gene variant or
CC fragment may be used for therapeutic purposes, where a patient could
CC benefit from expression or increased expression of a particular TACR2
CC protein isoform, or an expression vector encoding the isoform may be
CC administered to the patient. Haplotype information is useful in improving
CC the efficiency and output of several steps in drug discovery and
CC development process, including target validation, identifying lead
CC compounds, and early phase clinical trials. Information on polymorphisms
CC may be applied in studying biological functions of TACR2 as well as in
CC identifying drugs targeting this protein for the treatment of disorders
CC related to its abnormal expression or function. ABS64163-ABS64302
CC represent human TACR2 gene allele-specific oligonucleotide probes and
CC primers used to detect haplotypes of the TACR2 gene of the invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AGGCTGT 11
| | | | |
Db 3 AGGCTGT 9
RESULT 784
AAK98601/c

AAK98601 standard; DNA; 10 BP.
AAK98601;
16-APR-2002 (first entry)
Human enolase 3 gene allele specific primer SEQ ID NO: 72.
Human; enolase 3 (beta, muscle); ENO3; single nucleotide polymorphism;
SNP; haplotype analysis; isogene; primer; ss.
Homo sapiens.
WO200202579-A2.
10-JAN-2002.
02-JUL-2001; 2001WO-US020952.
30-JUN-2000; 2000US-0215236P.
(GENA-) GENAISSANCE PHARM INC.
Duda A, Finkel K, Koshy B, Parks KE;
WPI; 2002-154721/20.
Novel genetic variants of enolase 3, (beta, muscle) gene useful in
studying expression and function of the protein, and for screening drugs
to treat disorders of glycolytic pathway.
Claim 18; Page 14; 90pp; English.
The present invention provides the protein, cDNA and genomic sequences of
a human enolase 3 (beta, muscle) isogene containing a number of single
nucleotide polymorphisms (SNPs). The sequences can be used to identify
the haplotype of an individual and identify whether particular haplotypes
are linked to certain diseases. The present sequence is a primer for the
ENO3 gene described in the exemplification of the invention
Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TGAGGCT 9
| | | | |
Db 10 TGAGGCT 4
RESULT 785
ABK32812
ID ABK32812 standard; DNA; 10 BP.
XX
XX ABK32812;
XX
XX 23-APR-2002 (first entry)
XX
XX Human APPBP1 gene, allele-specific oligonucleotide #42.
XX
XX Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;
KW Alzheimer's disease; transgenic animal; platelet aggregation;
XX single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.
XX Homo sapiens.
XX
XX WO200202820-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 02-JUL-2001; 2001WO-US020951.
XX

PR 30-JUN-2000; 2000US-0215511P.
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Anestasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;
PI Stephens CJ;
PI
XX WPI; 2002-164539/21.
DR
XX
XX Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
PT polymorphic variants, useful e.g. in studying the expression and function
PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.
XX
XX Claim 19; Page 14; 104pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a sequence
CC which is a polymorphic variant of a reference sequence for the amyloid
CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
CC fragment. The polymorphic variants are useful in studying the expression
CC and function of APPBP1, in expressing APPBP1 protein for use in screening
CC for candidate drugs to treat diseases related to APPBP1 activity, in
CC studying the effect of the variation on the biological activity of
CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
CC the treatment of disorders such as Alzheimer's disease. The haplotyping
CC methods are useful in validating APPBP1 as a candidate target for
CC treating a specific condition or disease predicted to be associated with
CC APPBP1 activity, or in the design of clinical trials of candidate drugs
CC for treating a specific condition or disease associated with APPBP1
CC activity. The transgenic animals are useful for studying expression of
CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against APPBP1 protein, and for testing the efficacy of
CC therapeutic agents and compounds for disorders related to platelet
CC aggregation in a biological system. ABK32771-ABK32327 represent human
CC APPBP1 gene allele-specific oligonucleotides used in the method of the
XX invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGGCTG 10
Db 2 GAGGCTG 8
RESULT 786
AAD25697
ID AAD25697 standard; DNA; 10 BP.
XX
XX AAD25697;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human cyclin-dependent kinase 4 gene polymorphism detecting primer #9.
DE
XX
XX Human; cyclin-dependent kinase 4; CDK4; chromosome 12q13; therapy;
KW cancer; melanoma; protein synthesis disorder; drug screening; primer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200190115-A2.
FN
XX
XX 29-NOV-2001.
PD
XX
XX 18-MAY-2001; 2001WO-US016350.
PF
XX
XX 19-MAY-2000; 2000US-0205867P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Duda AE, Kazemi A, Koshy B, Sausker EA;
PI

XX WPI; 2002-083072/11.
XX
XX New genetic variants comprising haplotypes of the cyclin-dependent kinase
PT 4 (CDK4) gene, useful in improving the efficiency drug screening
PT protocols for compounds targeting CDK4.
XX
XX Claim 16; Page 13; 58pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising fragments
CC and haplotypes of the cyclin-dependent kinase 4 (CDK4) gene. Human CDK4
CC gene is located on chromosome 12q13 and contains 8 exons. The haplotypes
CC and polymorphisms of CDK4 gene are useful for validating whether CDK4 is
CC a suitable target for drugs to treat cancer, melanoma and disorders
CC associated with impaired protein synthesis in cells, screening for such
CC drugs and reducing bias in clinical trials of such drugs. Haplotype
CC information would be useful in improving the efficiency and output of
CC several steps in the drug discovery and development process, including
CC target validation, identifying lead compounds, early phase clinical
CC trials. The methods are useful in screening for compounds targeting CDK4
CC to treat a specific condition or disease predicted to be associated with
CC CDK4 activity. The present sequence is a primer used for detecting human
CC CDK4 gene polymorphism
XX
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TGTGGC 15
Db 3 TGTGGC 9
RESULT 787
AAS99395
ID AAS99395 standard; DNA; 10 BP.
XX
XX AAS99395;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #88.
DE
XX
XX Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
KW succinate-semialdehyde dehydrogenase; gene therapy; primer;
KW antisense technology; primer extension oligonucleotide;
KW 4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.
XX
XX Synthetic.
OS
XX
XX WO200190119-A2.
FN
XX
XX 29-NOV-2001.
PD
XX
XX 21-MAY-2001; 2001WO-US016558.
PF
XX
XX 19-MAY-2000; 2000US-0205849P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Kliem SE, Koshy B, Tanguay DA;
PI
XX
XX WPI; 2002-089912/12.
DR
XX
XX New genetic variants of human aldehyde dehydrogenase 5 family, member A1,
PT ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1
PT protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.
XX
XX Claim 18; Page 14; 151pp; English.
PS
XX
XX The invention describes an isolated polynucleotide comprising a

CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11

Db 4 AGGCTGT 10

RESULT 792

ABT14266/c

ID ABT14266 standard; DNA; 10 BP.

AC ABT14266;

XX

DT 20-FEB-2003 (first entry)

XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #36.

XX Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;

KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX Unidentified.

XX WO200281743-A2.

XX 17-OCT-2002.

XX 28-MAR-2002; 2002WO-GB001489.

XX 02-APR-2001; 2001GB-00008182.

XX (HAMI/) HAMILL B.

XX Hamill B;

XX WPI; 2003-075484/07.

XX Amplification of nucleotide sequences from polynucleotides by chain
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT solution, 2 attached to supports and both share complementary sequences.

XX Disclosure; Fig 17; 60pp; English.

XX The invention comprises a method for the PCR amplification of nucleic
CC acids. The method involves a set of primers, where two of the primers are
CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention
XX

SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11

Db 7 AGGCTGT 1

RESULT 793

ABZ81289

ID ABZ81289 standard; DNA; 10 BP.

XX ABZ81289;

AC ABZ81289;

XX 14-MAY-2003 (first entry)

XX Small proline-rich protein 1B related oligonucleotide.

XX Tumour; non-small cell lung cancer; molecular characteristic; cancer;

XX lung cancer; squamous cell carcinoma; adenocarcinoma; ss.

XX Homo sapiens.

XX Synthetic.

XX WO2003015613-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026027.

XX 16-AUG-2001; 2001US-0312400P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX (GENZ) GENZYME CORP.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Nacht M, Dracheva T, Sidransky D, Madden SL, Jen J;

XX WPI; 2003-268230/26.

XX Identifying lung cancer as squamous cell carcinoma or adenocarcinoma, by
PT determining level of product of gene e.g., glutathione peroxidase,
PT peroxiredoxin 1 and small proline-rich protein 3 in lung cancer sample.

XX Example 10; Fig 2C; 26pp; English.

XX The present invention describes a method for identifying lung cancer as
CC squamous cell carcinoma, which involves determining in an amount of a
CC gene product of a gene in a lung cancer sample, the gene selected from
CC glutathione peroxidase (GPX; NM_002083), glutathione S-transferase M3
CC (GSTM3; NM_000849), aldo-ketoreductase family 1, member B 10 (NM_020299),
CC peroxiredoxin 1 (PRDX1; NM_002574), small proline-rich protein 3 (SPRR3;
CC NM_005416), and tumour necrosis factor (TNF) receptor superfamily member
CC 18 (TNFRSF18; NM_004195), comparing the amount of the gene product to the
CC amount determined in a lung tissue sample which is non-pathological,
CC where an increased amount of the gene product in the lung cancer sample
CC relative to the lung tissue sample which is non-pathological identifies
CC the lung cancer as a squamous cell carcinoma. Also described is a method
CC for identifying a lung cancer as adenocarcinoma, which involves
CC determining an amount of a gene product of a small proline-rich protein 3
CC gene in a lung cancer sample, comparing the amount of the gene product to
CC the amount determined in a lung tissue sample which is non-pathological,
CC where a decreased amount of the gene product in the lung cancer sample
CC relative to the lung tissue sample which is non-pathological identifies
CC the lung cancer as adenocarcinoma. The methods are useful for identifying
CC lung cancers as a squamous cell carcinoma or an adenocarcinoma. The
CC present sequence represents an oligonucleotide which is used in an
CC example from the present invention
XX

SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGG 7

Db 3 CTTGAGG 9

RESULT 794

```
ADA63337
ID ADA63337 standard; DNA; 10 BP.
XX
AC ADA63337;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #359.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 19; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
DB |||||
4 GAGGCTG 10

RESULT 795
ADA63653
ID ADA63653 standard; DNA; 10 BP.
XX
AC ADA63653;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #417.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 18; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
DB |||||
4 GAGGCTG 10

RESULT 796
ADA62585
ID ADA62585 standard; DNA; 10 BP.
XX
AC ADA62585;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #222.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 19; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
```

```
PI Liu Q;
XX WPI; 2003-567233/53.
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX Disclosure; Page 16; 34pp; English.
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  9 TGTGGC 15
  2 TGTGGC 8
  |||||
  |||||

RESULT 797
ID ADA63654 standard; DNA; 10 BP.
XX
AC ADA63654;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #418.
XX
ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
XX
PR 24-MAR-1999; 99US-0126239P.
XX
PR 30-JUL-1999; 99US-0146595P.
XX
PR 30-JUL-1999; 99US-0146615P.
XX
PR 23-MAR-2000; 2000US-00535008.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
WPI; 2003-567233/53.
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX Disclosure; Page 19; 34pp; English.
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  9 TGTGGC 15
  2 TGTGGC 8
  |||||
  |||||

RESULT 798
ID ADA63308 standard; DNA; 10 BP.
XX
AC ADA63308;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #330.
XX
ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
XX
PR 24-MAR-1999; 99US-0126239P.
XX
PR 30-JUL-1999; 99US-0146595P.
XX
PR 30-JUL-1999; 99US-0146615P.
XX
PR 23-MAR-2000; 2000US-00535008.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
WPI; 2003-567233/53.
XX Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX Disclosure; Page 18; 34pp; English.
XX The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
  Query Match      38.9%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  4 GAGGCTG 10
  4 GAGGCTG 10
  |||||
  |||||

Search completed: September 9, 2004, 11:15:19
Job time : 2 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:17:53 ; Search time 0.001 Seconds
(without alignments)
89.388 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18

Sequence: 1 cttgagcgttggtgcac 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 237 seqs, 2483 residues

Total number of hits satisfying chosen parameters: 474

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 237 summaries

Database : rni21.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	100.0	18	1	US-09-256-465-21
2	12.4	68.9	18	1	5245022-14
3	12.2	67.8	17	1	US-09-371-772B-4769
4	12	66.7	17	1	US-09-094-557-14
5	12	66.7	18	1	US-09-256-465-22
6	11.8	65.6	18	1	US-09-242-937-6
7	11.4	63.3	17	1	US-09-866-108A-9833
8	11.4	63.3	17	1	US-09-866-108A-9834
9	11.4	63.3	17	1	US-09-866-108A-9835
10	11.4	63.3	17	1	US-09-866-108A-9836
11	11.4	63.3	17	1	US-09-866-108A-9837
12	11.2	62.2	17	1	US-08-584-040-1933
13	11.2	62.2	17	1	US-09-371-772B-478
14	10.8	60.0	16	1	US-09-509-565-33
15	10	55.6	11	1	US-08-959-853-6
16	10	55.6	15	1	US-08-889-296A-32
17	10	55.6	15	1	US-08-848-840A-32
18	10	55.6	15	1	US-08-961-469A-40
19	10	55.6	15	1	US-09-128-494-32
20	10	55.6	15	1	US-09-248-386-32
21	9.8	54.4	15	1	US-08-363-240A-146
22	9.8	54.4	15	1	US-08-595-684B-2148
23	9.8	54.4	15	1	US-09-038-073-2148
24	9.8	54.4	15	1	US-09-081-646-81
25	9.8	54.4	15	1	US-09-081-646-770
26	9.2	51.1	14	1	US-09-081-646-514
27	9	50.0	9	1	US-09-989-789-2478
28	8.8	48.9	12	1	US-08-651-835A-6
29	8.8	48.9	12	1	US-08-738-381-47
30	8.8	48.9	13	1	US-09-216-584-20
31	8.8	48.9	13	1	US-10-032-307-70
32	8.4	46.7	10	1	US-09-989-789-626
33	8.4	46.7	11	1	US-08-959-853-5

Sequence 7, Appli	1	US-09-613-826A-7	12	46.7	8.4	34
Sequence 13, Appli	1	US-09-613-826A-13	12	46.7	8.4	35
Sequence 14, Appli	1	US-09-613-826A-14	12	46.7	8.4	36
Sequence 5, Appli	1	US-09-621-275-5	12	46.7	8.4	37
Sequence 100, App	1	US-08-859-954-100	8	44.4	8	38
Sequence 2152, Ap	1	US-09-989-789-2152	9	44.4	8	39
Sequence 2326, Ap	1	US-09-989-789-2326	9	44.4	8	40
Sequence 21, Appli	1	PCT-US94-05655-21	9	44.4	8	41
Sequence 31, Appli	1	US-08-259-148A-31	10	44.4	8	42
Sequence 47, Appli	1	US-07-876-941A-47	10	44.4	8	43
Sequence 733, App	1	US-08-388-353-733	10	44.4	8	44
Sequence 734, App	1	US-08-388-353-734	10	44.4	8	45
Sequence 735, App	1	US-08-388-353-735	10	44.4	8	46
Sequence 733, App	1	US-08-488-551B-733	10	44.4	8	47
Sequence 734, App	1	US-08-488-551B-734	10	44.4	8	48
Sequence 735, App	1	US-08-488-551B-735	10	44.4	8	49
Sequence 8, Appli	1	US-08-308-892A-8	11	44.4	8	50
Sequence 15, Appli	1	US-08-597-467-15	11	44.4	8	51
Sequence 3, Appli	1	US-08-962-790-3	11	44.4	8	52
Sequence 7, Appli	1	US-08-205-507-7	11	44.4	8	53
Sequence 206, App	1	US-08-271-880A-206	11	43.3	7.8	54
Sequence 10, Appli	1	US-08-295-743-10	11	43.3	7.8	55
Sequence 12, Appli	1	US-08-295-743-12	11	43.3	7.8	56
Sequence 13, Appli	1	US-08-295-743-13	11	43.3	7.8	57
Sequence 14, Appli	1	US-08-295-743-14	11	43.3	7.8	58
Sequence 15, Appli	1	US-08-295-743-15	11	43.3	7.8	59
Sequence 23, Appli	1	US-08-295-743-23	11	43.3	7.8	60
Sequence 24, Appli	1	US-08-295-743-24	11	43.3	7.8	61
Sequence 25, Appli	1	US-08-295-743-25	11	43.3	7.8	62
Sequence 206, App	1	US-08-910-408-206	11	43.3	7.8	63
Sequence 14, Appli	1	US-09-249-215-206	11	43.3	7.8	64
Sequence 245, App	1	US-09-303-586-14	11	43.3	7.8	65
Sequence 318, App	1	US-09-249-155A-245	11	43.3	7.8	66
Sequence 16, Appli	1	US-09-409-926-16	11	43.3	7.8	67
Sequence 10, Appli	1	PCT-US93-02059-10	11	43.3	7.8	68
Sequence 12, Appli	1	PCT-US93-02059-12	11	43.3	7.8	69
Sequence 13, Appli	1	PCT-US93-02059-13	11	43.3	7.8	70
Sequence 14, Appli	1	PCT-US93-02059-14	11	43.3	7.8	71
Sequence 15, Appli	1	PCT-US93-02059-15	11	43.3	7.8	72
Sequence 21, Appli	1	PCT-US93-02059-21	11	43.3	7.8	73
Sequence 22, Appli	1	PCT-US93-02059-22	11	43.3	7.8	74
Sequence 24, Appli	1	PCT-US93-02059-24	11	43.3	7.8	75
Sequence 7, Appli	1	US-08-651-835A-7	12	43.3	7.8	76
Sequence 7, Appli	1	US-08-358-171-7	12	43.3	7.8	77
Sequence 7, Appli	1	US-09-090-947-7	12	43.3	7.8	78
Sequence 34, Appli	1	US-08-874-825-34	12	43.3	7.8	79
Sequence 34, Appli	1	US-08-863-824-34	12	43.3	7.8	80
Sequence 57, App	1	US-09-281-418-57	12	43.3	7.8	81
Sequence 189, App	1	US-09-281-418-189	12	43.3	7.8	82
Sequence 34, Appli	1	US-09-231-303-34	12	43.3	7.8	83
Sequence 2508, Ap	1	US-09-989-789-2508	12	43.3	7.8	84
Sequence 18, Appli	1	US-07-783-705A-14	9	41.1	7.4	85
Sequence 72, Appli	1	US-08-388-353-72	10	41.1	7.4	86
Sequence 73, Appli	1	US-08-388-353-73	10	41.1	7.4	87
Sequence 72, Appli	1	US-08-488-551B-72	10	41.1	7.4	88
Sequence 73, Appli	1	US-08-488-551B-73	10	41.1	7.4	89
Sequence 10, Appli	1	US-08-522-384-10	10	41.1	7.4	90
Sequence 8, Appli	1	US-08-522-384-8	10	41.1	7.4	91
Sequence 6, Appli	1	US-08-997-897-6	10	41.1	7.4	92
Sequence 50, Appli	1	US-09-156-836B-50	10	41.1	7.4	93
Sequence 123, App	1	US-09-914-259-123	10	41.1	7.4	94
Sequence 219, App	1	US-09-508-753B-219	10	41.1	7.4	95
Sequence 369, App	1	US-09-508-753B-369	10	41.1	7.4	96
Sequence 20, Appli	1	US-10-042-111-20	10	41.1	7.4	97
Sequence 1278, Ap	1	US-09-989-789-1278	10	41.1	7.4	98
Sequence 1, Appli	1	US-09-621-275-1	10	41.1	7.4	99
Sequence 82, Appli	1	US-08-481-658B-82	11	41.1	7.4	100
Sequence 82, Appli	1	US-08-477-504A-82	11	41.1	7.4	101
Sequence 82, Appli	1	US-08-486-756A-82	11	41.1	7.4	102
Sequence 82, Appli	1	US-08-485-862B-82	11	41.1	7.4	103

C 107	7.4	41.1	11	1	US-08-787-739-82	Sequence 82, Appl	180	6.4	35.6	9	1	US-09-989-789-2199	Sequence 2199, Ap
C 108	7.4	41.1	11	1	US-08-487-077A-82	Sequence 82, Appl	C 181	6.4	35.6	9	1	PCT-US94-05659-18	Sequence 18, Appl
C 109	7.4	41.1	11	1	US-08-485-863A-82	Sequence 82, Appl	182	6	33.3	8	1	US-08-187-749-21	Sequence 21, Appl
C 110	7.4	41.1	11	1	US-07-875-790B-15	Sequence 15, Appl	183	6	33.3	8	1	US-08-210-223-31	Sequence 31, Appl
C 111	7.4	41.1	11	1	US-08-485-049D-82	Sequence 82, Appl	184	6	33.3	8	1	US-08-859-954-97	Sequence 97, Appl
C 112	7.4	41.1	11	1	US-09-178-115-82	Sequence 82, Appl	C 185	6	33.3	8	1	US-08-859-954-325	Sequence 325, App
C 113	7.4	41.1	11	1	US-09-177-776-82	Sequence 82, Appl	C 186	6	33.3	8	1	US-08-859-954-326	Sequence 326, App
C 114	7.4	41.1	11	1	US-09-179-162A-3	Sequence 3, Appl	C 187	6	33.3	8	1	US-08-859-954-532	Sequence 532, App
C 115	7.4	41.1	11	1	US-09-249-155A-37	Sequence 37, Appl	188	6	33.3	8	1	US-08-859-954-543	Sequence 543, App
C 116	7.4	41.1	11	1	US-09-249-155A-266	Sequence 266, App	C 189	6	33.3	8	1	US-09-398-499-18	Sequence 18, Appl
C 117	7.4	41.1	11	1	US-09-950-459-3	Sequence 3, Appl	C 190	6	33.3	8	1	US-09-398-499-41	Sequence 41, Appl
C 118	7.4	38.9	9	1	US-08-253-575-10	Sequence 10, Appl	191	6	33.3	8	1	PCT-US95-01104-21	Sequence 21, Appl
C 119	7.4	38.9	9	1	US-09-989-789-531	Sequence 531, App	192	6	33.3	9	1	US-08-381-097A-13	Sequence 13, Appl
C 120	7.4	38.9	9	1	US-09-989-789-2156	Sequence 2156, Ap	193	6	33.3	9	1	US-08-798-738-1	Sequence 1, Appl
C 121	7.4	38.9	9	1	US-09-989-789-2127	Sequence 2127, Ap	C 194	6	33.3	9	1	US-08-899-324-12	Sequence 12, Appl
C 122	7.4	38.9	9	1	US-09-989-789-2128	Sequence 2128, Ap	195	6	33.3	9	1	US-08-757-024-952	Sequence 952, App
C 123	7.4	38.9	9	1	US-09-989-789-2129	Sequence 2129, Ap	C 196	6	33.3	9	1	US-08-329-892B-12	Sequence 12, Appl
C 124	7.4	38.9	10	1	US-09-263-790-27	Sequence 27, Appl	197	6	33.3	9	1	US-09-528-760A-21	Sequence 21, Appl
C 125	7.4	38.9	10	1	US-09-721-777-7	Sequence 7, Appl	198	6	33.3	9	1	US-09-951-843-21	Sequence 21, Appl
C 126	7.4	38.9	10	1	US-08-446-646-20	Sequence 20, Appl	C 199	6	33.3	9	1	US-09-989-789-441	Sequence 441, App
C 127	7.4	38.9	10	1	US-08-545-253A-16	Sequence 16, Appl	C 200	6	33.3	9	1	US-09-989-789-442	Sequence 442, App
C 128	7.4	38.9	10	1	US-08-388-353-732	Sequence 732, App	C 201	6	33.3	9	1	US-09-989-789-443	Sequence 443, App
C 129	7.4	38.9	10	1	US-08-388-353-736	Sequence 736, App	C 202	6	33.3	9	1	US-09-989-789-444	Sequence 444, App
C 130	7.4	38.9	10	1	US-08-488-551B-732	Sequence 732, App	C 203	6	33.3	9	1	US-09-989-789-465	Sequence 465, App
C 131	7.4	38.9	10	1	US-08-488-551B-736	Sequence 736, App	C 204	6	33.3	9	1	US-09-989-789-466	Sequence 466, App
C 132	7.4	38.9	10	1	US-08-719-337-16	Sequence 16, Appl	C 205	6	33.3	9	1	US-09-989-789-467	Sequence 467, App
C 133	7.4	38.9	10	1	US-08-522-384-4	Sequence 4, Appl	C 206	6	33.3	9	1	US-09-989-789-468	Sequence 468, App
C 134	7.4	38.9	10	1	US-08-522-384-86	Sequence 86, Appl	C 207	6	33.3	9	1	US-09-989-789-469	Sequence 469, App
C 135	7.4	38.9	10	1	US-09-255-432-2	Sequence 2, Appl	C 208	6	33.3	9	1	US-09-989-789-470	Sequence 470, App
C 136	7.4	38.9	10	1	US-09-154-750A-16	Sequence 16, Appl	C 209	6	33.3	9	1	US-09-989-789-532	Sequence 532, App
C 137	7.4	38.9	10	1	US-09-154-750A-19	Sequence 19, Appl	210	6	33.3	9	1	US-09-989-789-608	Sequence 608, App
C 138	7.4	38.9	10	1	US-09-989-789-556	Sequence 556, App	211	6	33.3	9	1	US-09-989-789-2084	Sequence 2084, Ap
C 139	7.4	38.9	10	1	US-09-989-789-1279	Sequence 1279, Ap	212	6	33.3	9	1	US-09-989-789-2086	Sequence 2086, Ap
C 140	7.4	38.9	10	1	US-09-989-789-1308	Sequence 1308, Ap	213	6	33.3	9	1	US-09-989-789-2161	Sequence 2161, Ap
C 141	7.4	38.9	10	1	US-09-989-789-1313	Sequence 1313, Ap	214	6	33.3	9	1	US-09-989-789-2162	Sequence 2162, Ap
C 142	7.4	38.9	10	1	US-09-989-789-1624	Sequence 1624, Ap	215	6	33.3	9	1	US-09-989-789-2166	Sequence 2166, Ap
C 143	7.4	38.9	10	1	US-09-989-789-1625	Sequence 1625, Ap	216	6	33.3	9	1	US-09-989-789-2177	Sequence 2177, Ap
C 144	7.4	38.9	10	1	US-09-758-073-2	Sequence 2, Appl	217	6	33.3	9	1	US-09-989-789-2185	Sequence 2185, Ap
C 145	7.4	38.9	10	1	US-09-869-080-3	Sequence 3, Appl	C 218	6	33.3	9	1	US-09-989-789-2204	Sequence 2204, Ap
C 146	6.8	37.8	10	1	US-07-651-710A-5	Sequence 5, Appl	219	6	33.3	9	1	US-09-989-789-2221	Sequence 2221, Ap
C 147	6.8	37.8	10	1	US-07-651-710A-13	Sequence 13, Appl	220	6	33.3	9	1	US-09-989-789-2222	Sequence 2222, Ap
C 148	6.8	37.8	10	1	US-08-388-353-162	Sequence 162, App	221	6	33.3	9	1	US-09-989-789-2230	Sequence 2230, Ap
C 149	6.8	37.8	10	1	US-08-488-551B-162	Sequence 162, App	C 222	6	33.3	9	1	US-09-989-789-2230	Sequence 2230, Ap
C 150	6.8	37.8	10	1	US-08-522-384-110	Sequence 110, App	C 223	6	33.3	9	1	US-09-989-789-2243	Sequence 2243, Ap
C 151	6.8	37.8	10	1	US-07-875-790B-14	Sequence 14, Appl	C 224	6	33.3	9	1	US-09-989-789-2273	Sequence 2273, Ap
C 152	6.8	37.8	10	1	US-09-398-499-47	Sequence 47, Appl	C 225	6	33.3	9	1	US-09-989-789-2338	Sequence 2338, Ap
C 153	6.8	37.8	10	1	US-08-618-834C-42	Sequence 42, Appl	226	6	33.3	9	1	US-09-989-789-2394	Sequence 2394, Ap
C 154	6.8	37.8	10	1	US-09-914-259-117	Sequence 117, App	227	6	33.3	9	1	US-09-989-789-2395	Sequence 2395, Ap
C 155	6.8	37.8	10	1	US-09-989-789-629	Sequence 629, App	228	6	33.3	9	1	US-09-989-789-2433	Sequence 2433, Ap
C 156	6.4	35.6	8	1	US-08-859-954-184	Sequence 184, App	229	6	33.3	9	1	US-09-989-789-2443	Sequence 2443, Ap
C 157	6.4	35.6	8	1	US-08-859-954-198	Sequence 198, App	230	6	33.3	9	1	US-09-989-789-2449	Sequence 2449, Ap
C 158	6.4	35.6	8	1	US-08-859-954-449	Sequence 449, App	231	6	33.3	9	1	US-09-989-789-2455	Sequence 2455, Ap
C 159	6.4	35.6	8	1	US-08-859-954-566	Sequence 566, App	232	6	33.3	9	1	US-09-989-789-2456	Sequence 2456, Ap
C 160	6.4	35.6	8	1	US-09-432-020B-24	Sequence 24, Appl	233	6	33.3	9	1	US-09-989-789-2471	Sequence 2471, Ap
C 161	6.4	35.6	8	1	US-09-398-499-3	Sequence 3, Appl	234	6	33.3	9	1	US-09-989-789-2473	Sequence 2473, Ap
C 162	6.4	35.6	8	1	US-09-398-499-5	Sequence 5, Appl	235	6	33.3	9	1	PCT-US94-05659-1	Sequence 1, Appl
C 163	6.4	35.6	8	1	US-09-398-499-12	Sequence 12, Appl	C 236	6	33.3	9	1	PCT-US94-05659-4	Sequence 4, Appl
C 164	6.4	35.6	8	1	US-09-398-499-21	Sequence 21, Appl	C 237	6	33.3	9	1	PCT-US94-05659-19	Sequence 19, Appl
C 165	6.4	35.6	8	1	US-09-398-499-26	Sequence 26, Appl							
C 166	6.4	35.6	8	1	US-09-398-499-28	Sequence 28, Appl							
C 167	6.4	35.6	8	1	US-09-398-499-35	Sequence 35, Appl							
C 168	6.4	35.6	8	1	US-09-398-499-44	Sequence 44, Appl							
C 169	6.4	35.6	8	1	US-09-878-693-1	Sequence 1, Appl							
C 170	6.4	35.6	9	1	US-08-461-607-21	Sequence 21, Appl							
C 171	6.4	35.6	9	1	US-09-363-600-21	Sequence 21, Appl							
C 172	6.4	35.6	9	1	US-09-432-020B-16	Sequence 16, Appl							
C 173	6.4	35.6	9	1	US-09-432-020B-20	Sequence 20, Appl							
C 174	6.4	35.6	9	1	US-09-380-836-6	Sequence 6, Appl							
C 175	6.4	35.6	9	1	US-09-989-789-2097	Sequence 2097, Ap							
C 176	6.4	35.6	9	1	US-09-989-789-2157	Sequence 2157, Ap							
C 177	6.4	35.6	9	1	US-09-989-789-2160	Sequence 2160, Ap							
C 178	6.4	35.6	9	1	US-09-989-789-2171	Sequence 2171, Ap							
C 179	6.4	35.6	9	1	US-09-989-789-2198	Sequence 2198, Ap							

ALIGNMENTS

RESULT 1

US-09-256-465-21
; Sequence 21, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465

RESULT 5

US-09-256-465-22
; Sequence 22, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-22

Query Match 66.7%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGGCTGTT 12

Db 7 CTTGAGGCTGTT 18

RESULT 6

US-09-242-937-6
; Sequence 6, Application US/09242937
; Patent No. 6448002
; GENERAL INFORMATION:
; APPLICANT: Invitex GmbH
; TITLE OF INVENTION: Method to detect clinically relevant mutations of the
; TITLE OF INVENTION: DNA sequence of ki-ras oncogene, its use and a test kit
; FILE REFERENCE: US Ser. No. 6448002 09/242,937
; CURRENT APPLICATION NUMBER: US/09/242,937
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: DE 196 35 609.1
; EARLIER FILING DATE: 1996-08-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-242-937-6

Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 11;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGGCG 16

Db 2 TTGAGGCTGTGGCG 16

RESULT 7

US-09-866-108A-9833/c
; Sequence 9833, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9833
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9833

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14

Db 17 TTGAGGCTGTGG 5

RESULT 8

US-09-866-108A-9834/c
; Sequence 9834, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

US-09-866-108A-9835

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 15 TTGAGGCTGTGG 3

RESULT 10

US-09-866-108A-9836/c
; Sequence 9836, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9836
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108A-9834

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 16 TTGAGGCTGTGG 4

RESULT 9

US-09-866-108A-9835/c
; Sequence 9835, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9835
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108A-9835

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 15 TTGAGGCTGTGG 3

RESULT 10

US-09-866-108A-9836/c
; Sequence 9836, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9836
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108A-9836

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 14 TTGAGGCTGTGG 2

RESULT 11

US-09-866-108A-9837/c
; Sequence 9837, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeoica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 9837
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-9837

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGG 14
Db 13 TTGAGGCTGTGG 1

RESULT 12
US-08-584-040-1933/c
Sequence 1933, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1933:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-1933

Query Match 62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTGAGGCTGTGGCG 16
Db 16 CTTGAGGTAGTTGGAG 1

RESULT 13
US-09-371-772B-478/c
Sequence 478, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
FILE REFERENCE: MBH800,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 478
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-478

Query Match 62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTGAGGCTGTGGCG 16
Db 16 CTTGAGGTAGTTGGAG 1

RESULT 14

US-09-509-565-33
; Sequence 33, Application US/09509565
; Patent No. 639340
; GENERAL INFORMATION:
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: NOGUCHI, YUJI
; APPLICANT: YOSHIKAWA, KOJI
; APPLICANT: SOEDA, SHINSUKE
; TITLE OF INVENTION: PLASMID VECTORS
; FILE REFERENCE: 0018-1105-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,565
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/JP9804611
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: JP9/303395
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 33
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-509-565-33

Query Match 60.0%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTGGC 15
| | | | | | | |
DB 3 TGGAGGCTGTAGC 16

RESULT 15
US-08-959-853-6/c
; Sequence 6, Application US/08959853
; Patent No. 609053
; GENERAL INFORMATION:
; APPLICANT: Robert S. Matson
; TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
; TITLE OF INVENTION: IN GENETIC ANALYSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; ZIP: 92834-3100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: WINDOWS 95 - WORDPERFECT 7.0
; SOFTWARE: ASCII (DOS) TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,853
; FILING DATE: herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: P.R. Harder
; REGISTRATION NUMBER: 20,022
; REFERENCE/DOCKET NUMBER: 45D-1566
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-6929
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-08-959-853-6

Query Match 55.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
| | | | | | | |
DB 11 GCTGTTGGCG 2

RESULT 16
US-08-889-296A-32/c
; Sequence 32, Application US/08889296A
; Patent No. 5872242
; GENERAL INFORMATION:
; APPLICANT: Monia, B.P., Cowsett, L.M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,296A
; FILING DATE: herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,734
; FILING DATE: April 3, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09346
; FILING DATE: October 1, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 958,134
; FILING DATE: October 5, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/007,996
; FILING DATE: January 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-889-296A-32

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
| | | | | | | |
DB 12 GCTGTTGGCG 3

RESULT 17
US-08-848-840A-32/c
; Sequence 32, Application US/08848840A
; Patent No. 5965722
; GENERAL INFORMATION:
; APPLICANT: Monia, et al.
; TITLE OF INVENTION: ANTISENSE INHIBITION OF ras GENE WITH
; TITLE OF INVENTION: CHIMERIC AND ALTERNATING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5965722ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,840A
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,289
; FILING DATE: 03-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,493
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/335,046
; FILING DATE: 07-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,256
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,866
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,037
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,734
; FILING DATE: 03-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,180
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-848-840A-32

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCTGTTGGCG 16
DB 12 GCTGTTGGCG 3

RESULT 18
US-08-961-469A-40/c
; Sequence 40, Application US/08961469A
; Patent No. 6083923
; GENERAL INFORMATION:
; APPLICANT: Greg Hardee, Richard Geary, Arthur Levin,
; APPLICANT: Mike Tempin, Randy Howard, Rahul Mehta
; TITLE OF INVENTION: LIPOSOMAL OLIGONUCLEOTIDE COMPOSITIONS
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,469A
; FILING DATE: October 31, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-779-2400
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-961-469A-40

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
DB 12 GCTGTTGGCG 3

RESULT 19
US-09-128-494-32/c
; Sequence 32, Application US/09128494
; Patent No. 6117848
; GENERAL INFORMATION:
; APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,494
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/889,296
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,734
FILING DATE: April 3, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09346
FILING DATE: October 1, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 958,134
FILING DATE: October 5, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/007,996
FILING DATE: January 21, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0213
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-128-494-32

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 20
US-09-248-386-32/c
Sequence 32, Application US/09248386
Patent No. 6359124
GENERAL INFORMATION:
APPLICANT: Monia, Brett P
APPLICANT: Frieler, Susan M
APPLICANT: Sanghvi, Yogesh S
APPLICANT: Cook, Phillip D
APPLICANT: Ecker, David J
TITLE OF INVENTION: Antisense Inhibition of RAS Gene with Chimeric and
FILE REFERENCE: IS183350
CURRENT APPLICATION NUMBER: US/09/248,386
CURRENT FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: 08/848,840
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 07/411,734
EARLIER FILING DATE: 1989-09-25
EARLIER APPLICATION NUMBER: PCT/US93/09346
EARLIER FILING DATE: 1993-10-01
EARLIER APPLICATION NUMBER: 07/715,196
EARLIER FILING DATE: 1991-06-14
EARLIER APPLICATION NUMBER: 07/958,134
EARLIER FILING DATE: 1992-10-05
EARLIER APPLICATION NUMBER: 08/007,996
EARLIER FILING DATE: 1993-01-21

EARLIER APPLICATION NUMBER: 07/703,619
EARLIER FILING DATE: 1991-05-21
EARLIER APPLICATION NUMBER: 08/040,903
EARLIER FILING DATE: 1993-03-31
EARLIER APPLICATION NUMBER: 07/040,526
EARLIER FILING DATE: 1987-04-20
EARLIER APPLICATION NUMBER: 08/174,379
EARLIER FILING DATE: 1993-12-28
EARLIER APPLICATION NUMBER: 08/040,933
EARLIER FILING DATE: 1993-03-31
EARLIER APPLICATION NUMBER: 08/300,072
EARLIER FILING DATE: 1994-09-02
EARLIER APPLICATION NUMBER: 08/039,979
EARLIER FILING DATE: 1993-03-30
EARLIER APPLICATION NUMBER: 08/395,168
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: 07/814,961
EARLIER FILING DATE: 1991-12-24
EARLIER APPLICATION NUMBER: 08/244,993
EARLIER FILING DATE: 1994-06-21
EARLIER APPLICATION NUMBER: 08/468,037
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6359124el Sequence
US-09-248-386-32

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
Db 12 GCTGTTGGCG 3

RESULT 21
US-08-363-240A-146
Sequence 146, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PREVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-146

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCGCTGTTGGCG 16
   ||||| :|: |||||
Db 3 GAGGUGUGCGCG 15

RESULT 22
US-08-585-684B-2148
; Sequence 2148, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
US-08-585-684B-2148

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGCGA 17
   ||||| :|: |||||
Db 1 AGGCAGUUGGCCA 13

RESULT 23
US-09-038-073-2148
; Sequence 2148, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-2148

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGCGA 17
   ||||| :|: |||||
Db 1 AGGCAGUUGGCCA 13

RESULT 24
US-09-081-646-81
; Sequence 81, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
```

; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081.646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-81

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGCGA 17
Db 2 ATGCTGTGTGTA 14

RESULT 25

US-09-081-646-770
; Sequence 770, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081.646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 770
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-770

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGCGA 17
Db 2 ATGCTGTGTGTA 14

RESULT 26

US-09-081-646-514
; Sequence 514, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664

; CURRENT APPLICATION NUMBER: US/09/081.646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-514

Query Match 51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGTGG 14
Db 1 CATGAGGATGTGG 14

RESULT 27

US-09-989-789-2478
; Sequence 2478, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 1 GAGGCTGTT 9

RESULT 28

US-08-651-835A-6
; Sequence 6, Application US/08651835A
; Patent No. 5707866
; GENERAL INFORMATION:
; APPLICANT: BRAKIER-GINGRAS, Lea
; APPLICANT: MELANCON, Pierre
; APPLICANT: COTE, Marc
; APPLICANT: PAYANT, Catherine
; TITLE OF INVENTION: USE OF DNA OLIGOMERS FOR INHIBITION OF
; TITLE OF INVENTION: HIV BY DECREASING RIBOSOMAL FRAMESHIFTING
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,835A
FILING DATE: 21-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,852
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,604
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 487-5800
TELEFAX: (201) 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-651-835A-6

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGCTGTTGGC 15
| | | | | | | | | |
Db 1 GCGGCTGCTGGC 12

RESULT 29

US-08-738-381-47/c
Sequence 47, Application US/08738381
Patent No. 6083694
GENERAL INFORMATION:
APPLICANT: John A. Hardy, Alison M. Goate
TITLE OF INVENTION: Method for Elucidation and
TITLE OF INVENTION: Detection of Polymorphisms, Splice Variants and
TITLE OF INVENTION: Proximal Coding Using Intronic Sequences of the
TITLE OF INVENTION: Mutations Alzheimer's S182 Gene
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,381
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/007,048
FILING DATE: October 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han

REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: NO
US-08-738-381-47

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTTG 13
| | | | | | | | | |
Db 12 TTGTTGCTGTTG 1

RESULT 30

US-09-216-584-20
Sequence 20, Application US/09216584
Patent No. 6548657
GENERAL INFORMATION:
APPLICANT: Alex, Burgin
APPLICANT: Leonid, Beigelman
APPLICANT: Laurent, Bellon
TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
FILE REFERENCE: MEH800-853-A; RPI 237/167
CURRENT APPLICATION NUMBER: US/09/216,584
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 09/094,381
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/068,212
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/049,002
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Accessible site within Kras transcript
US-09-216-584-20

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GCGTGTGGCGA 17
| | | | | | | | | |
Db 1 GCGTGTGGCGA 12

RESULT 31

US-10-032-307-70/c
Sequence 70, Application US/10032307
Patent No. 6683173
GENERAL INFORMATION:
APPLICANT: Dempcy, Robert O.
APPLICANT: Gall, Alexander A.
APPLICANT: Lokhov, Sergey G.
APPLICANT: Afonina, Irina A.
APPLICANT: Singer, Michael J.
APPLICANT: Kutyaev, Igor V.
APPLICANT: Vermeulen, Nicolaas M.J.

; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: T-m Leveling Methods
; FILE REFERENCE: 17682A-003630US
; CURRENT APPLICATION NUMBER: US/10/032.307
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/054,830
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/054,832
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/431,385
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: US 60/186,046
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/640,953
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/724,959
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/796,988
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:probe sequence
US-10-032-307-70

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTTGG 14
|||||
Db 12 TGAGGCGGTGG 1

RESULT 32
US-09-989-789-626
; Sequence 626, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-626

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
|||||
Db 1 GAGGCTGTTG 10

RESULT 33
US-08-959-853-5/c
; Sequence 5, Application US/08959853
; Patent No. 6090553

; GENERAL INFORMATION:
; APPLICANT: Robert S. Matson
; TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; ZIP: 92834-3100
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: WINDOWS 95 - WORDPERFECT 7.0
; SOFTWARE: ASCII (DOS) TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,853
; FILING DATE: herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: P.R. Harder
; REGISTRATION NUMBER: 20,022
; REFERENCE/DOCKET NUMBER: 45D-1566
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-6929
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-959-853-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
|||||
Db 11 GCTGTTGGCG 2

RESULT 34
US-09-613-826A-7
; Sequence 7, Application US/09613826A
; Patent No. 6440706
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: DIGITAL AMPLIFICATION
; FILE REFERENCE: 01107.00031
; CURRENT APPLICATION NUMBER: US/09/613,826A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/146,792
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-613-826A-7

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
|||||
Db 1 GCTGTTGGCG 10

RESULT 35

US-09-613-826A-13
; Sequence 13, Application US/09613826A
; Patent No. 6440706
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: DIGITAL AMPLIFICATION
; FILE REFERENCE: 01107.00031
; CURRENT APPLICATION NUMBER: US/09/613,826A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/146,792
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-613-826A-13

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 16
||| |||||
DB 1 GCTGTGGCG 10

RESULT 36

US-09-613-826A-14
; Sequence 14, Application US/09613826A
; Patent No. 6440706
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: DIGITAL AMPLIFICATION
; FILE REFERENCE: 01107.00031
; CURRENT APPLICATION NUMBER: US/09/613,826A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/146,792
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-613-826A-14

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 16
||| |||||
DB 1 GCTGTGGCG 10

RESULT 37

US-09-621-275-5
; Sequence 5, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60,084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-5

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCTG 10
||| |||||
DB 2 CTCGAGGCTG 11

RESULT 38

US-08-859-954-100
; Sequence 100, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 100:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-100

Query Match 44.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
Db 1 TTGAGGCT 8

RESULT 39

US-09-989-789-2152
; Sequence 2152, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2152
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2152

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGTGGCG 16
Db 2 TGTGTGGCG 9

RESULT 40

US-09-989-789-2326
; Sequence 2326, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2326

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
Db 1 CTGTTGGC 8

RESULT 41

US-09-989-789-2327
; Sequence 2327, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2327

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
Db 1 CTGTTGGC 8

RESULT 42

PCT-US94-05659-21
; Sequence 21, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF' RESPONSIVE ELEMENT, TNF'-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05659
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 PF
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-05659-21

Query Match      44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGCTGTT 12
Db 1 AGCTGTT 8

RESULT 43
US-08-259-148A-31/c
; Sequence 31, Application US/08259148A
; Patent No. 5741490
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Twu, Jr-Shin
; APPLICANT: Purdy, Michael A.
; APPLICANT: Tam, Albert W.
; APPLICANT: Krawczynski, Krzysztof Z.
; APPLICANT: Yarbough, Patrice D.
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,148A
; FILING DATE: 13-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 822,335
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,888
; FILING DATE: 05-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 420,921
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 367,486
; FILING DATE: 16-JUN-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 336,672
; FILING DATE: 11-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 208,997
; FILING DATE: 17-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0093.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-08-259-148A-31

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTGCGCA 17
Db 9 GTTGCGCA 2

RESULT 44
US-07-876-941A-47/c
; Sequence 47, Application US/07876941A
; Patent No. 5885768
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Tam, Albert W.
; APPLICANT: Mitchell, Carl
; TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,941A
; FILING DATE: 01-MAY-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 822,335
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,888
; FILING DATE: 05-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 420,921
; FILING DATE: 13-OCTOBER-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 367,486
; FILING DATE: 16-JUNE-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 336,672
; FILING DATE: 11-APRIL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 208,997
; FILING DATE: 17-JUNE-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0093.33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 47:
```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-07-876-941A-47

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTGGCGA 17
|||||||
Db 9 GTTGGCGA 2

RESULT 45
US-08-388-353-733/c
; Sequence 733, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 733:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-733

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
|||||||
Db 10 TTGAGGCT 3

RESULT 46
US-08-388-353-734/c
; Sequence 734, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 734:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-734

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
|||||||
Db 9 TTGAGGCT 2

RESULT 47
US-08-388-353-735/c
; Sequence 735, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York

/ COUNTRY: United States
/ ZIP: 11530
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/388,353
/ FILING DATE: 14-FEB-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DiGiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9606
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ TELEX: 230 901 SANS UR
/ INFORMATION FOR SEQ ID NO: 735:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-735

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
Db 8 TTGAGGCT 1

RESULT 48
US-08-488-551B-733/c
/ Sequence 733, Application US/08488551B
/ Patent No. 6015661
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas J. Deacon
/ APPLICANT: Dale A. McPhee
/ APPLICANT: David Cooper
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
/ NUMBER OF SEQUENCES: 841
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
/ STREET: 400 GARDEN CITY PLAZA
/ CITY: GARDEN CITY
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 11530-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,551B
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PM3864 (AU)
/ FILING DATE: 14-FEB-1994
/ APPLICATION NUMBER: PM4002 (AU)
/ FILING DATE: 21-FEB-1994
/ APPLICATION NUMBER: PM0284 (AU)
/ FILING DATE: 23-DEC-1994
/ APPLICATION NUMBER: US 08/388,353
/ FILING DATE: 14-FEB-1995
/ APPLICATION NUMBER: PM3021/95
/ FILING DATE: 17-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FRANK S. DIGIGLIO
/ REFERENCE/DOCKET NUMBER: 9606Z
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ INFORMATION FOR SEQ ID NO: 734:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA

/ ATTORNEY/AGENT INFORMATION:
/ NAME: FRANK S. DIGIGLIO
/ REFERENCE/DOCKET NUMBER: 9606Z
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ INFORMATION FOR SEQ ID NO: 733:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-488-551B-733

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
Db 10 TTGAGGCT 3

RESULT 49
US-08-488-551B-734/c
/ Sequence 734, Application US/08488551B
/ Patent No. 6015661
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas J. Deacon
/ APPLICANT: Dale A. McPhee
/ APPLICANT: David Cooper
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
/ NUMBER OF SEQUENCES: 841
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
/ STREET: 400 GARDEN CITY PLAZA
/ CITY: GARDEN CITY
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 11530-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,551B
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PM3864 (AU)
/ FILING DATE: 14-FEB-1994
/ APPLICATION NUMBER: PM4002 (AU)
/ FILING DATE: 21-FEB-1994
/ APPLICATION NUMBER: PM0284 (AU)
/ FILING DATE: 23-DEC-1994
/ APPLICATION NUMBER: US 08/388,353
/ FILING DATE: 14-FEB-1995
/ APPLICATION NUMBER: PM3021/95
/ FILING DATE: 17-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FRANK S. DIGIGLIO
/ REFERENCE/DOCKET NUMBER: 9606Z
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ INFORMATION FOR SEQ ID NO: 734:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA

US-08-488-551B-734

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
|||||
Db 9 TTGAGGCT 2

RESULT 50

US-08-488-551B-735/c
; Sequence 735, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 735:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-735

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
|||||
Db 8 TTGAGGCT 1

RESULT 51

US-08-308-892A-8/c

; Sequence 8, Application US/08308892A
; Patent No. 5500341
; GENERAL INFORMATION:
; APPLICANT: Spears, Patricia A.
; TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF
; MYCOBACTERIUM KANSASII
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,892A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3128
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-308-892A-8

Query Match 44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
|||||
Db 11 CTGTGGC 4

RESULT 52

US-08-597-467-15/c
; Sequence 15, Application US/08597467
; Patent No. 5824787
; GENERAL INFORMATION:
; APPLICANT: Singer, Paul A.
; TITLE OF INVENTION: POLYNUCLEOTIDE SIZING REAGENT
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,467
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,901
; FILING DATE: 03-DEC-1993

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..11
; US-08-597-467-15

Query Match 44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGGC 8
Db 9 CTTGAGGC 2

RESULT 53
US-08-962-790-3/c
; Sequence 3, Application US/08962790
; Patent No. 6043035
; GENERAL INFORMATION:
; APPLICANT: BERTINA, ROGER M.
; APPLICANT: POORT, SWIBERTUS R.
; APPLICANT: ROSENDAAL, FRITS R.
; APPLICANT: REITSMA, PIETER H.
; TITLE OF INVENTION: A METHOD FOR DETERMINING A RISK FACTOR FOR THROMBOSIS
; FILE REFERENCE: T/97317
; CURRENT APPLICATION NUMBER: US/08/962,790
; CURRENT FILING DATE: 1997-11-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
; US-08-962-790-3

Query Match 44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGGCT 9
Db 11 TTGAGGCT 4

RESULT 54
US-08-205-507-7
; Sequence 7, Application US/08205507
; Patent No. 5543507
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook, Muthiah Manoharan, and Thomas W.
; APPLICANT: Bruice
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5543507ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA

; ATTORNEY/AGENT INFORMATION:
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,507
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: March 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; US-08-205-507-7

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 55
US-08-271-880A-206
; Sequence 206, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,880A
; FILING DATE: July 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: two
```



```
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-880A-206

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGT 11
Db 1 CTTGAGGAGGT 11

RESULT 56
US-08-295-743-10
; Sequence 10, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
```

```
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a 2'-O-(octylhydrazino) functionality
US-08-295-743-10

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 57
US-08-295-743-12
; Sequence 12, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a octyl-hydroxylamine functionality
US-08-295-743-12

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 58
```

```
US-08-295-743-13
; Sequence 13, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,743
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a penty1-N-semicarbazide
; OTHER INFORMATION: functionality
US-08-295-743-13
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 59
US-08-295-743-14
; Sequence 14, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,743
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a penty1-N-semicarbazide
; OTHER INFORMATION: functionality
US-08-295-743-13
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 60
US-08-295-743-15
; Sequence 15, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,743
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate an ethyl hydrazide functionality
US-08-295-743-14
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11
```

```
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a heptan-7-ol functionality
US-08-295-743-15

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      1 GGCTGUCTGCG 11

RESULT 61
US-08-295-743-23
; Sequence 23, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESSEE: and No. 5719271ris
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a heptan-7-ol functionality
US-08-295-743-15

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      1 GGCTGUCTGCG 11

RESULT 62
US-08-295-743-24
; Sequence 24, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: nucleotide modified to
; OTHER INFORMATION: incorporate a heptan-7-ol functionality
US-08-295-743-24

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      1 GGCTGUCTGCG 11

RESULT 63
US-08-295-743-25
```

```
; OTHER INFORMATION: 2'-O-(hexylamino) uridine
; OTHER INFORMATION: nucleotide
US-08-295-743-23

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      1 GGCTGUCTGCG 11

RESULT 62
US-08-295-743-24
; Sequence 24, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: 2'-O-(hexylamino) uridine
; OTHER INFORMATION: nucleotide
US-08-295-743-24

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGGCG 16
Db      1 GGCTGUCTGCG 11

RESULT 63
US-08-295-743-25
```

; Sequence 25, Application US/08295743
; Patent No. 5719271
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5719271ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,743
; FILING DATE: 30-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: 2'-deoxyuridine
; US-08-295-743-25

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 1 GGCTGCTGCG 11

RESULT 64
US-08-910-408-206
; Sequence 206, Application US/08910408
; Patent No. 5972704
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,880
; FILING DATE: July 7, 1994
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-910-408-206
; Query Match 43.3%; Score 7.8; DB 1; Length 11;
; Best Local Similarity 81.8%; Pred. No. 48;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CTTGAGGCTGT 11
Db 1 CTTGAGGAGGT 11
RESULT 65
US-09-249-215-206
; Sequence 206, Application US/09249215
; Patent No. 6159692
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,215
; FILING DATE: 12-Feb-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,408
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-249-215-206

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTGT 11
Db 1 CTTGAGGAGGT 11

RESULT 66
US-09-303-586-14
; Sequence 14, Application US/09303586
; Patent No. 6369209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form Confirmation
; FILE REFERENCE: IGIS3310
; CURRENT APPLICATION NUMBER: US/09/303,586
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (6)-(7)
; OTHER INFORMATION: 2' aminolinker linkage
US-09-303-586-14

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 67
US-09-249-155A-245/c
; Sequence 245, Application US/09249155A
```

```
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-245

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTT 12
Db 11 TTGACCTGTT 1

RESULT 68
US-09-249-155A-318
; Sequence 318, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-318

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
Db 1 GTGGGTGTGG 11

RESULT 69
US-09-409-926-16
; Sequence 16, Application US/09409926
; Patent No. 6617442
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter F.
; APPLICANT: Wu, Hongjiang
```

; TITLE OF INVENTION: Human Nkase H1 and Oligonucleotide Compositions Thereof
; FILE REFERENCE: ISIS4186
; CURRENT APPLICATION NUMBER: US/09/409,926
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: No. 6617442el Sequence
US-09-409-926-16

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 70
PCT-US93-02059-10
; Sequence 10, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
PCT-US93-02059-10

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 71
PCT-US93-02059-12
; Sequence 12, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
PCT-US93-02059-12

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||: |||
Db 1 GGCTGUCTGCG 11

RESULT 72
PCT-US93-02059-13
; Sequence 13, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA

```
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; NAME: Joseph Lucci
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-13

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 73
PCT-US93-02059-14
; Sequence 14, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; NAME: Joseph Lucci
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-15

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 75
PCT-US93-02059-21
```

```
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-14

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 74
PCT-US93-02059-15
; Sequence 15, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; NAME: Joseph Lucci
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-15

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11

RESULT 75
PCT-US93-02059-21
```

```
; Sequence 21, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-21
```

```
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11
```

```
RESULT 76
PCT-US93-02059-22
; Sequence 22, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
; PCT-US93-02059-22
```

```
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 6 GGCTGTTGGCG 16
Db 1 GGCTGUCTGCG 11
```

```
RESULT 77
PCT-US93-02059-24
; Sequence 24, Application PC/TUS9302059
; GENERAL INFORMATION:
; APPLICANT: David Ecker
; TITLE OF INVENTION: Covalently Cross-Linked
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02059
; FILING DATE: 19930305
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 846,376
; FILING DATE: March 5, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: no
```


PCT-US93-02059-24

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16
|||||: |||
Db 1 GGCTGCTGCG 11

RESULT 78

US-08-651-835A-7
; Sequence 7, Application US/08651835A
; Patent No. 5707866
; GENERAL INFORMATION:
; APPLICANT: BRAKIER-GINGRAS, Lea
; APPLICANT: MELANCON, Pierre
; APPLICANT: COTE, Marc
; APPLICANT: PAYANT, Catherine
; TITLE OF INVENTION: USE OF DNA OLIGOMERS FOR INHIBITION OF
; TITLE OF INVENTION: HIV BY DECREASING RIBOSOMAL FRAMESHIFTING
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651.835A
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,852
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,604
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELEPHONE: (201) 487-5800
; TELEFAX: (201) 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-651-835A-7

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGG 14
|||||: |||
Db 2 GCGGCTGCTGG 12

RESULT 79

US-08-358-171-7/c
; Sequence 7, Application US/08358171
; Patent No. 5763578
; GENERAL INFORMATION:
; APPLICANT: FONG, Henry K.W.
; TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
; TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THERETO
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,171
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: FONG=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-358-171-7

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18
|||||: |||
Db 12 CTGTTGGGAGAC 2

RESULT 80

US-09-090-947-7/c
; Sequence 7, Application US/09090947
; Patent No. 6008338
; GENERAL INFORMATION:
; APPLICANT: FONG, Henry K.W.
; TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
; TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THERETO
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,947

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/358,171
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: FONG-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-090-947-7

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CTGTGGCGAC 18
||| ||| |||
Db 12 CTGTGGGAGAC 2

RESULT 81
US-08-874-825-34
; Sequence 34, Application US/08874825
; Patent No. 6057101
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Weijia
; APPLICANT: Knight, James
; APPLICANT: Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-874-825-34

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGA 17
||| ||| |||
Db 2 GCTGTGGTGA 12

RESULT 82
US-08-663-824-34
; Sequence 34, Application US/08663824
; Patent No. 6083693
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
; FILE REFERENCE: 7934-006
; CURRENT APPLICATION NUMBER: US/08/663,824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-663-824-34

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGA 17
||| ||| |||
Db 2 GCTGTGGTGA 12

RESULT 83
US-09-281-418-57
; Sequence 57, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fr
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mic
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 57
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-281-418-57
```

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AGCCTGTGGC 11
|||||

RESULT 84
US-09-281-418-189
; Sequence 189, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA R
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 189
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-189

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGGC 15
Db 1 AAGCTGTGGC 11
|||||

RESULT 85
US-09-231-303-34
; Sequence 34, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-231-303-34

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGCGCA 17
Db 2 GCTGTGCGTA 12
|||||

RESULT 86
US-09-989-789-2508
; Sequence 2508, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2508
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2508

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 1 GAGGCTCTT 9
|||||

RESULT 87
US-07-783-705A-14
; Sequence 14, Application US/07783705A
; Patent No. 5429939
; GENERAL INFORMATION:
; APPLICANT: Misawa, No. 5429939ihiko
; APPLICANT: Kobayashi, Kazuo
; APPLICANT: Nakamura, Katsumi
; APPLICANT: Yamano, Shigeyuki
; TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE
; TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61 Street
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/783,705A
; FILING DATE: 19911023
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-103078
; FILING DATE: 21-APR-1989
; APPLICATION NUMBER: JP 2-53225
; FILING DATE: 05-MAR-1990
; APPLICATION NUMBER: US 07/519,011
; FILING DATE: 19-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwadron, Janet I.
; REGISTRATION NUMBER: 33,778

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-708-1935
; TELEFAX: 212-246-5959
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-07-783-705A-14

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 1 GCAGTTGGC 9

RESULT 88
US-08-388-353-72/c
; Sequence 72, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-73

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 9 GCTGCTGGC 1

RESULT 90
US-08-488-551B-72/c
; Sequence 72, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-708-1935
; TELEFAX: 212-246-5959
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-07-783-705A-14

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 1 GCAGTTGGC 9

RESULT 88
US-08-388-353-72/c
; Sequence 72, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-73

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGGC 15
Db 9 GCTGCTGGC 1

RESULT 90
US-08-488-551B-72/c
; Sequence 72, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)

FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)

FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353

FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95

ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-72
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGCG 15
|||||
Db 10 GCTGTTGCG 2

RESULT 91

US-08-488-551B-73/c
Sequence 73, Application US/08488551B
Patent No. 6015661

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon

APPLICANT: Dale A. McPhee

APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 11530-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PM3864 (AU)

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-73
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTTGCG 15
|||||
Db 9 GCTGTTGCG 1

RESULT 92

US-08-522-384-10/c
Sequence 10, Application US/08522384
Patent No. 6110667

GENERAL INFORMATION:

APPLICANT: LOPEZ-NIETO, CARLOS E

APPLICANT: NIGAM, SANJAY KUMAR

TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR

FILE REFERENCE: 2458-4029

CURRENT APPLICATION NUMBER: US/08/522,384

CURRENT FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 10

LENGTH: 10

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Primer

US-08-522-384-10

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
|||||
Db 9 TTGAGGATG 1

RESULT 93

US-08-522-384-82/c
Sequence 82, Application US/08522384
Patent No. 6110667

GENERAL INFORMATION:

APPLICANT: LOPEZ-NIETO, CARLOS E

APPLICANT: NIGAM, SANJAY KUMAR

TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR

FILE REFERENCE: 2458-4029

CURRENT APPLICATION NUMBER: US/08/522,384

CURRENT FILING DATE: 1996-11-15

; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-82

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
||| |||
Db 9 GTTGGTGCAC 1

RESULT 94
US-08-997-897-6
; Sequence 6, Application US/08997897C
; Patent No. 6114514
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, RANJANA
; APPLICANT: KUMAR, DEEPAK
; APPLICANT: SRIVASTAVA, BRAHM SHANKER
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
; FILE REFERENCE: u011469-7
; CURRENT APPLICATION NUMBER: US/08/997,897C
; CURRENT FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-08-997-897-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
||| |||
Db 1 TTGAGGATG 9

RESULT 95
US-09-156-836B-6
; Sequence 6, Application US/09156836B
; Patent No. 6242585
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Ranjana
; APPLICANT: Kumar, Deepak
; APPLICANT: Srivastava, Brahm Shanker
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
; FILE REFERENCE: U 011876-4
; CURRENT APPLICATION NUMBER: US/09/156,836B
; CURRENT FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 08/997,897
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-156-836B-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTG 10
||| |||
Db 1 TTGAGGATG 9

RESULT 96
US-09-398-499-50
; Sequence 50, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-50

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGA 17
||| |||
Db 2 TGCTGGCGA 10

RESULT 97
US-09-914-259-123/c
; Sequence 123, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-123

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
||| |||
Db 10 CTGAGGCT 2

RESULT 98
US-09-508-753B-219
; Sequence 219, Application US/09508753B
; Patent No. 6544736

GENERAL INFORMATION:
; APPLICANT: AKIRA SHIMAMOTO
; APPLICANT: YASUHIRO FURUICHI
; APPLICANT: YUKO SHIBATA
; APPLICANT: HIROKO FUNAKI
; APPLICANT: EIJI OHARA
; APPLICANT: MASANORI WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 219
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-219

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCG 16
||| |||||
Db 2 CTTTGGCG 10

RESULT 99
US-09-508-753B-369/c
; Sequence 369, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: AKIRA SHIMAMOTO
; APPLICANT: YASUHIRO FURUICHI
; APPLICANT: YUKO SHIBATA
; APPLICANT: HIROKO FUNAKI
; APPLICANT: EIJI OHARA
; APPLICANT: MASANORI WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 369
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-369

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
||| |||||
Db 9 GAGGCTATT 1

RESULT 100
US-10-042-111-20
; Sequence 20, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jingding

; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-20

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
||| |||||
Db 2 GAGGCTGTT 10

RESULT 101
US-09-989-789-1278
; Sequence 1278, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1278

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
||| |||||
Db 2 AGGCTGTTG 10

RESULT 102
US-09-621-275-1
; Sequence 1, Application US/09621275
; Patent No. 6686150
; GENERAL INFORMATION:
; APPLICANT: Blackburn, Gary
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC
; FILE REFERENCE: A-67643-2/RET/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/621,275
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/144,698
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/238,351
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,034

```

; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60,084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/028,102
; PRIOR FILING DATE: 1996-10-09
; PRIOR APPLICATION NUMBER: 60/073,011
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-1

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTTGAGGCT 9
        ||| |||||
Db      2 CTCGAGGCT 10

RESULT 103
US-08-481-658B-82/c
; Sequence 82, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; APPLICANT: Zavada, Jan

```

```

; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-481-658B-82

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TGAGGCTGT 11
        ||| |||||
Db      11 TGAGCCTGT 3

RESULT 104
US-08-477-504A-82/c
; Sequence 82, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-477-504A-82

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 TGAGGCTGT 11
        ||| |||||
Db      11 TGAGCCTGT 3

RESULT 105
US-08-486-756A-82/c
; Sequence 82, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan

```


APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 3' acceptor consensus splice sequence
US-08-486-756A-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
||| ||||
Db 11 TGAGCCTGT 3

RESULT 106
US-08-485-862B-82/c
Sequence 82, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 3' acceptor consensus splice sequence
US-08-485-862B-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
||| ||||
Db 11 TGAGCCTGT 3

RESULT 107
US-08-787-739-82/c
Sequence 82, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-787-739-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 108
US-08-487-077A-82/c
; Sequence 82, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-487-077A-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 109
US-08-485-863A-82/c
; Sequence 82, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-485-863A-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 110
US-07-875-790B-15
; Sequence 15, Application US/07875790B
; Patent No. 6183984
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Fuchs, Elaine
; TITLE OF INVENTION: SEQUENCES FOR PROMOTING EPIDERMAL
;   CELL-SPECIFIC TRANSCRIPTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durke
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/875,790B
; FILING DATE: April 29, 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-875-790B-15

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
Db 3 CCTGAGGCT 11
|||||

RESULT 111
US-08-485-049D-82/c
; Sequence 82, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,049D
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
```

```
;
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
; US-08-485-049D-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGGCTGT 3
|||||

RESULT 112
US-09-178-115-82/c
; Sequence 82, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
; US-09-178-115-82
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 113
US-09-177-776-82/c
; Sequence 82, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
US-09-177-776-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 114
US-09-179-162A-3/c
; Sequence 3, Application US/09179162A
; Patent No. 6485901
; GENERAL INFORMATION:
; APPLICANT: Gildea, Brian D.
; APPLICANT: Coull, James M.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Fiandaca, Mark J.
; TITLE OF INVENTION: Methods, Kits and Compositions Pertaining To Linear
; TITLE OF INVENTION: Beacons

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
Db 11 TGAGCCTGT 3

RESULT 115
US-09-249-155A-37/c
; Sequence 37, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-37

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
Db 11 GTTGGTGAC 3

RESULT 116
US-09-249-155A-266/c
; Sequence 266, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
```

```
FILE REFERENCE: BP9703US
; CURRENT APPLICATION NUMBER: US/09/179,162A
; CURRENT FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/063,283
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: 5'Fluorescein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: 3' Dabcyl
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PROBE OR TARGET
US-09-179-162A-3
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 7 GCTGTTGTC 15
Db 9 GCTGTTGTC 1
```

```
RESULT 115
US-09-249-155A-37/c
; Sequence 37, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-37
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 10 GTTGGCGAC 18
Db 11 GTTGGTGAC 3
```

```
RESULT 116
US-09-249-155A-266/c
; Sequence 266, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
```

; TITLE OF INVENTION: Compositions and Methods for Wound
 ; TITLE OF INVENTION: Healing
 ; FILE REFERENCE: 00486.78503
 ; CURRENT APPLICATION NUMBER: US/09/249,155A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,737
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/097,937
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: US 60/102,051
 ; PRIOR FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 346
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 266
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-249-155A-266

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGAC 18
 |||||
 Db 11 GTTGGTGAC 3

RESULT 117

US-09-950-459-3/c
 ; Sequence 3, Application US/09950459
 ; Patent No. 6649349
 ; GENERAL INFORMATION:
 ; APPLICANT: Gildea, Brian D.
 ; APPLICANT: Coull, James M.
 ; APPLICANT: Hyldig-Nielsen, Jens J.
 ; APPLICANT: Flindaca, Mark J.
 ; TITLE OF INVENTION: Methods, Kits and Compositions Pertaining To Linear
 ; FILE REFERENCE: BP9703US-DV1
 ; CURRENT APPLICATION NUMBER: US/09/950,459
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/063,283
 ; PRIOR FILING DATE: 1997-10-27
 ; PRIOR APPLICATION NUMBER: 09/179,162
 ; PRIOR FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)
 ; OTHER INFORMATION: 5'Fluorescein
 ; NAME/KEY: misc_feature
 ; LOCATION: (11)
 ; OTHER INFORMATION: 3' Dabcyl
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 ; OTHER INFORMATION: PROBE OR TARGET
 US-09-950-459-3

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGC 15
 |||||
 Db 9 GCTGTGGC 1

RESULT 118

US-08-253-575-10
 ; Sequence 10, Application US/08253575
 ; Patent No. 5705375
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN OOVEN, ALBERT J.J.
 ; APPLICANT: RIETVELD, KILJUN
 ; APPLICANT: QUAX, WILHELMUS J.
 ; APPLICANT: VAN DEN ELZEN, PETRUS J.M.
 ; APPLICANT: PEN, JAN
 ; APPLICANT: HOKEMA, ANDREAS
 ; APPLICANT: SIJMONS, PETER C.
 ; TITLE OF INVENTION: TRANSGENIC PLANTS HAVING A MODIFIED
 ; TITLE OF INVENTION: CARBOHYDRATE CONTENT
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/253,575
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/849,422
 ; FILING DATE: 12-JUN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20033.00
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-253-575-10

Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGAC 18
 |||||
 Db 3 TGGCGAC 9

RESULT 119

US-09-989-789-531
 ; Sequence 531, Application US/09989789
 ; Patent No. 6588746
 ; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 531
 ; LENGTH: 9

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-531

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTGG 14
Db      2 CTGTGG 8
|||||

RESULT 120
US-09-989-789-2126
; Sequence 2126, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2126
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2126

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8
|||||

RESULT 121
US-09-989-789-2127
; Sequence 2127, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2127
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2127

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8
|||||

RESULT 122
US-09-989-789-2128
; Sequence 2128, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2128
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2128

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8
|||||

RESULT 123
US-09-989-789-2129
; Sequence 2129, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2129
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2129

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
Db      1 GAGGCTG 7
|||||

RESULT 124
US-09-263-790-27
; Sequence 27, Application US/09263790
; Patent No. PPI2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
```

```
Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8
|||||

RESULT 122
US-09-989-789-2128
; Sequence 2128, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2128
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2128

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTGT 11
Db      2 AGGCTGT 8
|||||

RESULT 123
US-09-989-789-2129
; Sequence 2129, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2129
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-2129

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
Db      1 GAGGCTG 7
|||||

RESULT 124
US-09-263-790-27
; Sequence 27, Application US/09263790
; Patent No. PPI2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
```

;; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
;; FILE REFERENCE: 2761-0120P
;; CURRENT APPLICATION NUMBER: US/09/263,790
;; CURRENT FILING DATE: 1999-03-05
;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 27
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: OPT 07 Primer - Used to develop the unique RAPD profiles of the
;; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-27

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||
Db 4 AGGCTGT 10

RESULT 125

US-09-721-777-7
;; Sequence 7, Application US/09721777
;; Patent No. P13279
;; GENERAL INFORMATION:
;; APPLICANT: Khanuja, Suman Preet Singh
;; APPLICANT: Kumar, Sushil
;; APPLICANT: Shasany, Ajit Kumar
;; APPLICANT: Dhawan, Sunita
;; APPLICANT: Darokar, Mahendra Pandurang
;; APPLICANT: Naqvi, Ali Arif
;; APPLICANT: Dhawan, Om Parkash
;; APPLICANT: Singh, Anil Kumar
;; APPLICANT: Patra, Nirmal Kumar
;; APPLICANT: Bahl, Janak Raj
;; APPLICANT: Bansal, Ram Prakash
;; TITLE OF INVENTION: Mint Plant Named Saksham
;; FILE REFERENCE: 033166-002
;; CURRENT APPLICATION NUMBER: US/09/721,777
;; CURRENT FILING DATE: 2000-11-27
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: OPT primer
US-09-721-777-7

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||
Db 4 AGGCTGT 10

RESULT 126

US-08-446-646-20
;; Sequence 20, Application US/08446646
;; Patent No. 5726038
;; GENERAL INFORMATION:
;; APPLICANT: Christiansen, Lars
;; APPLICANT: Petersen, Jens G.
;; TITLE OF INVENTION: A DNA Construct Encoding the YAP3 Signal
;; TITLE OF INVENTION: Peptide
;; NUMBER OF SEQUENCES: 24

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NO. 57260380 No. 5726038disk of No. 5726038th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; FILING DATE: 25-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 3987.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; ORIGINAL SOURCE:
;; ORGANISM: synthetic
US-08-446-646-20

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGCGAC 18
|||||
Db 3 TGGCGAC 9

RESULT 127

US-08-545-253A-16/c
;; Sequence 16, Application US/08545253A
;; Patent No. 5908978
;; GENERAL INFORMATION:
;; APPLICANT: O'Malley, David M.
;; APPLICANT: Sederoff, Ronald R.
;; APPLICANT: Grattapaglia, Dario
;; APPLICANT: Henry V. Amerson
;; APPLICANT: Phillip Wilcox
;; APPLICANT: E. George Kuhlman
;; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
;; TITLE OF INVENTION: SELECTION IN
;; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kenneth D. Sibley
;; STREET: Post Office Drawer 34009
;; CITY: Charlotte
;; STATE: No. 5908978th Carolina
;; COUNTRY: U.S.A.
;; ZIP: 28234
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: US/08/545,253A

```
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sibley, Kenneth D.
;; REGISTRATION NUMBER: 31,665
;; REFERENCE/DOCKET NUMBER: 5051-281
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 881-3140
;; TELEFAX: (919) 881-3175
;; TELEX: 575102
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-08-545-253A-16

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 7 AGGCTGT 1

RESULT 128
US-08-388-353-732/c
; Sequence 732, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 732:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-732

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGC 8
Db 7 TTGAGGC 1

RESULT 130
US-08-488-551B-732/c
; Sequence 732, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 732:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-732

Query Match 38.9%; Score 7; DB 1; Length 10;
```

```
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
Db 10 TGAGGCT 4

RESULT 129
US-08-388-353-736/c
; Sequence 736, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 736:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-736

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGC 8
Db 7 TTGAGGC 1

RESULT 130
US-08-488-551B-732/c
; Sequence 732, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 732:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-732

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTGAGGCT 9
Db 10 TTGAGGCT 4

RESULT 131
US-08-488-551B-736/c
Sequence 736, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 736:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-736
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTGAGGC 8
Db 7 TTGAGGC 1
RESULT 132
US-08-719-337-16/c
Sequence 16, Application US/08719337
Patent No. 6054634
GENERAL INFORMATION:
APPLICANT: O'Malley, David M.
APPLICANT: Sederoff, Ronald R.
APPLICANT: Grattapaglia, Dario
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
WOODY PERENNIALS USING GENETIC MARKERS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 6054634th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,337
FILING DATE: 25-SEP-1996
CLASSIFICATION: 047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175

TELEX: 575102
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-719-337-16

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 7 AGGCTGT 1
|||||

RESULT 133
US-08-522-384-4/c

; Sequence 4, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522.384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-4

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTTG 13
Db 7 GCTGTTG 1
|||||

RESULT 134
US-08-522-384-86/c

; Sequence 86, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522.384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-86

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GCTGTTG 13
Db 8 GCTGTTG 2
|||||

RESULT 135

US-09-255-432-2
; Sequence 2, Application US/09255432
; Patent No. 6258537
; GENERAL INFORMATION:
; APPLICANT: Keinath, et al.
; TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Judy C. Jarecki-Black, Ph.D.
; ADDRESSEE: Dority & Manning, P.A.
; STREET: 700 E. No. 6258537th Street, Suite 15
; CITY: Greenville
; STATE: South Carolina
; COUNTRY: USA
; ZIP: 29601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS Dos; Windows 95
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,432
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA: Claims Priority to Provisional Application
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy C. Jarecki-Black, Ph.D.
; REGISTRATION NUMBER: P44,170
; REFERENCE/DOCKET NUMBER: CXU-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (864) 271-1592
; TELEFAX: (864) 233-7342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other Nucleic Acid
; DESCRIPTION: Oligonucleotide Primer
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE: Operon Technologies (Alameda, CA)
; IMMEDIATE SOURCE: Operon Technologies
; POSITION IN GENOME: No. 6258537 Applicable
; UNITS:
; FEATURE:
; OTHER INFORMATION: Commercially Available Primer

; PUBLICATION INFORMATION:
; AUTHORS: Keinath, Anthony P., Farnham, M. W., and Zitter, T. A.
; TITLE: Morphological, Pathological, and Genetic Differentiation of
; JOURNAL: Phytopathology
; VOLUME: 85
; ISSUE: 3
; PAGES:
; DATE: 1995
US-09-255-432-2

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
Db 7 AGGCTGT 1
|||||

```
Db 4 AGGCTGT 10

US-09-154-750A-16
; Sequence 16, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-16

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
| | | | |
Db 1 AGGCTGT 7

RESULT 137
US-09-154-750A-19/c
; Sequence 19, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-19

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGC 15
| | | | |
Db 10 TGTGGC 4

RESULT 138
US-09-989-789-556
; Sequence 556, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 556
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-556

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGC 15
| | | | |
Db 2 TGTGGC 8

RESULT 139
US-09-989-789-1279
; Sequence 1279, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1279

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTG 10
| | | | |
Db 4 GAGGCTG 10

RESULT 140
US-09-989-789-1308
; Sequence 1308, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 10
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1308

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
      |||||
Db      4 GAGGCTG 10

RESULT 141
US-09-989-789-1313
; Sequence 1313, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1313
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1313

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
      |||||
Db      4 GAGGCTG 10

RESULT 142
US-09-989-789-1624
; Sequence 1624, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1624

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 GAGGCTG 10
      |||||
Db      4 GAGGCTG 10

RESULT 143
US-09-989-789-1625
; Sequence 1625, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1625

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAGGCTG 10
      |||||
Db      4 GAGGCTG 10

RESULT 144
US-09-758-073-2
; Sequence 2, Application US/09758073
; Patent No. 6610487
; GENERAL INFORMATION:
; APPLICANT: Keinath, et al.
; TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in
; TITLE OF INVENTION: Plants Using a Polymerase Chain Reaction Assay
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Judy C. Jarecki-Black, Ph.D.
; ADDRESSEE: Dority & Manning, P.A.
; STREET: 700 E. No. 6610487th Street, Suite 15
; CITY: Greenville
; STATE: South Carolina
; COUNTRY: USA
; ZIP: 29601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS Dos; Windows 95
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,073
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/078,103
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy C. Jarecki-Black, Ph.D.
; REGISTRATION NUMBER: P44,170
; REFERENCE/DOCKET NUMBER: CXU-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (864) 271-1592
; TELEFAX: (864) 233-7342
; INFORMATION FOR SEQ ID NO: 2;
```

SEQUENCE CHARACTERISTICS:
LENGTH: 10 Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other Nucleic Acid
DESCRIPTION: Oligonucleotide Primer
HYPOTHETICAL: NO
ANTI-SENSE: No
ORIGINAL SOURCE: Operon Technologies (Alameda, CA)
IMMEDIATE SOURCE: Operon Technologies
POSITION IN GENOME: No. 6610487 Applicable
UNITS:
FEATURE:
OTHER INFORMATION: Commercially Available Primer
PUBLICATION INFORMATION:
AUTHORS: Keinath, Anthony P., Farnham, M. W., and Zitter, T.
AUTHORS: A.
TITLE: Morphological, Pathological, and Genetic Differentiation
TITLE: of
TITLE: Cucurbits
JOURNAL: Phytopathology
VOLUME: 85
ISSUE: 3
PAGES:
DATE: 1995
US-09-758-073-2

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTGT 11
|||||
Db 4 AGGCTGT 10

RESULT 145
US-09-869-080-3/c
; Sequence 3, Application US/09869080
; Patent No. 6637366
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific And Industrial Research Organisation
; APPLICANT: Bedding, Robin A
; APPLICANT: Driver, Felice
; APPLICANT: Vella, Jacqueline
; APPLICANT: Butler, Karen L
; APPLICANT: Clark, Simone D
; TITLE OF INVENTION: Nematode Biopesticide
; FILE REFERENCE: 050179-0092
; CURRENT APPLICATION NUMBER: US/09/869,080
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/AU99/01152
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PP7927
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Heterorhabditis zealandica
US-09-869-080-3

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCT 9
|||||
Db 9 TGAGGCT 3

RESULT 146
US-07-651-710A-5
; Sequence 5, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAP-1 binding motif
US-07-651-710A-5

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCG 16
|||||
Db 1 GTTGTGGCG 10

RESULT 147
US-07-651-710A-13
; Sequence 13, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206

APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110
LENGTH: 10
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-110

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGT 11
Db 1 TGGTGGCTGT 10

RESULT 151

US-07-875-790B-14
Sequence 14, Application US/07875790B
Patent No. 6183984

GENERAL INFORMATION:
APPLICANT: Fuchs, Elaine
TITLE OF INVENTION: SEQUENCES FOR PROMOTING EPIDERMAL
TITLE OF INVENTION: CELL-SPECIFIC TRANSCRIPTION
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durke
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/875,790B
FILING DATE: April 29, 1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.

REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:046
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-07-875-790B-14

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTGTGGC 15
Db 1 GGCTGAGGC 10

RESULT 152

US-09-398-499-47
Sequence 47, Application US/09398499
Patent No. 6284466

GENERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 10

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-398-499-47

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGGCTGTGG 14
Db 1 ATGCTGTGG 10

RESULT 153

US-08-618-834C-42/c
Sequence 42, Application US/08618834C
Patent No. 6361937

GENERAL INFORMATION:
APPLICANT: Strayer, Lubert
TITLE OF INVENTION: Computer-Aided Nucleic Acid
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ritter, Van Pelt & Yi LLP
STREET: 4906 El Camino Real, Suite 205
CITY: Los Altos
STATE: CA
COUNTRY: USA
ZIP: 94022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FILING DATE: 19-MAR-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ritter, Michael J.
REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFFY002
TELEPHONE: 650-903-3500
TELEFAX: 650-903-3501

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```
; TOPOLOGY: linear
US-08-618-834C-42

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGT 11
Db 10 TTGATGTGT 1

RESULT 154
US-09-914-259-117
; Sequence 117, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
; OTHER INFORMATION: elements
US-09-914-259-117

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 1 TGGGGATGTT 10

RESULT 155
US-09-989-789-629
; Sequence 629, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 629
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-629

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCG 16
Db 1 GGTGTGGAG 10

; TOPOLOGY: linear
US-08-859-954-184
; Sequence 184, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-184

Query Match      35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGT 11
Db 1 GAGGATGT 8

RESULT 157
US-08-859-954-198
; Sequence 198, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
```


STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-198

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGT 11
||| |||
Db 1 GAGACTGT 8

RESULT 158
US-08-859-954-449
Sequence 449, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 449:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-449

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTT 12
||| |||
Db 1 AGGCTCTT 8

RESULT 159
US-08-859-954-566
Sequence 566, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 566:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-566

Query Match          35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TTGGCGAC 18
Db 1 TTGGAGAC 8

RESULT 160
US-09-432-020B-24
; Sequence 24, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 24
; LENGTH: 8
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CF195-8 probe; the 3'terminal thymidine contains
; OTHER INFORMATION: an aminopropanol which covalently binds to
; OTHER INFORMATION: the epoxysilaneized glass
US-09-432-020B-24

Query Match          35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
Db 1 TTGACGCT 8

RESULT 161
US-09-398-499-3
; Sequence 3, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-3

Query Match          35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCT 9
Db 1 TTGACGCT 8

RESULT 162
US-09-398-499-5
; Sequence 5, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-5

Query Match          35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCG 16
Db 1 TGCTGGCG 8

RESULT 163
US-09-398-499-12
; Sequence 12, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-12

Query Match          35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGGCGA 17
Db 1 GCTGGCGA 8

RESULT 164
US-09-398-499-21
; Sequence 21, Application US/09398499
; Patent No. 6284466
```

```
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-21
```

```
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 8 CTGTTGGC 15
||| |||||
DB 1 CTGTTGGC 8
```

```
RESULT 165
US-09-398-499-26/c
; Sequence 26, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-26
```

```
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GCTGTTGG 14
||| |||||
DB 8 GCTGTTGG 1
```

```
RESULT 166
US-09-398-499-28/c
; Sequence 28, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
```

```
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-28
```

```
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 9 TGCTGGCG 16
||| |||||
DB 8 TGCTGGCG 1
```

```
RESULT 167
US-09-398-499-35/c
; Sequence 35, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-35
```

```
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 10 GTTGGCGA 17
||| |||||
DB 8 GCTGGCGA 1
```

```
RESULT 168
US-09-398-499-44/c
; Sequence 44, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-44
```

```
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 8 CTGTTGGC 15
||| ||||
Db 8 CTGTTGGC 1

RESULT 169

US-09-878-693-1
; Sequence 1, Application US/09878693
; Patent No. 6677510
; GENERAL INFORMATION:
; APPLICANT: Windham, Mark T.
; APPLICANT: Trigiano, Robert N.
; APPLICANT: Witte, Willard T.
; TITLE OF INVENTION: Powdery Mildew Resistant Plants
; FILE REFERENCE: UTR-101X
; CURRENT APPLICATION NUMBER: US/09/878,693
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/210,603
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Random Primer
US-09-878-693-1

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGT 11
||| ||||
Db 1 GAGGCTGT 8

RESULT 170

US-08-461-607-21
; Sequence 21, Application US/08461607
; Patent No. 6054633
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Stambrook, Peter J.
; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,607
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,105
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..9
; OTHER INFORMATION: /note= "This sequence represents
; OTHER INFORMATION: mutation of base 2486 of Seq Id No. 60546333"
US-08-461-607-21

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
||| ||||
Db 1 CTGTTGGC 8

RESULT 171

US-09-363-600-21
; Sequence 21, Application US/09363600
; Patent No. 6232524
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Stambrook, Peter J.
; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,607
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature

LOCATION: 1..9
OTHER INFORMATION: /note= "this sequence represents
OTHER INFORMATION: mutation of base 2486 of Seq Id No. 62325243"
US-09-363-600-21

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGC 15
| | | | |
DB 1 CTGTGGC 8

RESULT 172

US-09-432-020B-16
; Sequence 16, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 16
; LENGTH: 9
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CF195 probe; the 3'terminal thymidine contains
; OTHER INFORMATION: an aminopropanol which covalently binds to
; OTHER INFORMATION: the epoxysilanzed glass
US-09-432-020B-16

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCT 9
| | | | |
DB 1 TTGAGGCT 8

RESULT 173

US-09-432-020B-20
; Sequence 20, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 20
; LENGTH: 9
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CF195-P probe; the 5' terminal thymidine is
; OTHER INFORMATION: phosphorylated and the 3' terminal thymidine
; OTHER INFORMATION: contains an aminopropanol which covalently binds
; OTHER INFORMATION: to the epoxysilanzed glass
US-09-432-020B-20

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCT 9
| | | | |
DB 1 TTGAGGCT 8

RESULT 174

US-09-380-836-6/C
; Sequence 6, Application US/09380836
; Patent No. 6551775
; GENERAL INFORMATION:
; APPLICANT: Lifton, Richard P.
; APPLICANT: Chang, Sue S.
; APPLICANT: Rossier, Bernard C.
; TITLE OF INVENTION: Method to Diagnose and Treat Pathological Conditions
; TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
; TITLE OF INVENTION: Pseudohypoaldosteronism Type-1
; FILE REFERENCE: 44574-5018-US
; CURRENT APPLICATION NUMBER: US/09/380,836
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/040,171
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US98/04681
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Segment of mutant beta ENaC allele
US-09-380-836-6

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGT 11
| | | | |
DB 9 GGGGCTGT 2

RESULT 175

US-09-989-789-2097
; Sequence 2097, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2097
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2097

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCG 16
||| |||||
Db 2 TGTGGCG 9

RESULT 176

US-09-989-789-2157
; Sequence 2157, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2157

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-2157

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGAGGC 8
||| |||||
Db 1 CTGGAGGC 8

RESULT 177

US-09-989-789-2160
; Sequence 2160, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2160

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-2160

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
||| |||||
Db 1 CTGTGGC 8

RESULT 178

US-09-989-789-2171
; Sequence 2171, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2171

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

US-09-989-789-2171

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGG 14
||| |||||
Db 1 GCGGTGG 8

RESULT 179

US-09-989-789-2198
; Sequence 2198, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2198

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

US-09-989-789-2198

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGC 15
||| |||||
Db 1 CTGTGGC 8

RESULT 180

US-09-989-789-2199
; Sequence 2199, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2199

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2199

Query Match      35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTGGC 15
Db      1 CTGTGGC 8

RESULT 181
PCT-US94-05659-18/c
; Sequence 18, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF-RESPONSIVE ELEMENT, TNF-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05659
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 FF
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-05659-18

Query Match      35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 AGGCTGTT 12
Db      9 AGGCAGTT 2

RESULT 182
US-08-187-749-21
; Sequence 21, Application US/08187749
; Patent No. 5525470
; GENERAL INFORMATION:
; APPLICANT: Cohen, S. Aharon,
; APPLICANT: Belenky, Alexei and
; APPLICANT: Ott, Christopher M.
; TITLE OF INVENTION: DNA Sequencing Using
; TITLE OF INVENTION: High Pressure Capillary
; TITLE OF INVENTION: Electrophoresis
;

; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,749
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-187-749-21

Query Match      33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTGAGG 7
Db      1 TTGAGG 6

RESULT 183
US-08-210-222-31
; Sequence 31, Application US/08210222
; Patent No. 5599917
; GENERAL INFORMATION:
; APPLICANT: Coppola, George R.
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Bertelsen, Arthur H.
; TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,222
; FILING DATE: Unassigned
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.

```

REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 23550-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 BASES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
HYPOTHETICAL: NO
US-08-210-222-31

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0;

Qy 3 TTGAGCT 9
Db 1 UGAGCU 7

RESULT 184
US-08-859-954-97
Sequence 97, Application US/08859954
Patent No. 6083695

GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-97

Query Match 33.3%; Score 6; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTGAGG 7
Db 1 TTGAGG 6

RESULT 185
US-08-859-954-325/c
Sequence 325, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-325

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAG 6
Db 6 CTTGAG 1

RESULT 186
US-08-859-954-326/c
Sequence 326, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin

APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 326:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-326

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAG 6
|||||
DB 6 CTTGAG 1

RESULT 187
US-08-859-954-532/C
Sequence 532, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-532

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCTGT 11
|||||
DB 6 GGCTGT 1

RESULT 188
US-08-859-954-543
Sequence 543, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246

; INFORMATION FOR SEQ ID NO: 543:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 ; US-08-859-954-543

Query Match 33.3%; Score 6; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
 Db 2 AGGCTG 7

RESULT 189
 US-09-398-499-18
 ; Sequence 41, Application US/09398499
 ; Patent No. 6284466
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Andrew K.
 ; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
 ; FILE REFERENCE: UNL 2963
 ; CURRENT APPLICATION NUMBER: US/09/398,499
 ; CURRENT FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/101,011
 ; PRIOR FILING DATE: 1998-09-18
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 8
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Primer
 US-09-398-499-18

Query Match 33.3%; Score 6; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGA 17
 Db 2 TGGCGA 7

RESULT 190
 US-09-398-499-41/c
 ; Sequence 41, Application US/09398499
 ; Patent No. 6284466
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Andrew K.
 ; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
 ; FILE REFERENCE: UNL 2963
 ; CURRENT APPLICATION NUMBER: US/09/398,499
 ; CURRENT FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/101,011
 ; PRIOR FILING DATE: 1998-09-18
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 8
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Primer
 US-09-398-499-41

Query Match 33.3%; Score 6; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGA 17
 Db 7 TGGCGA 2

RESULT 191
 PCT-US95-01104-21
 ; Sequence 21, Application PC/TUS9501104
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, S. Aharon,
 ; APPLICANT: Belenky, Alexei and
 ; APPLICANT: Ott, Christopher M.
 ; TITLE OF INVENTION: A Method of Sequencing
 ; TITLE OF INVENTION: Short Oligonucleotides
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lappin & Kusmer
 ; STREET: 200 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01104
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kerner, Ann-Louise
 ; REGISTRATION NUMBER: 33,523
 ; REFERENCE/DOCKET NUMBER: HYZ-013PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-330-1300
 ; TELEFAX: 617-330-1311
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US95-01104-21

Query Match 33.3%; Score 6; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGG 7
 Db 1 TTGAGG 6

RESULT 192
 US-08-381-097A-13
 ; Sequence 13, Application US/08381097A
 ; Patent No. 5643890
 ; GENERAL INFORMATION:
 ; APPLICANT: Iverson, Patrick L.
 ; APPLICANT: Mata, John E.
 ; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
 ; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
 ; TITLE OF INVENTION: of Cancer and Other Diseases

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,097A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: unmc 63092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-381-097A-13

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGGG 7
Db 2 TTGGG 7

RESULT 193
US-08-798-738-1
Sequence 1, Application US/08798738
Patent No. 5885833
GENERAL INFORMATION:
APPLICANT: MUELLER, Rolf
APPLICANT: ZWICKER, Joerk
APPLICANT: SEDLACEK, Hans-Herald
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS FOR THE CELL
TITLE OF INVENTION: CYCLE-REGULATED EXPRESSION OF GENES AND THERAPEUTIC
METHODS OF UTILIZING SUCH CONSTRUCTS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,738
FILING DATE: 13-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 19605274.2
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/318
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-798-738-1

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTGGCG 16
Db 2 TTGGCG 7

RESULT 194
US-08-899-324-12/C
Sequence 12, Application US/08899324
Patent No. 5945329
GENERAL INFORMATION:
APPLICANT: Breddam, Klaus
APPLICANT: Keilland-Brandt, Morten
APPLICANT: Mortensen, Uffe
APPLICANT: Olesen, Kjeld
APPLICANT: Stennicke, Henning
APPLICANT: Wagner, Fred
TITLE OF INVENTION: CUSTOMIZED PROTEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5945329west Center, 90 S. 7th Street
CITY: Minneapolis
STATE: MN
COUNTRY: U.S.A.
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,324
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/329,892
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 8648.44USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-899-324-12

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
| | | | |
Db 7 TGAGGC 2

RESULT 195

US-08-757-024-952
; Sequence 952, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/757,024
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102

; INFORMATION FOR SEQ ID NO: 952:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-952

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
| | | | |
Db 1 AGGCTG 6

RESULT 196

US-08-329-892B-12/c
; Sequence 12, Application US/08329892B
; Patent No. 6187579
; GENERAL INFORMATION:

; APPLICANT: Breddam, Klaus
; APPLICANT: Keilland-Brandt, Morten
; APPLICANT: Mortensen, Uffe
; APPLICANT: Olesen, Kjeld
; APPLICANT: Stennicke, Henning
; APPLICANT: Wagner, Fred
; TITLE OF INVENTION: CUSTOMIZED PROTEASE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6187579west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA: US/08/329,892B
; APPLICATION NUMBER: US/08/329,892B
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/144,704
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 8648.44US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-329-892B-12

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
| | | | |
Db 7 TGAGGC 2

RESULT 197

US-09-528-760A-21
; Sequence 21, Application US/09528760A
; Patent No. 6312924
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Feldhaus, Andrew L.
; TITLE OF INVENTION: Murine Interferon-Alpha
; FILE REFERENCE: 99-11
; CURRENT APPLICATION NUMBER: US/09/528,760A
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,045
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/155,739
; PRIOR FILING DATE: 1999-09-23

```
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence.
US-09-528-760A-21

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTGAG 6
Db      3 CTTGAG 8
|||||

RESULT 198
US-09-951-843-21
; Sequence 21, Application US/09951843
; Patent No. 6548056
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Feldhaus, Andrew L.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Interferon-Alpha
; FILE REFERENCE: 99-11D1
; CURRENT APPLICATION NUMBER: US/09/951,843
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/528,760
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,045
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/155,739
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence.
US-09-951-843-21

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTGAG 6
Db      3 CTTGAG 8
|||||

RESULT 199
US-09-989-789-441/c
; Sequence 441, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 441
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-443

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTG 10
Db      7 AGGCTG 2
|||||

RESULT 200
US-09-989-789-442/c
; Sequence 442, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 442
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-442

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTG 10
Db      7 AGGCTG 2
|||||

RESULT 201
US-09-989-789-443/c
; Sequence 443, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 443
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-443

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTG 10
Db      7 AGGCTG 2
|||||
```

```
Db          7 AGGCTG 2

RESULT 202
US-09-989-789-444/c
; Sequence 444, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 444
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-444

Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
           |||||
Db          7 AGGCTG 2

RESULT 203
US-09-989-789-465/c
; Sequence 465, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 465
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-465

Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
           |||||
Db          7 AGGCTG 2

RESULT 204
US-09-989-789-466/c
; Sequence 466, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 466
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-466

Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
           |||||
Db          7 AGGCTG 2

RESULT 205
US-09-989-789-467/c
; Sequence 467, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-467

Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
           |||||
Db          7 AGGCTG 2

RESULT 206
US-09-989-789-468/c
; Sequence 468, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 468
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
```

```
/ OTHER INFORMATION: DNA
US-09-989-789-468

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
Db 7 AGGCTG 2

RESULT 207
US-09-989-789-469/c
; Sequence 469, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 469
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-469

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
Db 7 AGGCTG 2

RESULT 208
US-09-989-789-470/c
; Sequence 470, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 470
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-470

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
Db 7 AGGCTG 2

RESULT 209
US-09-989-789-532/c
; Sequence 532, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 532
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-532

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GGCGAC 18
Db 9 GGCGAC 4

RESULT 210
US-09-989-789-608
; Sequence 608, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-608

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
Db 3 TGAGGC 8

RESULT 211
US-09-989-789-2084
; Sequence 2084, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
```

; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2084
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2084

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCT 9
|||
Db 4 GAGGCT 9

RESULT 212
US-09-989-789-2086
; Sequence 2086, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2086
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2086

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCT 9
|||
Db 4 GAGGCT 9

RESULT 213
US-09-989-789-2161
; Sequence 2161, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2161
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2161

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
|||
Db 3 TGAGGC 8

RESULT 214
US-09-989-789-2162
; Sequence 2162, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2162
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2162

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
|||
Db 3 TGAGGC 8

RESULT 215
US-09-989-789-2166
; Sequence 2166, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2166
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2166

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCT 9
|||
Db 4 GAGGCT 9

RESULT 216


```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2204
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2204

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 GGCAC 18
        |||||
Db      9 GGCAC 4

RESULT 219
US-09-989-789-2221
; Sequence 2221, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2221
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2221

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTG 10
        |||||
Db      2 AGGCTG 7

RESULT 220
US-09-989-789-2222
; Sequence 2222, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2222
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2222

Query Match      33.3%; Score 6; DB 1; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
 |||||
Db 2 AGGCTG 7

RESULT 221

US-09-989-789-2230
; Sequence 2230, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2230
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2230

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGG 14
 |||||
Db 2 TGTGG 7

RESULT 222

US-09-989-789-2243/c
; Sequence 2243, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2243
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2243

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCGCAG 18
 |||||
Db 9 GCGCAG 4

RESULT 223

US-09-989-789-2273
; Sequence 2273, Application US/09989789

; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2273
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2273

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGCTG 10
 |||||
Db 2 AGGCTG 7

RESULT 224

US-09-989-789-2338/c
; Sequence 2338, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2338
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2338

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCGCAG 18
 |||||
Db 9 GCGCAG 4

RESULT 225

US-09-989-789-2387
; Sequence 2387, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2387

; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2387

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GCGGAC 18
|||
Db 4 GCGGAC 9

RESULT 226
US-09-989-789-2394
; Sequence 2394, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2394
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2394

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGA 17
|||
Db 2 TGGCGA 7

RESULT 227
US-09-989-789-2395
; Sequence 2395, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2395
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2395

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCGA 17
|||
Db 2 TGGCGA 7

RESULT 228
US-09-989-789-2433
; Sequence 2433, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2433
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2433

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTGGC 15
|||
Db 3 GTTGGC 8

RESULT 229
US-09-989-789-2443
; Sequence 2443, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2443
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2443

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGC 8
|||
Db 1 TGAGGC 6

RESULT 230
US-09-989-789-2449
; Sequence 2449, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2449
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2449
```

```
Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      10 GTTGCC 15
         |||||
Db       3 GTTGCC 8
```

```
RESULT 231
US-09-989-789-2455
; Sequence 2455, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2455
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2455
```

```
Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 TGAGGC 8
         |||||
Db       1 TGAGGC 6
```

```
RESULT 232
US-09-989-789-2456
; Sequence 2456, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2456
; LENGTH: 9
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2456
```

```
Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 TGAGGC 8
         |||||
Db       1 TGAGGC 6
```

```
RESULT 233
US-09-989-789-2471
; Sequence 2471, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2471
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2471
```

```
Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 GAGGCT 9
         |||||
Db       4 GAGGCT 9
```

```
RESULT 234
US-09-989-789-2473
; Sequence 2473, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2473
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2473
```

```
Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 GAGGCT 9
```

```
Db          |||||
            4 GAGGCT 9

RESULT 235
PCT-US94-05659-1
; Sequence 1, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF' RESPONSIVE ELEMENT, TNF'-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 PF
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US94-05659-1
;
Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
            |||||
Db          1 AGGCTG 6

PCT-US94-05659-1
; Sequence 4, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF' RESPONSIVE ELEMENT, TNF'-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 PF
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US94-05659-1
;
Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
            |||||
Db          1 AGGCTG 6

PCT-US94-05659-4/c
; Sequence 1, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF' RESPONSIVE ELEMENT, TNF'-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 PF
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US94-05659-19
;
Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          13 GCGGAC 18
            |||||
Db          8 GCGGAC 3

PCT-US94-05659-19
; Sequence 19, Application PC/TUS9405659
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: TNF' RESPONSIVE ELEMENT, TNF'-INDUCED DNA-BINDING
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC93-01 PF
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US94-05659-4
;
Query Match          33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 AGGCTG 10
            |||||
Db          9 AGGCTG 4
```

Search completed: September 9, 2004, 11:17:54
Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:21:29 ; Search time 0.001 Seconds
(without alignments)
83.808 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18

Sequence: 1 cttgagctgttgcgac 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 211 seqs, 2328 residues

Total number of hits satisfying chosen parameters: 422

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 211 summaries

Database : rnpb1.seq *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	12.2	67.8	17	US-10-138-674-4769
C 2	12.2	67.8	17	US-10-287-949A-4769
C 3	12	66.7	17	US-09-816-127-14
C 4	11.8	65.6	18	US-09-969-373-3190
C 5	11.4	63.3	17	US-09-866-108-9833
C 6	11.4	63.3	17	US-09-866-108-9834
C 7	11.4	63.3	17	US-09-866-108-9835
C 8	11.4	63.3	17	US-09-866-108-9836
C 9	11.4	63.3	17	US-09-866-108-9837
C 10	11.4	63.3	17	US-10-723-361-9833
C 11	11.4	63.3	17	US-10-723-361-9834
C 12	11.4	63.3	17	US-10-723-361-9835
C 13	11.4	63.3	17	US-10-723-361-9836
C 14	11.4	63.3	17	US-10-723-361-9837
C 15	11.2	62.2	17	US-10-163-552-822
C 16	11.2	62.2	17	US-10-230-006-585
C 17	11.2	62.2	17	US-10-138-674-478
C 18	11.2	62.2	17	US-10-287-949A-478
C 19	11.2	62.2	17	US-10-712-672-968
C 20	10.4	57.8	13	US-09-877-478-5987
C 21	10.4	57.8	13	US-10-342-902-5987
C 22	10.4	57.8	13	US-10-669-841-2390
C 23	10.2	56.7	15	US-09-880-313A-16
C 24	10.2	56.7	15	US-09-880-313A-30
C 25	10	55.6	15	US-09-775-818-15
C 26	10	55.6	15	US-09-870-002-32
C 27	10	55.6	15	US-10-643-130-32
C 28	10	55.6	15	US-10-663-999-15
C 29	9.8	54.4	15	US-10-440-850-881
C 30	9.8	54.4	15	US-10-376-341-239
C 31	9.4	52.2	11	US-10-450-797-536
C 32	9.4	52.2	13	US-09-949-041A-44
C 33	9.4	52.2	14	US-08-591-486B-73
C 34	9.4	52.2	14	US-09-860-738C-40
C 35	9.4	52.2	14	US-09-860-738C-58
C 36	9.4	52.2	14	US-09-860-738C-82
C 37	9.4	52.2	14	US-09-860-738C-92
C 38	9.4	52.2	14	US-09-998-018-15
C 39	9	50.0	9	US-09-983-789-2478
C 40	9	50.0	9	US-09-990-186-2478
C 41	9	50.0	9	US-09-989-994-2478
C 42	8.8	48.9	13	US-10-005-956-877
C 43	8.8	48.9	13	US-10-156-433-20
C 44	8.8	48.9	13	US-10-112-814-20
C 45	8.8	48.9	13	US-10-176-972A-70
C 46	8.4	46.7	10	US-09-989-789-626
C 47	8.4	46.7	10	US-09-990-186-626
C 48	8.4	46.7	10	US-09-748-710-24
C 49	8.4	46.7	10	US-09-989-994-626
C 50	8.4	46.7	10	US-10-293-222-39
C 51	8.4	46.7	10	US-10-033-145-1906
C 52	8.4	46.7	10	US-10-330-627-347
C 53	8.4	46.7	10	US-10-673-938-68
C 54	8.4	46.7	10	US-10-673-938-77
C 55	8.4	46.7	10	US-10-673-938-89
C 56	8.4	46.7	11	US-10-055-728-24
C 57	8.4	46.7	11	US-10-310-677-24
C 58	8.4	46.7	12	US-09-238-351-5
C 59	8.4	46.7	12	US-09-245-105A-5
C 60	8.4	46.7	12	US-10-096-718-20
C 61	8.4	46.7	12	US-10-096-718-40
C 62	8	44.4	9	US-09-989-789-2152
C 63	8	44.4	9	US-09-989-789-2326
C 64	8	44.4	9	US-09-989-789-2327
C 65	8	44.4	9	US-09-990-186-2152
C 66	8	44.4	9	US-09-990-186-2326
C 67	8	44.4	9	US-09-990-186-2327
C 68	8	44.4	9	US-09-989-994-2152
C 69	8	44.4	9	US-09-989-994-2326
C 70	8	44.4	9	US-09-989-994-2327
C 71	8	44.4	10	US-10-033-145-940
C 72	8	44.4	10	US-10-330-627-292
C 73	8	44.4	10	US-10-330-627-1261
C 74	8	44.4	10	US-10-401-194-113
C 75	7.8	43.3	11	US-09-836-737A-4
C 76	7.8	43.3	11	US-09-249-155-245
C 77	7.8	43.3	11	US-09-880-313A-59
C 78	7.8	43.3	11	US-09-970-971A-14
C 79	7.8	43.3	11	US-09-918-715-65
C 80	7.8	43.3	11	US-10-098-816-14
C 81	7.8	43.3	11	US-10-314-322-245
C 82	7.8	43.3	11	US-10-314-322-318
C 83	7.8	43.3	11	US-10-450-797-499
C 84	7.8	43.3	12	US-10-001-670-34
C 85	7.4	41.1	9	US-09-989-789-2508
C 86	7.4	41.1	9	US-09-989-994-2508
C 87	7.4	41.1	9	US-09-916-466-147
C 88	7.4	41.1	9	US-09-277-494-147
C 89	7.4	41.1	10	US-09-238-351-1
C 90	7.4	41.1	10	US-09-989-789-1278
C 91	7.4	41.1	10	US-09-990-186-1278
C 92	7.4	41.1	10	US-09-989-994-1278
C 93	7.4	41.1	10	US-10-293-222-71
C 94	7.4	41.1	10	US-09-245-105A-1
C 95	7.4	41.1	10	US-10-033-145-1121
C 96	7.4	41.1	10	US-10-033-145-1229
C 97	7.4	41.1	10	US-10-033-145-1995
C 98	7.4	41.1	10	US-10-055-713-87
C 99	7.4	41.1	10	US-10-113-030-3
C 100	7.4	41.1	10	US-10-142-111-20
C 101	7.4	41.1	10	US-10-055-711-91
C 102	7.4	41.1	10	US-10-358-818-3
C 103	7.4	41.1	10	US-10-223-765-392
C 104	7.4	41.1	10	US-10-330-627-495
C 105	7.4	41.1	10	US-10-330-627-1121
C 106	7.4	41.1	10	US-10-330-627-1121
C 107	7.4	41.1	10	US-10-330-627-1121
C 108	7.4	41.1	10	US-10-330-627-1121
C 109	7.4	41.1	10	US-10-330-627-1121
C 110	7.4	41.1	10	US-10-330-627-1121
C 111	7.4	41.1	10	US-10-330-627-1121
C 112	7.4	41.1	10	US-10-330-627-1121
C 113	7.4	41.1	10	US-10-330-627-1121
C 114	7.4	41.1	10	US-10-330-627-1121
C 115	7.4	41.1	10	US-10-330-627-1121
C 116	7.4	41.1	10	US-10-330-627-1121
C 117	7.4	41.1	10	US-10-330-627-1121
C 118	7.4	41.1	10	US-10-330-627-1121
C 119	7.4	41.1	10	US-10-330-627-1121
C 120	7.4	41.1	10	US-10-330-627-1121
C 121	7.4	41.1	10	US-10-330-627-1121
C 122	7.4	41.1	10	US-10-330-627-1121
C 123	7.4	41.1	10	US-10-330-627-1121
C 124	7.4	41.1	10	US-10-330-627-1121
C 125	7.4	41.1	10	US-10-330-627-1121
C 126	7.4	41.1	10	US-10-330-627-1121
C 127	7.4	41.1	10	US-10-330-627-1121
C 128	7.4	41.1	10	US-10-330-627-1121
C 129	7.4	41.1	10	US-10-330-627-1121
C 130	7.4	41.1	10	US-10-330-627-1121
C 131	7.4	41.1	10	US-10-330-627-1121
C 132	7.4	41.1	10	US-10-330-627-1121
C 133	7.4	41.1	10	US-10-330-627-1121
C 134	7.4	41.1	10	US-10-330-627-1121
C 135	7.4	41.1	10	US-10-330-627-1121
C 136	7.4	41.1	10	US-10-330-627-1121
C 137	7.4	41.1	10	US-10-330-627-1121
C 138	7.4	41.1	10	US-10-330-627-1121
C 139	7.4	41.1	10	US-10-330-627-1121
C 140	7.4	41.1	10	US-10-330-627-1121
C 141	7.4	41.1	10	US-10-330-627-1121
C 142	7.4	41.1	10	US-10-330-627-1121
C 143	7.4	41.1	10	US-10-330-627-1121
C 144	7.4	41.1	10	US-10-330-627-1121
C 145	7.4	41.1	10	US-10-330-627-1121
C 146	7.4	41.1	10	US-10-330-627-1121
C 147	7.4	41.1	10	US-10-330-627-1121
C 148	7.4	41.1	10	US-10-330-627-1121
C 149	7.4	41.1	10	US-10-330-627-1121
C 150	7.4	41.1	10	US-10-330-627-1121
C 151	7.4	41.1	10	US-10-330-627-1121
C 152	7.4	41.1	10	US-10-330-627-1121
C 153	7.4	41.1	10	US-10-330-627-1121
C 154	7.4	41.1	10	US-10-330-627-1121
C 155	7.4	41.1	10	US-10-330-627-1121
C 156	7.4	41.1	10	US-10-330-627-1121
C 157	7.4	41.1	10	US-10-330-627-1121
C 158	7.4	41.1	10	US-10-330-627-1121
C 159	7.4	41.1	10	US-10-330-627-1121
C 160	7.4	41.1	10	US-10-330-627-1121
C 161	7.4	41.1	10	US-10-330-627-1121
C 162	7.4	41.1	10	US-10-330-627-1121
C 163	7.4	41.1	10	US-10-330-627-1121
C 164	7.4	41.1	10	US-10-330-627-1121
C 165	7.4	41.1	10	US-10-330-627-1121
C 166	7.4	41.1	10	US-10-330-627-1121
C 167	7.4	41.1	10	US-10-330-627-1121
C 168	7.4	41.1	10	US-10-330-627-1121
C 169	7.4	41.1	10	US-10-330-627-1121
C 170	7.4	41.1	10	US-10-330-627-1121
C 171	7.4	41.1	10	US-10-330-627-1121
C 172	7.4	41.1	10	US-10-330-627-1121
C 173	7.4	41.1	10	US-10-330-627-1121
C 174	7.4	41.1	10	US-10-330-627-1121
C 175	7.4	41.1	10	US-10-330-627-1121
C 176	7.4	41.1	10	US-10-330-627-1121
C 177	7.4	41.1	10	US-10-330-627-1121
C 178	7.4	41.1	10	US-10-330-627-1121
C 179	7.4	41.1	10	US-10-330-627-1121
C 180	7.4	41.1	10	US-10-330-627-1121
C 181	7.4	41.1	10	US-10-330-627-1121
C 182	7.4	41.1	10	US-10-330-627-1121
C 183	7.4	41.1	10	US-10-330-627-1121
C 184	7.4	41.1	10	US-10-330-627-1121
C 185	7.4	41.1	10	US-10-330-627-1121
C 186	7.4	41.1	10	US-10-330-627-1121
C 187	7.4	41.1	10	US-10-330-627-1121
C 188	7.4	41.1	10	US-10-330-627-1121
C 189	7.4	41.1	10	US-10-330-627-1121
C 190	7.4	41.1	10	US-10-330-627-1121
C 191	7.4	41.1	10	US-10-330-627-1121
C 192	7.4	41.1	10	US-10-

```
c 107 7.4 41.1 10 1 US-10-080-608A-123 Sequence 123, App
c 108 7.4 41.1 10 1 US-10-160-358-117 Sequence 117, App
c 109 7.4 41.1 10 1 US-10-370-685-33 Sequence 33, Appl
c 110 7.4 41.1 10 1 US-10-004-378A-185 Sequence 185, App
c 111 7.4 41.1 10 1 US-10-418-552-73 Sequence 73, Appl
c 112 7.4 41.1 10 1 US-10-650-454-92 Sequence 92, Appl
c 113 7.4 41.1 10 1 US-10-470-180-87 Sequence 87, Appl
c 114 7.4 41.1 11 1 US-09-950-459-3 Sequence 37, Appl
c 115 7.4 41.1 11 1 US-09-772-719-82 Sequence 82, Appl
c 116 7.4 41.1 11 1 US-09-249-155-37 Sequence 37, Appl
c 117 7.4 41.1 11 1 US-09-967-237-82 Sequence 82, Appl
c 118 7.4 41.1 11 1 US-09-918-715-10 Sequence 10, Appl
c 119 7.4 41.1 11 1 US-10-314-322-37 Sequence 37, Appl
c 120 7.4 41.1 11 1 US-10-314-322-266 Sequence 266, App
c 121 7.4 41.1 11 1 US-10-376-559-3 Sequence 3, Appl
c 122 7.4 41.1 11 1 US-10-450-797-316 Sequence 316, App
c 123 7.4 41.1 11 1 US-10-450-797-836 Sequence 836, App
c 124 7.4 41.1 11 1 US-10-450-797-1381 Sequence 1381, Ap
c 125 7.4 41.1 11 1 US-10-027-632-177591 Sequence 177591,
c 126 7.4 38.9 8 1 US-10-027-632-177591 Sequence 177591,
c 127 7.4 38.9 9 1 US-09-989-789-531 Sequence 531, App
c 128 7.4 38.9 9 1 US-09-989-789-2126 Sequence 2126, Ap
c 129 7.4 38.9 9 1 US-09-989-789-2127 Sequence 2127, Ap
c 130 7.4 38.9 9 1 US-09-989-789-2128 Sequence 2128, Ap
c 131 7.4 38.9 9 1 US-09-989-789-2129 Sequence 2129, Ap
c 132 7.4 38.9 9 1 US-09-990-186-531 Sequence 531, App
c 133 7.4 38.9 9 1 US-09-990-186-2126 Sequence 2126, Ap
c 134 7.4 38.9 9 1 US-09-990-186-2127 Sequence 2127, Ap
c 135 7.4 38.9 9 1 US-09-990-186-2128 Sequence 2128, Ap
c 136 7.4 38.9 9 1 US-09-990-186-2129 Sequence 2129, Ap
c 137 7.4 38.9 9 1 US-09-989-994-531 Sequence 531, App
c 138 7.4 38.9 9 1 US-09-989-994-2126 Sequence 2126, Ap
c 139 7.4 38.9 9 1 US-09-989-994-2127 Sequence 2127, Ap
c 140 7.4 38.9 9 1 US-09-989-994-2128 Sequence 2128, Ap
c 141 7.4 38.9 9 1 US-09-989-994-2129 Sequence 2129, Ap
c 142 7.4 38.9 9 1 US-10-182-327-110 Sequence 110, App
c 143 7.4 38.9 10 1 US-09-758-073-2 Sequence 2, Appl
c 144 7.4 38.9 10 1 US-09-989-789-556 Sequence 556, App
c 145 7.4 38.9 10 1 US-09-989-789-1279 Sequence 1279, Ap
c 146 7.4 38.9 10 1 US-09-989-789-1308 Sequence 1308, Ap
c 147 7.4 38.9 10 1 US-09-989-789-1313 Sequence 1313, Ap
c 148 7.4 38.9 10 1 US-09-989-789-1314 Sequence 1314, Ap
c 149 7.4 38.9 10 1 US-09-989-789-1624 Sequence 1624, Ap
c 150 7.4 38.9 10 1 US-09-989-789-1625 Sequence 1625, Ap
c 151 7.4 38.9 10 1 US-09-990-186-556 Sequence 556, App
c 152 7.4 38.9 10 1 US-09-990-186-1279 Sequence 1279, Ap
c 153 7.4 38.9 10 1 US-09-990-186-1308 Sequence 1308, Ap
c 154 7.4 38.9 10 1 US-09-990-186-1313 Sequence 1313, Ap
c 155 7.4 38.9 10 1 US-09-990-186-1624 Sequence 1624, Ap
c 156 7.4 38.9 10 1 US-09-990-186-1625 Sequence 1625, Ap
c 157 7.4 38.9 10 1 US-09-989-994-556 Sequence 556, App
c 158 7.4 38.9 10 1 US-09-989-994-1279 Sequence 1279, Ap
c 159 7.4 38.9 10 1 US-09-989-994-1308 Sequence 1308, Ap
c 160 7.4 38.9 10 1 US-09-989-994-1313 Sequence 1313, Ap
c 161 7.4 38.9 10 1 US-09-989-994-1624 Sequence 1624, Ap
c 162 7.4 38.9 10 1 US-09-989-994-1625 Sequence 1625, Ap
c 163 7.4 38.9 10 1 US-10-033-145-679 Sequence 679, App
c 164 7.4 38.9 10 1 US-10-033-145-1549 Sequence 1549, Ap
c 165 7.4 38.9 10 1 US-10-033-145-1843 Sequence 1843, Ap
c 166 7.4 38.9 10 1 US-10-033-145-1923 Sequence 1923, Ap
c 167 7.4 38.9 10 1 US-10-033-145-2122 Sequence 2122, App
c 168 7.4 38.9 10 1 US-10-330-627-178 Sequence 178, App
c 169 7.4 38.9 10 1 US-10-330-627-410 Sequence 410, App
c 170 7.4 38.9 10 1 US-10-330-627-411 Sequence 411, App
c 171 7.4 38.9 10 1 US-10-330-627-548 Sequence 548, App
c 172 7.4 38.9 10 1 US-10-330-627-912 Sequence 912, App
c 173 7.4 38.9 10 1 US-10-330-627-1025 Sequence 1025, Ap
c 174 7.4 38.9 10 1 US-10-330-627-1262 Sequence 1262, Ap
c 175 7.4 38.9 10 1 US-10-330-627-1560 Sequence 1560, Ap
c 176 7.4 38.9 10 1 US-10-160-358-98 Sequence 98, Appl
c 177 6.8 37.8 10 1 US-09-989-789-629 Sequence 629, App
c 178 6.8 37.8 10 1 US-09-846-033B-240 Sequence 240, App
c 179 6.8 37.8 10 1 US-09-990-186-629 Sequence 629, App
c 180 6.8 37.8 10 1 US-09-989-994-629 Sequence 629, App
```

```
c 181 6.8 37.8 10 1 US-10-293-222-96 Sequence 96, Appl
c 182 6.8 37.8 10 1 US-10-293-222-102 Sequence 102, App
c 183 6.8 37.8 10 1 US-10-293-222-341 Sequence 341, App
c 184 6.8 37.8 10 1 US-10-033-145-152 Sequence 152, App
c 185 6.8 37.8 10 1 US-10-033-145-193 Sequence 193, App
c 186 6.8 37.8 10 1 US-10-033-145-200 Sequence 200, App
c 187 6.8 37.8 10 1 US-10-033-145-210 Sequence 210, App
c 188 6.8 37.8 10 1 US-10-033-145-414 Sequence 414, App
c 189 6.8 37.8 10 1 US-10-033-145-604 Sequence 604, App
c 190 6.8 37.8 10 1 US-10-033-145-646 Sequence 646, App
c 191 6.8 37.8 10 1 US-10-033-145-1324 Sequence 1324, Ap
c 192 6.8 37.8 10 1 US-10-033-145-1451 Sequence 1451, Ap
c 193 6.8 37.8 10 1 US-10-033-145-1686 Sequence 1686, Ap
c 194 6.8 37.8 10 1 US-10-033-145-1973 Sequence 1973, Ap
c 195 6.8 37.8 10 1 US-10-033-145-2032 Sequence 2032, Ap
c 196 6.8 37.8 10 1 US-10-033-145-2037 Sequence 2037, Ap
c 197 6.8 37.8 10 1 US-10-033-145-2103 Sequence 2103, Ap
c 198 6.8 37.8 10 1 US-10-033-145-2123 Sequence 2123, Ap
c 199 6.8 37.8 10 1 US-10-006-069A-240 Sequence 240, App
c 200 6.8 37.8 10 1 US-10-176-464A-43 Sequence 43, Appl
c 201 6.8 37.8 10 1 US-10-329-465-48 Sequence 48, Appl
c 202 6.8 37.8 10 1 US-10-330-627-279 Sequence 279, App
c 203 6.8 37.8 10 1 US-10-330-627-280 Sequence 280, App
c 204 6.8 37.8 10 1 US-10-330-627-963 Sequence 963, App
c 205 6.8 37.8 10 1 US-10-330-627-1029 Sequence 1029, Ap
c 206 6.8 37.8 10 1 US-10-330-627-1321 Sequence 1321, Ap
c 207 6.8 37.8 10 1 US-10-330-627-1348 Sequence 1348, Ap
c 208 6.8 37.8 10 1 US-10-330-627-1376 Sequence 1376, Ap
c 209 6.8 37.8 10 1 US-10-330-627-1508 Sequence 1508, Ap
c 210 6.8 37.8 10 1 US-10-080-608A-117 Sequence 117, App
c 211 6.8 37.8 10 1 US-10-197-019-84 Sequence 84, Appl
c 212 6.8 37.8 10 1 US-10-370-685-27 Sequence 27, Appl
```

ALIGNMENTS

```
RESULT 1
US-10-138-674-4769/c
; Sequence 4769, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4769
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4769
```

```
Query Match 67.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTTGAGGCTGTGGCGA 17
|||||
Db 17 CTTGAGGCTGTGGCGA 1
```

```
RESULT 2
US-10-287-949A-4769/c
; Sequence 4769, Application US/10287949A
; Publication No. US20040102389A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jalme
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4769
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4769

Query Match      67.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTTGAGGCTGTTGGCGA 17
Db      17 CTTGAGGTAGTTGGAGA 1

RESULT 3
US-09-816-127-14/c
; Sequence 14, Application US/09816127
; Patent No. US20020104122A1
; GENERAL INFORMATION:
; APPLICANT: KAKITANI, MAKOTO
; APPLICANT: UMEMOTO, NAOYUKI
; APPLICANT: ISHIDA, ISAO
; APPLICANT: IWAMATSU, AKIHIRO
; APPLICANT: YOSHIKAWA, MASAAKI
; APPLICANT: YOSHIKAWA, KUNIKO
; APPLICANT: YOSHIKAWA, MASASHI
; APPLICANT: YAMAKAKA, NAOTO
; APPLICANT: TAKEUCHI, YOUNJI
; TITLE OF INVENTION: METHODS FOR PRODUCING A PLANT WITH ENHANCED RESISTANCE
; TITLE OF INVENTION: TO PATHOGENIC FUNGI
; FILE REFERENCE: 081356/0160
; CURRENT APPLICATION NUMBER: US/09/816,127
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 09/094,557
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 08/591,566
; PRIOR FILING DATE: 1997-07-14
; PRIOR APPLICATION NUMBER: PCT/JP96/03653
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-816-127-14

Query Match      66.7%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTGAGGCTGTTGGCGA 17
Db      17 TTGGKGTGTTGGCGA 2
```

RESULT 4

```
US-09-969-373-3190/c
; Sequence 3190, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Ebertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10152679A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3190
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3190

Query Match      65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGGCTGTTGGCGAC 18
Db      15 GAGGCTGTTGGAGAC 1

RESULT 5
US-09-866-108-9833/c
; Sequence 9833, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yizhong
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9833
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9833

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 17 TTGAGGCTGTGG 5

RESULT 6
US-09-866-108-9834/c
; Sequence 9834, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9834
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-866-108-9834

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 16 TTGAGGCTGTGG 4

RESULT 7
US-09-866-108-9835/c
; Sequence 9835, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9835
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9835

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGG 14
|||||
Db 15 TTGAGGCTGTGG 3

```
RESULT 8
US-09-866-108-9836/c
; Sequence 9836, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9836
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9836

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTGG 14
Db 14 TTGAGGCTGTTGG 2

RESULT 9
US-09-866-108-9837/c
; Sequence 9837, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AND MUSCLE
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
```

```
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9837
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9837

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTGG 14
Db 13 TTGAGGCTGTTGG 1

RESULT 10
US-10-723-361-9833/c
; Sequence 9833, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AND MUSCLE
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
```


; Sequence 9836, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aescmca Sequence Listing Engine
; SEQ ID NO 9836
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-9836

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTGG 14
Db 14 TTGAGGCTGTGG 2

RESULT 14
US-10-723-361-9837/c
; Sequence 9837, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aescmca Sequence Listing Engine
; SEQ ID NO 9837
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-9837

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TTGAGGCTGTGG 14
Db 13 TTGAGGCTGTGG 1

RESULT 15
US-10-163-552-822
; Sequence 822, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 822
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-822

Query Match 62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TGAGGCTGTGGCGAC 18
Db 1 UGAGACUGAGGCGUAC 16

RESULT 16
US-10-230-006-585
; Sequence 585, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC COND
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006

```
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 585
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-585

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 CTTGAGGCTGTTGGCG 16
   ||||| |||||
Db 1 CCUGGGGCGUCUGGCG 16

RESULT 17
US-10-138-674-478/c
; Sequence 478, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-478

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CTTGAGGCTGTTGGCG 16
   ||||| |||||
Db 16 CTTGAGGTAGTTGGAG 1

RESULT 18
US-10-287-949A-478/c
; Sequence 478, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-10-287-949A-478

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CTTGAGGCTGTTGGCG 16
   ||||| |||||
Db 16 CTTGAGGTAGTTGGAG 1

RESULT 19
US-10-712-672-968/c
; Sequence 968, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 968
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-968

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTTGGCGA 17
   ||||| |||||
Db 16 TTGATGATGCTGGCGA 1

RESULT 20
US-09-877-478-5987
; Sequence 5987, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
```

; PRIOR APPLICATION NUMBER: US 08/434,504
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5987
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B virus
 US-09-877-478-5987

Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTGGC 15
 |||||: |||
 DB 2 GAGGCGUAGGC 13

RESULT 21
 US-10-342-902-5987
 ; Sequence 5987, Application US/10342902
 ; Publication No. US20040054156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics, Inc.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Morrissey, Dave
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 ; FILE REFERENCE: 400/075 (MBH800-845-1)
 ; CURRENT APPLICATION NUMBER: US/10/342,902
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 09/877,478
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 09/531,025
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: US 09/636,385
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: US 09/696,347
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 08/193,627
 ; PRIOR FILING DATE: 1994-02-07
 ; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6592
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5987
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B virus
 US-10-342-902-5987

Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTGGC 15
 |||||: |||
 DB 2 GAGGCGUAGGC 13

RESULT 22
 US-10-669-841-2390
 ; Sequence 2390, Application US/10669841
 ; Publication No. US20040127446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna Therapeutics, Inc.
 ; APPLICANT: Lawrence, Blatt

; APPLICANT: Dennis, Macejak
 ; APPLICANT: James, McSwiggen
 ; APPLICANT: David, Morrissey
 ; APPLICANT: Pamela, Pavco
 ; APPLICANT: Patrice, Lee
 ; APPLICANT: Kenneth, Draper
 ; APPLICANT: Elisabeth, Roberts
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
 ; FILE REFERENCE: 400/042US (MBH802-249-E)
 ; CURRENT APPLICATION NUMBER: US/10/669,841
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US02/09187
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: US 60/296,876
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/335,059
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 60/337,055
 ; PRIOR FILING DATE: 2001-12-05
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 09/817,879
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 09/740,332
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: US 09/611,931
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 09/504,321
 ; PRIOR FILING DATE: 2000-02-15
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 16207
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2390
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B Virus
 US-10-669-841-2390

Query Match 57.8%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTGGC 15
 |||||: |||
 DB 2 GAGGCGUAGGC 13

RESULT 23
 US-09-880-313A-16
 ; Sequence 16, Application US/09880313A
 ; Publication No. US20030044791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Flemington, Erik K
 ; TITLE OF INVENTION: Adaptors and Methods of Use
 ; FILE REFERENCE: 9397/1000
 ; CURRENT APPLICATION NUMBER: US/09/880,313A
 ; CURRENT FILING DATE: 2001-06-13
 ; NUMBER OF SEQ ID NOS: 276
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-09-880-313A-16

Query Match 56.7%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 25;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCG 16
| | | | | | | |
Db 1 TCGAGGCTGCAGGCG 15

RESULT 24

US-09-880-313A-30
; Sequence 30, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-30

Query Match 56.7%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGAGGCTGTGGCG 16
| | | | | | | |
Db 1 TCGAGGCTGCAGGCG 15

RESULT 25

US-09-775-818-15
; Sequence 15, Application US/09775818
; Patent No. US20010044100A1
; GENERAL INFORMATION:
; APPLICANT: Laboratory of Molecular Biophotonics
; TITLE OF INVENTION: Method for selectively separating live cells expressing
; TITLE OF INVENTION: a specific gene
; FILE REFERENCE: FP00-0043-00
; CURRENT APPLICATION NUMBER: US/09/775,818
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: JP 2000/028117
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: JP 2000/130793
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-775-818-15

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
| | | | | | | |
Db 4 TGAGGCTGTT 13

RESULT 26

US-09-870-002-32/c
; Sequence 32, Application US/09870002
; Publication No. US20030013670A1

; GENERAL INFORMATION:
; APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1 for WINDOWS
; CURRENT APPLICATION NUMBER: US/09/870,002
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/575,554
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0463
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-870-002-32

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGGCG 16
| | | | | | | |
Db 12 GCTGTGGCG 3

RESULT 27
US-10-643-130-32/c
; Sequence 32, Application US/10643130
; Publication No. US20040072786A1
; GENERAL INFORMATION:
; APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1 for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/643,130
; FILING DATE: 18-Aug-2003
; CLASSIFICATION: <Unknown>


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/575,554
; FILING DATE: 22-May-2000
; APPLICATION NUMBER: 09/128,494
; FILING DATE: August 3, 1998
; APPLICATION NUMBER: 08/411,734
; FILING DATE: April 3, 1995
; APPLICATION NUMBER: PCT/US93/09346
; FILING DATE: October 1, 1993
; APPLICATION NUMBER: 07/958,134
; FILING DATE: October 5, 1992
; APPLICATION NUMBER: 08/007,996
; FILING DATE: January 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0463
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-643-130-32
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 16
Db 12 GCTGTGGCG 3

RESULT 28
US-10-663-999-15
; Sequence 15, Application US/10663999
; Publication No. US20040161771A1
; GENERAL INFORMATION:
; APPLICANT: Laboratory of Molecular Biophotonics
; TITLE OF INVENTION: Method for selectively separating live cells expressing
; FILE REFERENCE: FP00-0043-00
; CURRENT APPLICATION NUMBER: US/10/663,999
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US/09/775,818
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: JP 2000/028117
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: JP 2000/130793
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-663-999-15
Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGGCTGTT 12
Db 4 TCAGGCTGTT 13

; PRIOR APPLICATION DATA:
; Sequence 881, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Reve
; TITLE OF INVENTION: Immune Responses
; FILE REFERENCE: 250/130 (MBH00-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,850
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 881
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-440-850-881
Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTGGCGA 17
Db 1 AGGCAGUUGGCCA 13

RESULT 30
US-10-376-341-239
; Sequence 239, Application US/10376341
; Publication No. US20040002473A1
; GENERAL INFORMATION:
; APPLICANT: KURECK, Jens
; APPLICANT: ERDMANN, Volker A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES AGAINST VR1
; FILE REFERENCE: 029310.52142US
; CURRENT APPLICATION NUMBER: US/10/376,341
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/EP01/10081
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 100 43 674.9
; PRIOR FILING DATE: 2000-09-02
; PRIOR APPLICATION NUMBER: 100 43 702.8
; PRIOR FILING DATE: 2000-09-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-376-341-239
Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCAGGCTCTTGGC 15
Db 3 TCAGGCTCTTGGC 15
```

RESULT 31

US-10-450-797-536/c
; Sequence 536, Application US/10450797
; Publication No. US20040142335A1

; GENERAL INFORMATION:

; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 536
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-536

Query Match 52.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGGC 15

Db 11 ATGCTGTTGGC 1

RESULT 32

US-09-949-041A-44
; Sequence 44, Application US/09949041A
; Publication No. US20030104387A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rif
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-949-041A-44

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGGCG 16

Db 1 GACTGTTGGCG 11

RESULT 33

US-08-591-486B-73
; Sequence 73, Application US/08591486B
; Publication No. US20020037866A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg F
; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Gotingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-73

Query Match 52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGAC 18

Db 1 CTGTTGGCGAC 11

RESULT 34

US-09-860-738C-40/c

; Sequence 40, Application US/09860738C

; Publication No. US20030040620A1

; GENERAL INFORMATION:

; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:

```
; OTHER INFORMATION: Primer
US-09-860-738C-40
Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   ||||| |||||
Db 14 TGAGGTTGTTG 4

RESULT 35
US-09-860-738C-58/c
; Sequence 58, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-58

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   ||||| |||||
Db 14 TGAGGTTGTTG 4

RESULT 36
US-09-860-738C-82/c
; Sequence 82, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-82

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   ||||| |||||
Db 14 TGAGGTTGTTG 4

RESULT 37
US-09-860-738C-82/c
; Sequence 92, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-92
```

```
US-09-860-738C-92/c
; Sequence 92, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-92

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   ||||| |||||
Db 14 TGAGGTTGTTG 4

RESULT 38
US-09-999-018-15/c
; Sequence 15, Application US/09999018
; Publication No. US20030064376A1
; GENERAL INFORMATION:
; APPLICANT: Makarov, Vladimir
; APPLICANT: Kamberov, Emanuel
; APPLICANT: Sleptsova, Irina
; TITLE OF INVENTION: Genome Walking By Selective Amplification of Nick-Translate DNA
; FILE REFERENCE: RUBC:018US/10111436
; CURRENT APPLICATION NUMBER: US/09/999,018
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-999-018-15

Query Match          52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTTG 13
   ||||| |||||
Db 14 TGAGGTTGTTG 4

RESULT 39
US-09-989-789-2478
; Sequence 2478, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
||| |||||
Db 1 GAGGCTGTT 9

RESULT 40
US-09-990-186-2478
; Sequence 2478, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
||| |||||
Db 1 GAGGCTGTT 9

RESULT 41
US-09-989-994-2478
; Sequence 2478, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2478

Query Match 50.0%; Score 9; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
||| |||||
Db 1 GAGGCTGTT 9

RESULT 42
US-10-005-956-877
; Sequence 877, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 877
; LENGTH: 13
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-877

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGCTGTGGC 15
||| |||||
Db 1 GAAGCTGTGGC 12

RESULT 43
US-10-156-433-20
; Sequence 20, Application US/10156433
; Publication No. US20030144489A1
; GENERAL INFORMATION:
; APPLICANT: Burgin, Alex
; APPLICANT: Beigelman, Leonid
; APPLICANT: Bellon, Laurent
; APPLICANT: Zinnen, Shawn
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MHB00-943-E (500.007)
; CURRENT APPLICATION NUMBER: US/10/156,433
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/112,814
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-433-20

```
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGCGCA 17
Db      1 GGGTGTTCACGA 12

RESULT 44
US-10-112-814-20
; Sequence 20, Application US/10112814
; Publication No. US20030170844A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: M8H00-943-D; 400.005
; CURRENT APPLICATION NUMBER: US/10/112,814
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Kras transcript
US-10-112-814-20

Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTTGCGCA 17
Db      1 GGGTGTTCACGA 12

RESULT 45
US-10-176-972A-70/c
; Sequence 70, Application US/10176972A
; Publication No. US20030235822A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Gall, Alexander A.
; APPLICANT: Lokhov, Sergey G.
; APPLICANT: Afonina, Irina A.
; APPLICANT: Singer, Michael J.
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Vermeulen, Nicolaas M.J.
; TITLE OF INVENTION: Systems and Methods for Predicting Oligonucleotide Melting
; FILE REFERENCE: 17682A-003640US
; CURRENT APPLICATION NUMBER: US/10/176,972A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/054,830
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/054,832
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/431,385
; PRIOR FILING DATE: 1999-11-01
```

```
; PRIOR APPLICATION NUMBER: US 09/640,953
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/724,959
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/796,988
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:probe sequence
US-10-176-972A-70

Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGAGGCTGTTCG 14
Db      12 TGAGGCGGGTGG 1

RESULT 46
US-09-989-789-626
; Sequence 626, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-626

Query Match      46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GAGGCTGTTCG 13
Db      1 GAGGCTGTTCG 10

RESULT 47
US-09-990-186-626
; Sequence 626, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-626

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
Db 1 GAGGCTGTTG 10

RESULT 48
US-09-748-710-24
; Sequence 24, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; FILE REFERENCE: ARCD:343US
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-748-710-24

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGA 17
Db 1 CTGTTGGTGA 10

RESULT 49
US-09-989-994-626
; Sequence 626, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-626

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTTG 13
Db 1 GAGGCTGTTG 10

RESULT 50
US-10-293-222-39
; Sequence 39, Application US/10293222
; Publication No. US2004003332A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-39

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGA 17
Db 1 CTGTTGGTGA 10

RESULT 51
US-10-033-145-1906
; Sequence 1906, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1906
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1906

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 1 TCAGGCTGTT 10

```
RESULT 52
US-10-330-627-347
; Sequence 347, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-347

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTTGGCGA 17
Db 1 CTGTTGGTGA 10

RESULT 53
US-10-673-938-68/c
; Sequence 68, Application US/10673938
; Publication No. US20040152108A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Jonathan M
; APPLICANT: Bryant, Darryn E
; APPLICANT: Adams, Peter
; TITLE OF INVENTION: A method for sequence analysis
; FILE REFERENCE: 2512891
; CURRENT APPLICATION NUMBER: US/10/673,938
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00397
; PRIOR FILING DATE: 2002-03-28
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence string
US-10-673-938-68

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 10 TGAGGCTCTT 1

RESULT 54
US-10-673-938-77/c
; Sequence 77, Application US/10673938
; Publication No. US20040152108A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Jonathan M
```

```
; APPLICANT: Bryant, Darryn E
; APPLICANT: Adams, Peter
; TITLE OF INVENTION: A method for sequence analysis
; FILE REFERENCE: 2512891
; CURRENT APPLICATION NUMBER: US/10/673,938
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00397
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: USSN 60/279,238
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence string
US-10-673-938-77

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 10 TGAGGCTCTT 1

RESULT 55
US-10-673-938-89/c
; Sequence 89, Application US/10673938
; Publication No. US20040152108A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Jonathan M
; APPLICANT: Bryant, Darryn E
; APPLICANT: Adams, Peter
; TITLE OF INVENTION: A method for sequence analysis
; FILE REFERENCE: 2512891
; CURRENT APPLICATION NUMBER: US/10/673,938
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/AU02/00397
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: USSN 60/279,238
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 188
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence string
US-10-673-938-89

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
Db 10 TGAGGCTCTT 1

RESULT 56
US-10-055-728-24
; Sequence 24, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyt, Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
```

; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence H860440
US-10-055-728-24

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
|||||
Db 2 AGGCTGCTGG 11

RESULT 57
US-10-310-677-24
; Sequence 24, Application US/10310677
; Publication No. US2003021972A1
; GENERAL INFORMATION:
; APPLICANT: Kuyil v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG sequence
; OTHER INFORMATION: H860440
; NAME/KEY: misc feature
; LOCATION: (1)..(11)
US-10-310-677-24

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTGG 14
|||||
Db 2 AGGCTGCTGG 11

RESULT 58
US-09-238-351-5
; Sequence 5, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz

; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; FILE REFERENCE: A67643/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; CURRENT FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-5

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTG 10
|||||
Db 2 CTCGAGGCTG 11

RESULT 59
US-09-245-105A-5
; Sequence 5, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Yu, Changjun
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-5

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCTG 10
|||||
Db 2 CTCGAGGCTG 11

RESULT 60
US-10-096-718-20/c

; Sequence 20, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft word
; SEQ ID NO 20
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-20

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
||| |||||
DB 10 GATGCTGTTG 1

RESULT 61
US-10-096-718-40
; Sequence 40, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft word
; SEQ ID NO 40
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-40

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
||| |||||
DB 3 GATGCTGTTG 12

RESULT 62
US-09-989-789-2152
; Sequence 2152, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2152
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2152

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 16
|||||
DB 2 TGTGGCG 9

RESULT 63
US-09-989-789-2326
; Sequence 2326, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2326

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 15
|||||
DB 1 CTGTGGC 8

RESULT 64
US-09-989-789-2327
; Sequence 2327, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2327

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 65

US-09-990-186-2152
; Sequence 2152, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2152
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2152

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGTGGC 16
|||||
Db 2 TGTGTGGC 9

RESULT 66

US-09-990-186-2326
; Sequence 2326, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2326

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 67

US-09-990-186-2327
; Sequence 2327, Application US/09990186
; Publication No. US20030068675A1

; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2327

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 68

US-09-989-994-2152
; Sequence 2152, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2152
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2152

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGTGGC 16
|||||
Db 2 TGTGTGGC 9

RESULT 69

US-09-989-994-2326
; Sequence 2326, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2326
; LENGTH: 9

;
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2326

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 70
US-09-989-994-2327
; Sequence 2327, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2327
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2327

Query Match 44.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 71
US-10-033-145-940/c
; Sequence 940, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 940
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-940

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGGCTG 10
|||||
Db 10 TGAGGCTG 3

RESULT 72
US-10-330-627-292/c
; Sequence 292, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-292

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCTGTGT 13
|||||
Db 9 GGCTGTGT 2

RESULT 73
US-10-330-627-1261
; Sequence 1261, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1261

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGGC 15
|||||
Db 1 CTGTTGGC 8

RESULT 74
US-10-401-194-113
; Sequence 113, Application US/10401194
; Publication No. US20030219810A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Barnes, Glenn T.
; APPLICANT: Bertin, John
; TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN CARD4 GENE
; FILE REFERENCE: MPI02-04PIRNM
; CURRENT APPLICATION NUMBER: US/10/401,194
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/368,184
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-194-113

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGGCTG 10
|||||
DB 2 TGAGGCTG 9

RESULT 75

US-09-836-737A-4
; Sequence 4, Application US/09836737A
; Patent No. US2002025561A1
; GENERAL INFORMATION:
; APPLICANT: Hodgson, Clague; Nature Technology Corporation
; TITLE OF INVENTION: Vectors for gene self-assembly
; FILE REFERENCE: 01-04/17/01
; CURRENT APPLICATION NUMBER: US/09/836,737A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/197,882
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Plasmid
US-09-836-737A-4

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTTGCGA 17
|||||
DB 1 GCTGTTGCGA 11

RESULT 76

US-09-249-155-245/c
; Sequence 245, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 245

; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-245

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
|||||
DB 11 TTGAACCTGTT 1

RESULT 77

US-09-880-313A-59/c
; Sequence 59, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-59

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGCG 16
|||||
DB 11 GGCTGACGGCG 1

RESULT 78

US-09-970-971A-14
; Sequence 14, Application US/09970971A
; Publication No. US20030096979A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew M.
; TITLE OF INVENTION: Oligonucleotides Having DNA Form and B-DNA Form Conformational
; FILE REFERENCE: ISIS4789
; CURRENT APPLICATION NUMBER: US/09/970,971A
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030096979A1el Sequence
; NAME/KEY: misc.feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-aminolinker
US-09-970-971A-14

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGC 16
|||||: |||
Db 1 GGCTGCTGGC 11

RESULT 79
US-10-918-715-65
; Sequence 65, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-65

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGGC 15
|||||: |||
Db 1 AGGCTCTGGC 11

RESULT 80
US-10-098-816-14
; Sequence 14, Application US/10098816
; Publication No. US20030105311A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/10/098,816
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/303,586
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: 2' aminolinker linkage
US-10-098-816-14

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGC 16
|||||: |||
Db 1 GGCTGCTGGC 11

RESULT 81
US-10-314-322-245/c
; Sequence 245, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-245

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGTT 12
|||||: |||
Db 11 TTGAACCTGTT 1

RESULT 82
US-10-314-322-318
; Sequence 318, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-318

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGCTGTGG 14
| | | | |
Db 1 GTGGGTGTGG 11

RESULT 83

US-10-450-797-499
; Sequence 499, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 499
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-499

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTTGGCGAC 18
| | | | |
Db 1 CTGTTGGCGAC 11

RESULT 84

US-10-001-670-34
; Sequence 34, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/10/001,670
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/231,303
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 08/663,824
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-001-670-34

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 62;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 17
| | | | |
Db 2 GCTGTGGCGA 12

RESULT 85

US-09-989-789-2508
; Sequence 2508, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2508
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2508

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
| | | | |
Db 1 GAGGCTCTT 9

RESULT 86

US-09-990-186-2508
; Sequence 2508, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2508
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2508

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
| | | | |
Db 1 GAGGCTCTT 9

RESULT 87

US-09-989-994-2508
; Sequence 2508, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2508
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2508

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
|||:|:|
Db 1 GAGGCTCTT 9

RESULT 88
US-09-916-466-147
; Sequence 147, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Akhtar, Saghir
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 9
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-916-466-147

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
|||:|:|
Db 1 GGCUGCUGG 9

RESULT 89
US-10-277-494-147
; Sequence 147, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
; TITLE OF INVENTION: Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-K (400/064)
; CURRENT APPLICATION NUMBER: US/10/277,494
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 9
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-277-494-147

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 6 GGCTGTTGG 14
|||:|:|
Db 1 GGCUGCUGG 9

RESULT 90
US-09-238-351-1
; Sequence 1, Application US/09238351
; Patent No. US20020006643A1
; GENERAL INFORMATION:
; APPLICANT: Kayyem, Jon Faiz
; APPLICANT: Bamdad, Cynthia
; TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
; TITLE OF INVENTION: Detection
; FILE REFERENCE: A67643/RTT/RMS
; CURRENT APPLICATION NUMBER: US/09/238,351
; CURRENT FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 09/014,304
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: 60/073,011
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/084,425
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/078,102
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-1

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
|||:|:|
Db 2 CTCGAGGCT 10

RESULT 91
US-09-989-789-1278
; Sequence 1278, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1278

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 5 AGGCTGTTG 13
Db 2 AGGCTGTGG 10

RESULT 92
US-09-990-186-1278
; Sequence 1278, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1278

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTG 13
Db 2 AGGCTGTGG 10

RESULT 93
US-09-989-994-1278
; Sequence 1278, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1278

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGGCTGTTG 13
Db 2 AGGCTGTGG 10

RESULT 94
US-10-293-222-71/c
; Sequence 71, Application US/10293222
; Publication No. US2004003392A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-293-222-71

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGAGGCTGT 11
Db 9 TGAGGATGT 1

RESULT 95
US-09-245-105A-1
; Sequence 1, Application US/09245105A
; Publication No. US20030087228A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Yu, Changjun
; TITLE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
; FILE REFERENCE: A-67652/RFT/RMS
; CURRENT APPLICATION NUMBER: US/09/245,105A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/084,425
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084,509
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/135,183
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-1

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
Db 2 CTCGAGGCT 10

RESULT 96
US-10-033-145-1121
; Sequence 1121, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
```


; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1121
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1121

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGCCTGTTG 13
||| |||||
DB 1 AGCCTGTTG 9

RESULT 97
US-10-033-145-1229/c
; Sequence 1229, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1229
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1229

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGAGGCTG 10
||| |||||
DB 10 TTGGGGCTG 2

RESULT 98
US-10-033-145-1995
; Sequence 1995, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1995
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-033-145-1995

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCCTGTTGG 14
||| |||||
DB 1 GCCTGTTGG 9

RESULT 99
US-10-055-713-87
; Sequence 87, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; FILE REFERENCE: 8325-0026 / S26-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 14 target sequence
US-10-055-713-87

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
||| |||||
DB 2 CTTGAGGCT 10

RESULT 100
US-10-113-030-3
; Sequence 3, Application US/10113030
; Publication No. US20030077610A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, John
; APPLICANT: Fuller, Carl
; APPLICANT: Sood, Anup
; APPLICANT: Kumar, Shiv
; TITLE OF INVENTION: Terminal-Phosphate-Labeled Nucleotides and Methods of Use
; FILE REFERENCE: PB0156-1
; CURRENT APPLICATION NUMBER: US/10/113,030
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/315,798
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Template
US-10-113-030-3

Query Match 41.1%; Score 7.4; DB 1; Length 10;

```
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGGCTGTTG 13
Db 2 AGGCTGCTG 10

RESULT 101
US-10-142-111-20
; Sequence 20, Application US/10142111
; Publication No. US20030101485A1
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jingding
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/142,111
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-142-111-20

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGCTGTT 12
Db 2 GAGGCTGTT 10

RESULT 102
US-10-055-711-91
; Sequence 91, Application US/10055711
; Publication No. US20030108880A1
; GENERAL INFORMATION:
; APPLICANT: REBAR, Edward
; APPLICANT: JAMIESON, Andrew
; TITLE OF INVENTION: MODIFIED ZINC FINGER BINDING PROTEINS
; FILE REFERENCE: 8325-0025
; CURRENT APPLICATION NUMBER: US/10/055,711
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP #14 target
US-10-055-711-91

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
Db 2 CTTGAGGCT 10

RESULT 103
US-10-358-818-3
```

```
; Sequence 3, Application US/10358818
; Publication No. US20030162213A1
; GENERAL INFORMATION:
; APPLICANT: Fuller, Carl
; APPLICANT: Kumar, Shiv
; APPLICANT: Sood, Anup
; APPLICANT: Nelson, John
; TITLE OF INVENTION: Terminal-Phosphate-Labeled Nucleotides and Methods of Use
; FILE REFERENCE: PB0156-1CIP
; CURRENT APPLICATION NUMBER: US/10/358,818
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/315,798
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 10/113,030
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Template
US-10-358-818-3
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 5 AGGCTGTTG 13
Db 2 AGGCTGCTG 10
```

RESULT 104

```
US-10-223-765-292
; Sequence 292, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-292
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CTTGAGGCT 9
Db 2 CTTGAGGCT 10
```

RESULT 105

US-10-330-627-495
; Sequence 495, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 495
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-495

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
|||||||
Db 2 GGCTGTTGG 10

RESULT 106
US-10-330-627-1121
; Sequence 1121, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1121

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTGGGGCTG 10
|||||||
Db 2 TTGGGGCTG 10

RESULT 107
US-10-080-608A-123/c
; Sequence 123, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
; OTHER INFORMATION: elements
US-10-080-608A-123

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
|||||||
Db 10 CTGGAGGCT 2

RESULT 108
US-10-160-358-117
; Sequence 117, Application US/10160358
; Publication No. US20030198969A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Cappola, Gina-Marie
; APPLICANT: Koshiy, Beena
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE
; FILE REFERENCE: TACR2 MWH-0225US
; CURRENT APPLICATION NUMBER: US/10/160,358
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/47394
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/247,649
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-358-117

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
|||||||
Db 1 CTTGAGGCT 9

RESULT 109
US-10-370-685-33/c
; Sequence 33, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA

; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: PNA complementary joining portion
US-10-370-685-33

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
||| |||||
Db 10 CTGGAGGCT 2

RESULT 110
US-10-004-378A-185
; Sequence 185, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazaryna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Casman, Stacie J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Vernet, Corrine A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Agee, Michele
; APPLICANT: Rastelli, Luca
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie
; APPLICANT: Edinger, Schlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Peyman, John A
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David J
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A

; TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding Th
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-179
; CURRENT APPLICATION NUMBER: US/10/004,378A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/242,882
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,765
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/300,206
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/242,789
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,768
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,767
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/243,622
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/273,047
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/243,591
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,950
; PRIOR FILING DATE: 2000-10-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 185
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SAGE library
; OTHER INFORMATION: tag sequence
US-10-004-378A-185

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AGCGTGTG 13
||| |||||
Db 1 AGCGTGTG 9

RESULT 111
US-10-418-552-73
; Sequence 73, Application US/10418552
; Publication No. US20030233672A1
; GENERAL INFORMATION:
; APPLICANT: Li, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; APPLICANT: VAN EENENNAAM, Alison
; APPLICANT: VENKATRAMESH, Mylavaram
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR REGULATION OF PLANT GAMMA-METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029 (S29-US1)
; CURRENT APPLICATION NUMBER: US/10/418,552
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,488
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/385,992
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/442,470
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: AGMT14 target
US-10-418-552-73

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
||| |||||
Db 2 CTTGAGGCT 10

RESULT 112
US-10-650-454-92
; Sequence 92, Application US/10650454
; Publication No. US20040091990A1
; GENERAL INFORMATION:
; APPLICANT: Li, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF PLANT GAMMA-TOCOPHEROL
; FILE REFERENCE: 8325-0029.30 (S29-US2)
; CURRENT APPLICATION NUMBER: US/10/650,454
; CURRENT FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: 60/406,849
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ZFP14 target
US-10-650-454-92

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
DB 2 CTTGTGGCT 10
|||||

RESULT 113

US-10-470-180-87
; Sequence 87, Application US/10470180
; Publication No. US20040128717A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; TITLE OF INVENTION: REGULATION IN PLANTS
; FILE REFERENCE: 8325-0026.30 / S26-US2
; CURRENT APPLICATION NUMBER: US/10/470,180
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: PCT/US02/01906
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 14 target sequence
US-10-470-180-87

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
DB 2 CTTGTGGCT 10
|||||

RESULT 114

US-09-950-459-3/c
; Sequence 3, Application US/09950459
; Patent No. US20020064772A1
; GENERAL INFORMATION:
; APPLICANT: Gildea, Brian D.
; APPLICANT: Coull, James M.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Fiandaca, Mark J.
; TITLE OF INVENTION: Methods, Kits and Compositions Pertaining To Linear
; TITLE OF INVENTION: Beacons
; FILE REFERENCE: BP9703US-DV1
; CURRENT APPLICATION NUMBER: US/09/950,459
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/063,283

; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 09/179,162
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: 5'Fluorescein
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: 3' Dabcyl
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PROBE OR TARGET
US-09-950-459-3

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGC 15
DB 9 GCTGTGGC 1
|||||

RESULT 115

US-09-772-719-82/c
; Sequence 82, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-09-772-719-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
|||||
Db 11 TGAGCCTGT 3

RESULT 116

US-09-249-155-37/c
; Sequence 37, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; PRIOR FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-37

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGCGGAC 18
|||||
Db 11 GTTGTGAC 3

RESULT 117

US-09-967-237-82/c
; Sequence 82, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.58-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
US-09-967-237-82

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGAGGCTGT 11
|||||
Db 11 TGAGCCTGT 3

RESULT 118

US-09-918-715-10/c
; Sequence 10, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-10

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAGGCT 9
|||||
Db 11 CTTGAGGAT 3

RESULT 119

US-10-314-322-37/c
; Sequence 37, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-37

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTTGCGGAC 18
|||||

```
Db 11 GTTGGTGAC 3

; OTHER INFORMATION: PROBE OR TARGET
US-10-376-559-3

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGC 15
Db 9 GCTGTGGC 1

RESULT 120
US-10-314-322-266/c
; Sequence 266, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-266

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTTGGGAC 18
Db 11 GTTGGTGAC 3

RESULT 121
US-10-376-559-3/c
; Sequence 3, Application US/10376559
; Publication No. US200302327A1
; GENERAL INFORMATION:
; APPLICANT: Gildea, Brian D.
; APPLICANT: Coull, James M.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Fiandaca, Mark J.
; TITLE OF INVENTION: Methods, Kits and Compositions Pertaining To Linear
; TITLE OF INVENTION: Beacons
; FILE REFERENCE: BP9702US-CPI-DV2
; CURRENT APPLICATION NUMBER: US/10/376,559
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/063,283
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 09/179,162
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: 5'Fluorescein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: 3' Dabcyl
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

; OTHER INFORMATION: PROBE OR TARGET
US-10-376-559-3

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
Db 11 CTTGAGGAT 3

RESULT 123
US-10-450-797-836/c
; Sequence 836, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 836
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-836

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGAGGCT 9
Db 11 CTTGAGGAT 3

RESULT 123
US-10-450-797-836/c
; Sequence 836, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 836
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-836

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 3 TGAGGCTGT 11
|||||
Db 9 TGAGGATGT 1

RESULT 124

US-10-450-797-1381
; Sequence 1381, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1381
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1381

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCTGTTGG 14
|||||
Db 2 GGCTGTTGG 10

RESULT 125

US-10-027-632-177591
; Sequence 177591, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177591
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177591

Query Match 38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TTGAGGC 8
|||||
Db 2 TTGAGGC 8

RESULT 126

US-10-027-632-177591
; Sequence 177591, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177591
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177591

Query Match 38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGAGGC 8
|||||
Db 2 TTGAGGC 8

RESULT 127

US-09-989-789-531
; Sequence 531, Application US/09989789
; Patent No. US2002006379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-531

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGG 14
|||||||
Db 2 CTGTTGG 8

RESULT 128

US-09-989-789-2126
; Sequence 2126, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2126
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2126

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||||
Db 2 AGGCTGT 8

RESULT 129

US-09-989-789-2127
; Sequence 2127, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2127
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2127

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||||
Db 2 AGGCTGT 8

RESULT 130

US-09-989-789-2128
; Sequence 2128, Application US/09989789
; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2128
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2128

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||||
Db 2 AGGCTGT 8

RESULT 131

US-09-989-789-2129
; Sequence 2129, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2129
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2129

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||||
Db 1 GAGGCTG 7

RESULT 132

US-09-990-186-531
; Sequence 531, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-531

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGG 14
|||
Db 2 CTGTTGG 8

RESULT 133
US-09-990-186-2126
; Sequence 2126, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2126
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2126

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||
Db 2 AGGCTGT 8

RESULT 134
US-09-990-186-2127
; Sequence 2127, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2127
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2127

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||
Db 2 AGGCTGT 8

RESULT 135
US-09-990-186-2128
; Sequence 2128, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2128
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2128

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||
Db 2 AGGCTGT 8

RESULT 136
US-09-990-186-2129
; Sequence 2129, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2129
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2129

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||
Db 1 GAGGCTG 7

RESULT 137
US-09-989-994-531
; Sequence 531, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang

```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-531

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTTGG 14
        |||||
Db       2 CTGTTGG 8

RESULT 138
US-09-989-994-2126
; Sequence 2126, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2126
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2126

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGCTGT 11
        |||||
Db       2 AGGCTGT 8

RESULT 139
US-09-989-994-2127
; Sequence 2127, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2127
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2127

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGCTGT 11
        |||||
Db       2 AGGCTGT 8

RESULT 140
US-09-989-994-2128
; Sequence 2128, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2128
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2128

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGGCTGT 11
        |||||
Db       2 AGGCTGT 8

RESULT 141
US-09-989-994-2129
; Sequence 2129, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2129
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2129

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
        |||||
```


; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-556

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGC 15
|||||||

Db 2 TGTGGC 8
|||||||

RESULT 145

US-09-989-789-1279
; Sequence 1279, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1279

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||||

Db 4 GAGGCTG 10
|||||||

RESULT 146

US-09-989-789-1308
; Sequence 1308, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1308

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||||

Db 4 GAGGCTG 10
|||||||

RESULT 147
US-09-989-789-1313
; Sequence 1313, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1313
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1313

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||||

Db 4 GAGGCTG 10
|||||||

RESULT 148

US-09-989-789-1624
; Sequence 1624, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1624

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
|||||||

Db 4 GAGGCTG 10
|||||||

RESULT 149

US-09-989-789-1625
; Sequence 1625, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2

```
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1625
```

```
Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GAGGCTG 10
        |||
Db      4 GAGGCTG 10
```

RESULT 150

```
US-09-990-186-556
; Sequence 556, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 556
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-556
```

```
Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 TGTGGC 15
        |||
Db      2 TGTGGC 8
```

RESULT 151

```
US-09-990-186-1279
; Sequence 1279, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
```

US-09-990-186-1279

```
Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GAGGCTG 10
        |||
Db      4 GAGGCTG 10
```

RESULT 152

```
US-09-990-186-1308
; Sequence 1308, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1308
```

```
Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GAGGCTG 10
        |||
Db      4 GAGGCTG 10
```

RESULT 153

```
US-09-990-186-1313
; Sequence 1313, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1313
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1313
```

```
Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GAGGCTG 10
        |||
Db      4 GAGGCTG 10
```

```
RESULT 154
US-09-990-186-1624
; Sequence 1624, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1624

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
        |||||
Db      4 GAGGCTG 10

RESULT 155
US-09-990-186-1625
; Sequence 1625, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1625

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
        |||||
Db      4 GAGGCTG 10

RESULT 156
US-09-989-994-556
; Sequence 556, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-556

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
        |||||
Db      4 GAGGCTG 10

RESULT 157
US-09-989-994-1279
; Sequence 1279, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1279

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
        |||||
Db      4 GAGGCTG 10

RESULT 158
US-09-989-994-1308
; Sequence 1308, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1308
```

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
| | | | |
Db 4 GAGGCTG 10

RESULT 159
US-09-989-994-1313
; Sequence 1313, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1313
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1313

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
| | | | |
Db 4 GAGGCTG 10

RESULT 160
US-09-989-994-1624
; Sequence 1624, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1624

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
| | | | |
Db 4 GAGGCTG 10

RESULT 161
US-09-989-994-1625

; Sequence 1625, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1625

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTG 10
| | | | |
Db 4 GAGGCTG 10

RESULT 162
US-10-033-145-679
; Sequence 679, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 679
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-679

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTTGG 14
| | | | |
Db 2 CTGTTGG 8

RESULT 163
US-10-033-145-1549
; Sequence 1549, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800


```
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1549
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-033-145-1549

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 AGGCTGT 11
Db      3 AGGCTGT 9

RESULT 164
US-10-033-145-1843/c
; Sequence 1843, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1843
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-033-145-1843

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GCTGTGT 13
Db      8 GCTGTGT 2

RESULT 165
US-10-033-145-1923
; Sequence 1923, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1923
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-033-145-1923

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGCTGTT 12
Db      4 GGCTGTT 10

RESULT 168
US-10-033-627-410
; Sequence 410, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-330-627-178

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTGAGG 7
Db      9 CTTGAGG 3

RESULT 167
US-10-330-627-178
; Sequence 178, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-330-627-178

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTGAGG 7
Db      9 CTTGAGG 3

RESULT 167
US-10-330-627-178
; Sequence 178, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-330-627-178

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGCTGTT 12
Db      4 GGCTGTT 10

RESULT 168
US-10-330-627-410
; Sequence 410, Application US/10330627
; Publication No. US20030175771A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 1564
; SEQ ID NO 410
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-410

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
Db      2 GAGGCTG 8

RESULT 169
US-10-330-627-411
; Sequence 411, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-411

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
Db      2 GAGGCTG 8

RESULT 170
US-10-330-627-548/c
; Sequence 548, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-548

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGCTG 10
Db      2 GAGGCTG 8

RESULT 171
US-10-330-627-912/c
; Sequence 912, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 912
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-912

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTTG 13
Db      9 GCTGTTG 3

RESULT 172
US-10-330-627-1025
; Sequence 1025, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1025

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTTG 13
Db      9 GCTGTTG 3

RESULT 173
US-10-330-627-1025
; Sequence 1025, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1025

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 7 GCTGTTG 13
|||||
Db 1 GCTGTTG 7

RESULT 173

US-10-330-627-1262/c
; Sequence 1262, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1262
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1262

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGGCT 9
|||||
Db 9 TGAGGCT 3

RESULT 174

US-10-330-627-1560/c
; Sequence 1560, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1560
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1560

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGAGGCT 9
|||||
Db 9 TGAGGCT 3

RESULT 175

US-10-160-358-98
; Sequence 98, Application US/10160358
; Publication No. US20030198969A1
; GENERAL INFORMATION:
; APPLICANT: Genenase Pharmaceuticals, Inc.

; APPLICANT: Bieglecki, Karyn
; APPLICANT: Cappola, Gina-Marie
; APPLICANT: Koshy, Beena
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE
; FILE REFERENCE: TACR2.MWH-0225US
; CURRENT APPLICATION NUMBER: US/10/160,358
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/47394
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/247,649
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-358-98

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGCTGT 11
|||||
Db 3 AGGCTGT 9

RESULT 176

US-09-989-789-629
; Sequence 629, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 629
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-629

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTTGGCG 16
|||||
Db 1 GCTGTTGGAG 10

RESULT 177

US-09-846-033B-240
; Sequence 240, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.

```
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
;
US-09-846-033B-240

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCTGTTGGCG 16
Db      1 GCTGGGGCG 10
      |||||
RESULT 178
US-09-990-186-629
; Sequence 629, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 629
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-990-186-629

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCTGTTGGCG 16
Db      1 GCTGGGGCG 10
      |||||
RESULT 179
US-09-989-994-629
; Sequence 629, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 629

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCTGTTGGCG 16
Db      1 GGTGTTGGAG 10
      |||||
RESULT 180
US-10-293-222-96
; Sequence 96, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-293-222-96

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTGGC 15
Db      1 GGCTCTGGC 10
      |||||
RESULT 181
US-10-293-222-102/c
; Sequence 102, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-293-222-102

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
   ||| ||| |||
Db 10 TGAAGCAGTT 1

RESULT 182
US-10-293-222-341
; Sequence 341, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 341
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-341

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGC 15
   ||| ||| |||
Db 1 GGCTGGGGC 10

RESULT 183
US-10-033-145-152/c
; Sequence 152, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 152
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-152

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
   ||| ||| |||
Db 10 TGAAGCAGTT 1

RESULT 184
US-10-033-145-193/c
; Sequence 193, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 193
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-193

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
   ||| ||| |||
Db 10 TGAAGCAGTT 1

RESULT 185
US-10-033-145-200/c
; Sequence 200, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 200
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-200

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGC 15
   ||| ||| |||
Db 10 GGCCCTGGC 1

RESULT 186
US-10-033-145-210
; Sequence 210, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
```

; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-210

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTTGGC 15
||| ||| |||
Db 1 GGCAGTAGGC 10

RESULT 187
US-10-033-145-414
; Sequence 414, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 414
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-414

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
||| ||| |||
Db 1 TGATGCTGAT 10

RESULT 188
US-10-033-145-604
; Sequence 604, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 604
; LENGTH: 10

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-604

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
||| ||| |||
Db 1 TGATGATGTT 10

RESULT 189
US-10-033-145-646/c
; Sequence 646, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-646

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
||| ||| |||
Db 10 GAGCCTTTTG 1

RESULT 190
US-10-033-145-1324
; Sequence 1324, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1324
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1324

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGGCTGTTGG 14
||| ||| |||
Db 1 AGGATGTGGG 10

RESULT 191
 US-10-033-145-1451
 ; Sequence 1451, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1451
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1451

Query Match 37.8%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 82;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 AGGCTGTTGG 14
 |||||
 Db 1 AGGCTTAGG 10

RESULT 192
 US-10-033-145-1686
 ; Sequence 1686, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1686
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1686

Query Match 37.8%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 82;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GAGGCTCTTG 13
 |||||
 Db 1 GAGGCTCTG 10

RESULT 193
 US-10-033-145-1973
 ; Sequence 1973, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1973
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1973

Query Match 37.8%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 82;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 GCTGTTGGCG 16
 |||||
 Db 1 GCTGTAGGG 10

RESULT 194
 US-10-033-145-2032/c
 ; Sequence 2032, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2032
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-2032

Query Match 37.8%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 82;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGAGGCTGTT 12
 |||||
 Db 10 TGAGGATCTT 1

RESULT 195
 US-10-033-145-2037/c
 ; Sequence 2037, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2037
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-10-033-145-2037

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAGGCTGTT 12
||| |||||
Db 10 TAAAGCTGTT 1

RESULT 196

US-10-033-145-2103
; Sequence 2103, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2103

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGGCTGTTG 13
||| |||||
Db 1 GGGGCTGTGG 10

RESULT 197

US-10-033-145-2123/c
; Sequence 2123, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2123
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2123

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGAGGCTGT 11
||| |||||
Db 10 TTGGGCGAGT 1

RESULT 198

US-10-006-069A-240
; Sequence 240, Application US/10006069A
; Publication No. US20030021776A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005830US
; CURRENT APPLICATION NUMBER: US/10/006,069A
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/846,033
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-10-006-069A-240

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 16
||| |||||
Db 1 GCTGGGGCG 10

RESULT 199

US-10-176-464A-43
; Sequence 43, Application US/10176464A
; Publication No. US20030165902A1
; GENERAL INFORMATION:
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Lee, Helen
; APPLICANT: Messer, Chad
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOYPES OF THE F2R GENE
; FILE REFERENCE: P2R MWH-1457US
; CURRENT APPLICATION NUMBER: US/10/176,464A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/30876
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/236,603
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-176-464A-43

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTGTGGC 15


```
Db      ||| ||| |||
1 GCGCGTTAGC 10

RESULT 200
US-10-329-465-48/c
; Sequence 48, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-48

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GGCTGTGGC 15
Db      ||| ||| |||
10 GGTTTGGC 1

RESULT 201
US-10-330-627-279
; Sequence 279, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-279

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGGCTGTTG 13
Db      ||| ||| |||
1 GGGGCTGTGG 10

RESULT 202
US-10-330-627-280
; Sequence 280, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
```

```
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-280

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GAGGCTGTTG 13
Db      ||| ||| |||
1 GGGGCTGTGG 10

RESULT 203
US-10-330-627-963/c
; Sequence 963, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 963
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-963

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TGTGGCGAC 18
Db      ||| ||| |||
10 TGATGGCGC 1

RESULT 204
US-10-330-627-1029
; Sequence 1029, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1029
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1029

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      6 GGCTGTTGGC 15
Db      1 GGCTGGGGGC 10
      ||||| |||

RESULT 205
US-10-330-627-1321
; Sequence 1321, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1321
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1321

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      6 GGCTGTTGGC 15
Db      1 GGCTCCTGGC 10
      ||||| |||

RESULT 206
US-10-330-627-1348
; Sequence 1348, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1348
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1348

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      5 AGGCTGTTGG 14
      ||||| |||

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1029

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      6 GGCTGTTGGC 15
Db      1 GGCTGGGGGC 10
      ||||| |||

RESULT 207
US-10-330-627-1376/c
; Sequence 1376, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1376
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1376

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      3 TCAGGCTGTT 12
Db      10 TGAAGCAGTT 1
      ||||| |||

RESULT 208
US-10-330-627-1508
; Sequence 1508, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1508
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1508

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 2;

QY      6 GGCTGTTGGC 15
Db      1 GGCTGGGGGC 10
      ||||| |||

RESULT 209
US-10-080-608A-117
; Sequence 117, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
```

; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
; OTHER INFORMATION: elements
US-10-080-608A-117

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
||| |||||
Db 1 TGGGGATGTT 10

RESULT 210

US-10-197-019-84
; Sequence 84, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MWH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-84

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
||| |||||
Db 1 TGTGCTGTT 10

RESULT 211

US-10-370-685-27
; Sequence 27, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27

; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: PNA complementary joining portion
US-10-370-685-27

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGGCTGTT 12
||| |||||
Db 1 TGGGGATGTT 10

Search completed: September 9, 2004, 11:21:30
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:24:52 ; Search time 0.001 Seconds
(without alignments)
156.312 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18
Sequence: 1 gtgagcattcattcctt 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 396 seqs, 4342 residues

Total number of hits satisfying chosen parameters: 792

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 396 summaries

Database : rge32.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
C 1	12.4	68.9	15	1	AR033668	1	ACCESSION:AR033668
C 2	12.4	68.9	15	1	AR113490	1	ACCESSION:AR113490
C 3	12.4	68.9	15	1	I57897	1	ACCESSION:I57897
C 4	12.4	68.9	15	1	BD207401	1	ACCESSION:BD207401
C 5	11.8	65.6	17	1	AX139142	1	ACCESSION:AX139142
C 6	11.8	65.6	17	1	BD014758	1	ACCESSION:BD014758
C 7	11.4	63.3	17	1	AX139154	1	ACCESSION:AX139154
C 8	11.4	63.3	17	1	BD013438	1	ACCESSION:BD013438
C 9	11.2	62.2	17	1	AX727596	1	ACCESSION:AX727596
C 10	11	61.1	14	1	A35654	1	ACCESSION:A35654
C 11	10.8	60.0	15	1	AR180366	1	ACCESSION:AR180366
C 12	10	55.6	10	1	BD239875	1	ACCESSION:BD239875
C 13	10	55.6	14	1	I46929	1	ACCESSION:I46929
C 14	10	55.6	15	1	AR033669	1	ACCESSION:AR033669
C 15	10	55.6	15	1	AR113491	1	ACCESSION:AR113491
C 16	10	55.6	15	1	I57898	1	ACCESSION:I57898
C 17	10	55.6	15	1	BD207402	1	ACCESSION:BD207402
C 18	9.8	54.4	14	1	A42517	1	ACCESSION:A42517
C 19	9.8	54.4	14	1	A88709	1	ACCESSION:A88709
C 20	9.8	54.4	14	1	BD066222	1	ACCESSION:BD066222
C 21	9.8	54.4	15	1	AR033495	1	ACCESSION:AR033495
C 22	9.8	54.4	15	1	AR113317	1	ACCESSION:AR113317
C 23	9.8	54.4	15	1	I57724	1	ACCESSION:I57724
C 24	9.8	54.4	15	1	AR180531	1	ACCESSION:AR180531
C 25	9.8	54.4	15	1	BD207228	1	ACCESSION:BD207228
C 26	9.4	52.2	12	1	BD174826	1	ACCESSION:BD174826
C 27	9.4	52.2	14	1	A35614	1	ACCESSION:A35614
C 28	9	50.0	10	1	AR107783	1	ACCESSION:AR107783
C 29	9	50.0	10	1	AR107805	1	ACCESSION:AR107805
C 30	9	50.0	10	1	AR107806	1	ACCESSION:AR107806
C 31	9	50.0	11	1	AX394637	1	ACCESSION:AX394637
C 32	9	50.0	11	1	AX394655	1	ACCESSION:AX394655
C 33	9	50.0	11	1	AX625339	1	ACCESSION:AX625339

ACCESSION:AX632760	11	1	AX632760	50.0	9	34
ACCESSION:AJ599093	12	1	AX599093	50.0	9	35
ACCESSION:AR100991	12	1	AR100991	48.9	8	C 36
ACCESSION:AR371424	12	1	AR371424	48.9	8	C 37
ACCESSION:AR107819	10	1	AR107819	46.7	8	38
ACCESSION:BD239322	10	1	BD239322	46.7	8	39
ACCESSION:E04663	10	1	E04663	46.7	8	C 40
ACCESSION:AR029409	11	1	AR029409	46.7	8	41
ACCESSION:AR030100	11	1	AR030100	46.7	8	C 42
ACCESSION:AR049977	11	1	AR049977	46.7	8	43
ACCESSION:AR058872	11	1	AR058872	46.7	8	44
ACCESSION:AR058873	11	1	AR058873	46.7	8	45
ACCESSION:AR058874	11	1	AR058874	46.7	8	46
ACCESSION:AR079577	11	1	AR079577	46.7	8	47
ACCESSION:AR079578	11	1	AR079578	46.7	8	48
ACCESSION:AR079579	11	1	AR079579	46.7	8	49
ACCESSION:AR123286	11	1	AR123286	46.7	8	50
ACCESSION:AR123287	11	1	AR123287	46.7	8	51
ACCESSION:AR123288	11	1	AR123288	46.7	8	52
ACCESSION:AR123288	11	1	AR123288	46.7	8	53
ACCESSION:AR123288	11	1	AR123288	46.7	8	54
ACCESSION:AR123288	11	1	AR123288	46.7	8	55
ACCESSION:AR123288	11	1	AR123288	46.7	8	56
ACCESSION:AR123288	11	1	AR123288	46.7	8	57
ACCESSION:AR123288	11	1	AR123288	46.7	8	58
ACCESSION:AR123288	11	1	AR123288	46.7	8	59
ACCESSION:AR123288	11	1	AR123288	46.7	8	60
ACCESSION:AR123288	11	1	AR123288	46.7	8	61
ACCESSION:AR123288	11	1	AR123288	46.7	8	62
ACCESSION:AR123288	11	1	AR123288	46.7	8	63
ACCESSION:AR123288	11	1	AR123288	46.7	8	64
ACCESSION:AR123288	11	1	AR123288	46.7	8	65
ACCESSION:AR123288	11	1	AR123288	46.7	8	66
ACCESSION:AR123288	11	1	AR123288	46.7	8	67
ACCESSION:AR123288	11	1	AR123288	46.7	8	68
ACCESSION:AR123288	11	1	AR123288	46.7	8	69
ACCESSION:AR123288	11	1	AR123288	46.7	8	70
ACCESSION:AR123288	11	1	AR123288	46.7	8	71
ACCESSION:AR123288	11	1	AR123288	46.7	8	72
ACCESSION:AR123288	11	1	AR123288	46.7	8	73
ACCESSION:AR123288	11	1	AR123288	46.7	8	74
ACCESSION:AR123288	11	1	AR123288	46.7	8	75
ACCESSION:AR123288	11	1	AR123288	46.7	8	76
ACCESSION:AR123288	11	1	AR123288	46.7	8	77
ACCESSION:AR123288	11	1	AR123288	46.7	8	78
ACCESSION:AR123288	11	1	AR123288	46.7	8	79
ACCESSION:AR123288	11	1	AR123288	46.7	8	80
ACCESSION:AR123288	11	1	AR123288	46.7	8	81
ACCESSION:AR123288	11	1	AR123288	46.7	8	82
ACCESSION:AR123288	11	1	AR123288	46.7	8	83
ACCESSION:AR123288	11	1	AR123288	46.7	8	84
ACCESSION:AR123288	11	1	AR123288	46.7	8	85
ACCESSION:AR123288	11	1	AR123288	46.7	8	86
ACCESSION:AR123288	11	1	AR123288	46.7	8	87
ACCESSION:AR123288	11	1	AR123288	46.7	8	88
ACCESSION:AR123288	11	1	AR123288	46.7	8	89
ACCESSION:AR123288	11	1	AR123288	46.7	8	90
ACCESSION:AR123288	11	1	AR123288	46.7	8	91
ACCESSION:AR123288	11	1	AR123288	46.7	8	92
ACCESSION:AR123288	11	1	AR123288	46.7	8	93
ACCESSION:AR123288	11	1	AR123288	46.7	8	94
ACCESSION:AR123288	11	1	AR123288	46.7	8	95
ACCESSION:AR123288	11	1	AR123288	46.7	8	96
ACCESSION:AR123288	11	1	AR123288	46.7	8	97
ACCESSION:AR123288	11	1	AR123288	46.7	8	98
ACCESSION:AR123288	11	1	AR123288	46.7	8	99
ACCESSION:AR123288	11	1	AR123288	46.7	8	100
ACCESSION:AR123288	11	1	AR123288	46.7	8	101
ACCESSION:AR123288	11	1	AR123288	46.7	8	102
ACCESSION:AR123288	11	1	AR123288	46.7	8	103
ACCESSION:AR123288	11	1	AR123288	46.7	8	104
ACCESSION:AR123288	11	1	AR123288	46.7	8	105
ACCESSION:AR123288	11	1	AR123288	46.7	8	106

c 107	7.8	43.3	11	1	AX624355	ACCESSION:AX624355	c 180	7.4	41.1	10	1	E39654	ACCESSION:E39654
108	7.8	43.3	11	1	AX626174	ACCESSION:AX626174	181	7.4	41.1	10	1	I90236	ACCESSION:I90236
109	7.8	43.3	11	1	AX626909	ACCESSION:AX626909	182	7.4	41.1	10	1	I90236	ACCESSION:AR219658
110	7.8	43.3	11	1	AX628589	ACCESSION:AX628589	183	7.4	41.1	10	1	AR225432	ACCESSION:AR225432
c 111	7.8	43.3	11	1	AX628882	ACCESSION:AX628882	184	7.4	41.1	10	1	AR241699	ACCESSION:AR241699
c 112	7.8	43.3	11	1	AX629288	ACCESSION:AX629288	185	7.4	41.1	10	1	AR303338	ACCESSION:AR303338
c 113	7.8	43.3	11	1	AX629753	ACCESSION:AX629753	186	7.4	41.1	10	1	AR303662	ACCESSION:AR303662
c 114	7.8	43.3	11	1	AX630084	ACCESSION:AX630084	187	7.4	41.1	10	1	AR303664	ACCESSION:AR303664
c 115	7.8	43.3	11	1	AX630434	ACCESSION:AX630434	188	7.4	41.1	10	1	AR344453	ACCESSION:AR344453
c 116	7.8	43.3	11	1	AX631267	ACCESSION:AX631267	189	7.4	41.1	10	1	AR344454	ACCESSION:AR344454
c 117	7.8	43.3	11	1	AX631362	ACCESSION:AX631362	190	7.4	41.1	10	1	AR350756	ACCESSION:AR350756
c 118	7.8	43.3	11	1	AX631776	ACCESSION:AX631776	191	7.4	41.1	10	1	AR433132	ACCESSION:AR433132
c 119	7.8	43.3	11	1	AX632856	ACCESSION:AX632856	192	7.4	41.1	10	1	AX152820	ACCESSION:AX152820
c 120	7.8	43.3	11	1	S83243	ACCESSION:S83243	193	7.4	41.1	10	1	AX152965	ACCESSION:AX152965
c 121	7.8	43.3	12	1	A13913	ACCESSION:A13913	194	7.4	41.1	10	1	AX153006	ACCESSION:AX153006
c 122	7.8	43.3	12	1	AR005058	ACCESSION:AR005058	195	7.4	41.1	10	1	AX153007	ACCESSION:AX153007
c 123	7.8	43.3	12	1	AR034968	ACCESSION:AR034968	196	7.4	41.1	10	1	AX153251	ACCESSION:AX153251
c 124	7.8	43.3	12	1	AR060874	ACCESSION:AR060874	197	7.4	41.1	10	1	AX301460	ACCESSION:AX301460
c 125	7.8	43.3	12	1	AR082052	ACCESSION:AR082052	198	7.4	41.1	10	1	AX301515	ACCESSION:AX301515
c 126	7.8	43.3	12	1	AR101008	ACCESSION:AR101008	199	7.4	41.1	10	1	AX301571	ACCESSION:AX301571
c 127	7.8	43.3	12	1	AR110808	ACCESSION:AR110808	200	7.4	41.1	10	1	AX301574	ACCESSION:AX301574
c 128	7.8	43.3	12	1	AR118443	ACCESSION:AR118443	201	7.4	41.1	10	1	AX301623	ACCESSION:AX301623
c 129	7.8	43.3	12	1	AR151011	ACCESSION:AR151011	202	7.4	41.1	10	1	AX302568	ACCESSION:AX302568
c 130	7.8	43.3	12	1	AR162278	ACCESSION:AR162278	203	7.4	41.1	10	1	AX316766	ACCESSION:AX316766
c 131	7.8	43.3	12	1	AR167736	ACCESSION:AR167736	204	7.4	41.1	10	1	AX321517	ACCESSION:AX321517
c 132	7.8	43.3	12	1	E29620	ACCESSION:E29620	205	7.4	41.1	10	1	AX351118	ACCESSION:AX351118
c 133	7.8	43.3	12	1	E38726	ACCESSION:E38726	206	7.4	41.1	10	1	AX510722	ACCESSION:AX510722
c 134	7.8	43.3	12	1	E64152	ACCESSION:E64152	207	7.4	41.1	10	1	BD065288	ACCESSION:BD065288
c 135	7.8	43.3	12	1	I07917	ACCESSION:I07917	208	7.4	41.1	10	1	BD083377	ACCESSION:BD083377
c 136	7.8	43.3	12	1	I18287	ACCESSION:I18287	209	7.4	41.1	10	1	BD084309	ACCESSION:BD084309
c 137	7.8	43.3	12	1	I24500	ACCESSION:I24500	210	7.4	41.1	10	1	BD161423	ACCESSION:BD161423
c 138	7.8	43.3	12	1	I28894	ACCESSION:I28894	211	7.4	41.1	10	1	BD166941	ACCESSION:BD166941
c 139	7.8	43.3	12	1	I33032	ACCESSION:I33032	212	7.4	41.1	11	1	AR001155	ACCESSION:AR001155
c 140	7.8	43.3	12	1	I79628	ACCESSION:I79628	213	7.4	41.1	11	1	AR003033	ACCESSION:AR003033
c 141	7.8	43.3	12	1	AR199158	ACCESSION:AR199158	214	7.4	41.1	11	1	AR007243	ACCESSION:AR007243
c 142	7.8	43.3	12	1	AR218167	ACCESSION:AR218167	215	7.4	41.1	11	1	AR030101	ACCESSION:AR030101
c 143	7.8	43.3	12	1	AR222607	ACCESSION:AR222607	216	7.4	41.1	11	1	AR033007	ACCESSION:AR033007
c 144	7.8	43.3	12	1	AR231645	ACCESSION:AR231645	217	7.4	41.1	11	1	AR062447	ACCESSION:AR062447
c 145	7.8	43.3	12	1	AR277890	ACCESSION:AR277890	218	7.4	41.1	11	1	AR164474	ACCESSION:AR164474
c 146	7.8	43.3	12	1	AR371441	ACCESSION:AR371441	219	7.4	41.1	11	1	AR170029	ACCESSION:AR170029
c 147	7.8	43.3	12	1	AR382247	ACCESSION:AR382247	220	7.4	41.1	11	1	AR170456	ACCESSION:AR170456
c 148	7.8	43.3	12	1	AR408045	ACCESSION:AR408045	221	7.4	41.1	11	1	I06332	ACCESSION:I06332
c 149	7.8	43.3	12	1	AX319642	ACCESSION:AX319642	222	7.4	41.1	11	1	I27733	ACCESSION:I27733
c 150	7.8	43.3	12	1	AX319823	ACCESSION:AX319823	223	7.4	41.1	11	1	I28614	ACCESSION:I28614
c 151	7.8	43.3	12	1	AX350611	ACCESSION:AX350611	224	7.4	41.1	11	1	I29747	ACCESSION:I29747
c 152	7.8	43.3	12	1	AX710994	ACCESSION:AX710994	225	7.4	41.1	11	1	I38544	ACCESSION:I38544
c 153	7.8	43.3	12	1	BD001135	ACCESSION:BD001135	226	7.4	41.1	11	1	I38545	ACCESSION:I38545
c 154	7.8	43.3	12	1	BD001564	ACCESSION:BD001564	227	7.4	41.1	11	1	I38546	ACCESSION:I38546
c 155	7.8	43.3	12	1	BD143760	ACCESSION:BD143760	228	7.4	41.1	11	1	I38547	ACCESSION:I38547
c 156	7.8	43.3	12	1	BD168622	ACCESSION:BD168622	229	7.4	41.1	11	1	I38549	ACCESSION:I38549
c 157	7.4	41.1	10	1	A41388	ACCESSION:A41388	230	7.4	41.1	11	1	I76877	ACCESSION:I76877
c 158	7.4	41.1	10	1	A52292	ACCESSION:A52292	231	7.4	41.1	11	1	I87829	ACCESSION:I87829
c 159	7.4	41.1	10	1	AR018730	ACCESSION:AR018730	232	7.4	41.1	11	1	I90241	ACCESSION:I90241
c 160	7.4	41.1	10	1	AR030114	ACCESSION:AR030114	233	7.4	41.1	11	1	I91421	ACCESSION:I91421
c 161	7.4	41.1	10	1	AR036561	ACCESSION:AR036561	234	7.4	41.1	11	1	AR209671	ACCESSION:AR209671
c 162	7.4	41.1	10	1	AR092691	ACCESSION:AR092691	235	7.4	41.1	11	1	AR262556	ACCESSION:AR262556
c 163	7.4	41.1	10	1	AR106675	ACCESSION:AR106675	236	7.4	41.1	11	1	AR301423	ACCESSION:AR301423
c 164	7.4	41.1	10	1	AR107804	ACCESSION:AR107804	237	7.4	41.1	11	1	AR301582	ACCESSION:AR301582
c 165	7.4	41.1	10	1	AR107807	ACCESSION:AR107807	238	7.4	41.1	11	1	AR301866	ACCESSION:AR301866
c 166	7.4	41.1	10	1	AR107818	ACCESSION:AR107818	239	7.4	41.1	11	1	AR301736	ACCESSION:AR301736
c 167	7.4	41.1	10	1	AR107829	ACCESSION:AR107829	240	7.4	41.1	11	1	AR369671	ACCESSION:AR369671
c 168	7.4	41.1	10	1	AR124891	ACCESSION:AR124891	241	7.4	41.1	11	1	AR394634	ACCESSION:AR394634
c 169	7.4	41.1	10	1	AR124892	ACCESSION:AR124892	242	7.4	41.1	11	1	AR394654	ACCESSION:AR394654
c 170	7.4	41.1	10	1	AR147934	ACCESSION:AR147934	243	7.4	41.1	11	1	AR470521	ACCESSION:AR470521
c 171	7.4	41.1	10	1	BD237032	ACCESSION:BD237032	244	7.4	41.1	11	1	AR470565	ACCESSION:AR470565
c 172	7.4	41.1	10	1	BD238639	ACCESSION:BD238639	245	7.4	41.1	11	1	AR470673	ACCESSION:AR470673
c 173	7.4	41.1	10	1	BD238706	ACCESSION:BD238706	246	7.4	41.1	11	1	AR471180	ACCESSION:AR471180
c 174	7.4	41.1	10	1	BD239080	ACCESSION:BD239080	247	7.4	41.1	11	1	AR471634	ACCESSION:AR471634
c 175	7.4	41.1	10	1	BD239761	ACCESSION:BD239761	248	7.4	41.1	11	1	AR471749	ACCESSION:AR471749
c 176	7.4	41.1	10	1	BD240709	ACCESSION:BD240709	249	7.4	41.1	11	1	AR622982	ACCESSION:AR622982
c 177	7.4	41.1	10	1	BD248504	ACCESSION:BD248504	250	7.4	41.1	11	1	AR623272	ACCESSION:AR623272
c 178	7.4	41.1	10	1	E16894	ACCESSION:E16894	251	7.4	41.1	11	1	AR623334	ACCESSION:AR623334
c 179	7.4	41.1	10	1	E39572	ACCESSION:E39572	252	7.4	41.1	11	1	AR623425	ACCESSION:AR623425

C 253	7.4	41.1	11	1	AX624155	ACCESSION:AX624155	326	7	38.9	10	1	BD166594	ACCESSION:BD166594
C 254	7.4	41.1	11	1	AX624862	ACCESSION:AX624862	327	7	38.9	10	1	BD167838	ACCESSION:BD167838
C 255	7.4	41.1	11	1	AX624990	ACCESSION:AX624990	328	7	38.9	10	1	BD188967	ACCESSION:BD188967
C 256	7.4	41.1	11	1	AX625292	ACCESSION:AX625292	C 329	6.8	37.8	10	1	A35589	ACCESSION:A35589
C 257	7.4	41.1	11	1	AX625529	ACCESSION:AX625529	C 330	6.8	37.8	10	1	A67805	ACCESSION:A67805
C 258	7.4	41.1	11	1	AX626124	ACCESSION:AX626124	C 331	6.8	37.8	10	1	AR070981	ACCESSION:AR070981
C 259	7.4	41.1	11	1	AX626351	ACCESSION:AX626351	C 332	6.8	37.8	10	1	AR074451	ACCESSION:AR074451
C 260	7.4	41.1	11	1	AX626497	ACCESSION:AX626497	C 333	6.8	37.8	10	1	AR081131	ACCESSION:AR081131
C 261	7.4	41.1	11	1	AX626864	ACCESSION:AX626864	C 334	6.8	37.8	10	1	AR085328	ACCESSION:AR085328
C 262	7.4	41.1	11	1	AX627293	ACCESSION:AX627293	C 335	6.8	37.8	10	1	AR088076	ACCESSION:AR088076
C 263	7.4	41.1	11	1	AX627788	ACCESSION:AX627788	C 336	6.8	37.8	10	1	AR104235	ACCESSION:AR104235
C 264	7.4	41.1	11	1	AX627937	ACCESSION:AX627937	C 337	6.8	37.8	10	1	AR107341	ACCESSION:AR107341
C 265	7.4	41.1	11	1	AX628236	ACCESSION:AX628236	C 338	6.8	37.8	10	1	AR107831	ACCESSION:AR107831
C 266	7.4	41.1	11	1	AX628722	ACCESSION:AX628722	C 339	6.8	37.8	10	1	AR119433	ACCESSION:AR119433
C 267	7.4	41.1	11	1	AX628820	ACCESSION:AX628820	C 340	6.8	37.8	10	1	AR124889	ACCESSION:AR124889
C 268	7.4	41.1	11	1	AX629012	ACCESSION:AX629012	C 341	6.8	37.8	10	1	AR143499	ACCESSION:AR143499
C 269	7.4	41.1	11	1	AX629072	ACCESSION:AX629072	C 342	6.8	37.8	10	1	AR171403	ACCESSION:AR171403
C 270	7.4	41.1	11	1	AX629086	ACCESSION:AX629086	C 343	6.8	37.8	10	1	AR171404	ACCESSION:AR171404
C 271	7.4	41.1	11	1	AX629138	ACCESSION:AX629138	C 344	6.8	37.8	10	1	AR171574	ACCESSION:AR171574
C 272	7.4	41.1	11	1	AX629363	ACCESSION:AX629363	C 345	6.8	37.8	10	1	AR171575	ACCESSION:AR171575
C 273	7.4	41.1	11	1	AX629761	ACCESSION:AX629761	C 346	6.8	37.8	10	1	BD238784	ACCESSION:BD238784
C 274	7.4	41.1	11	1	AX629808	ACCESSION:AX629808	C 347	6.8	37.8	10	1	BD239431	ACCESSION:BD239431
C 275	7.4	41.1	11	1	AX630199	ACCESSION:AX630199	C 348	6.8	37.8	10	1	BD240019	ACCESSION:BD240019
C 276	7.4	41.1	11	1	AX630295	ACCESSION:AX630295	C 349	6.8	37.8	10	1	BD243164	ACCESSION:BD243164
C 277	7.4	41.1	11	1	AX630403	ACCESSION:AX630403	C 350	6.8	37.8	10	1	BD243165	ACCESSION:BD243165
C 278	7.4	41.1	11	1	AX630693	ACCESSION:AX630693	C 351	6.8	37.8	10	1	BD248496	ACCESSION:BD248496
C 279	7.4	41.1	11	1	AX630755	ACCESSION:AX630755	C 352	6.8	37.8	10	1	E40334	ACCESSION:E40334
C 280	7.4	41.1	11	1	AX630846	ACCESSION:AX630846	C 353	6.8	37.8	10	1	E54721	ACCESSION:E54721
C 281	7.4	41.1	11	1	AX631576	ACCESSION:AX631576	C 354	6.8	37.8	10	1	I21680	ACCESSION:I21680
C 282	7.4	41.1	11	1	AX632283	ACCESSION:AX632283	C 355	6.8	37.8	10	1	I22203	ACCESSION:I22203
C 283	7.4	41.1	11	1	AX632411	ACCESSION:AX632411	C 356	6.8	37.8	10	1	AR201714	ACCESSION:AR201714
C 284	7.4	41.1	11	1	AX632713	ACCESSION:AX632713	C 357	6.8	37.8	10	1	AR212997	ACCESSION:AR212997
C 285	7.4	41.1	11	1	AX632798	ACCESSION:AX632798	C 358	6.8	37.8	10	1	AR220101	ACCESSION:AR220101
C 286	7.4	41.1	11	1	BD124173	ACCESSION:BD124173	C 359	6.8	37.8	10	1	AR222980	ACCESSION:AR222980
C 287	7.4	41.1	11	1	BD124332	ACCESSION:BD124332	C 360	6.8	37.8	10	1	AR303352	ACCESSION:AR303352
C 288	7.4	41.1	11	1	BD124436	ACCESSION:BD124436	C 361	6.8	37.8	10	1	AR303429	ACCESSION:AR303429
C 289	7.4	41.1	11	1	BD124486	ACCESSION:BD124486	C 362	6.8	37.8	10	1	AR303522	ACCESSION:AR303522
C 290	7.4	38.9	9	1	AX205264	ACCESSION:AX205264	C 363	6.8	37.8	10	1	AR303557	ACCESSION:AR303557
C 291	7.4	38.9	9	1	AX205264	ACCESSION:AX205264	C 364	6.8	37.8	10	1	AR303686	ACCESSION:AR303686
C 292	7.4	38.9	9	1	AX669023	ACCESSION:AX669023	C 365	6.8	37.8	10	1	AR304507	ACCESSION:AR304507
C 293	7.4	38.9	9	1	AX669028	ACCESSION:AX669028	C 366	6.8	37.8	10	1	AR306855	ACCESSION:AR306855
C 294	7.4	38.9	10	1	AR058729	ACCESSION:AR058729	C 367	6.8	37.8	10	1	AR334451	ACCESSION:AR334451
C 295	7.4	38.9	10	1	AR107870	ACCESSION:AR107870	C 368	6.8	37.8	10	1	AR351726	ACCESSION:AR351726
C 296	7.4	38.9	10	1	AR134572	ACCESSION:AR134572	C 369	6.8	37.8	10	1	AR351825	ACCESSION:AR351825
C 297	7.4	38.9	10	1	AR134573	ACCESSION:AR134573	C 370	6.8	37.8	10	1	AR351826	ACCESSION:AR351826
C 298	7.4	38.9	10	1	AR134582	ACCESSION:AR134582	C 371	6.8	37.8	10	1	AR362545	ACCESSION:AR362545
C 299	7.4	38.9	10	1	BD238699	ACCESSION:BD238699	C 372	6.8	37.8	10	1	AR369273	ACCESSION:AR369273
C 300	7.4	38.9	10	1	BD238707	ACCESSION:BD238707	C 373	6.8	37.8	10	1	AX030211	ACCESSION:AX030211
C 301	7.4	38.9	10	1	BD239507	ACCESSION:BD239507	C 374	6.8	37.8	10	1	AX113035	ACCESSION:AX113035
C 302	7.4	38.9	10	1	BD239938	ACCESSION:BD239938	C 375	6.8	37.8	10	1	AX152839	ACCESSION:AX152839
C 303	7.4	38.9	10	1	BD240530	ACCESSION:BD240530	C 376	6.8	37.8	10	1	AX152854	ACCESSION:AX152854
C 304	7.4	38.9	10	1	BD248497	ACCESSION:BD248497	C 377	6.8	37.8	10	1	AX152855	ACCESSION:AX152855
C 305	7.4	38.9	10	1	E39663	ACCESSION:E39663	C 378	6.8	37.8	10	1	AX152970	ACCESSION:AX152970
C 306	7.4	38.9	10	1	AR214814	ACCESSION:AR214814	C 379	6.8	37.8	10	1	AX153025	ACCESSION:AX153025
C 307	7.4	38.9	10	1	AR303309	ACCESSION:AR303309	C 380	6.8	37.8	10	1	AX153430	ACCESSION:AX153430
C 308	7.4	38.9	10	1	AR303407	ACCESSION:AR303407	C 381	6.8	37.8	10	1	AX189811	ACCESSION:AX189811
C 309	7.4	38.9	10	1	AR303484	ACCESSION:AR303484	C 382	6.8	37.8	10	1	AX150715	ACCESSION:AX150715
C 310	7.4	38.9	10	1	AR303574	ACCESSION:AR303574	C 383	6.8	37.8	10	1	AX667819	ACCESSION:AX667819
C 311	7.4	38.9	10	1	AX152105	ACCESSION:AX152105	C 384	6.8	37.8	10	1	AX668181	ACCESSION:AX668181
C 312	7.4	38.9	10	1	AX152122	ACCESSION:AX152122	C 385	6.8	37.8	10	1	AX668182	ACCESSION:AX668182
C 313	7.4	38.9	10	1	AX152124	ACCESSION:AX152124	C 386	6.8	37.8	10	1	AX753456	ACCESSION:AX753456
C 314	7.4	38.9	10	1	AX152559	ACCESSION:AX152559	C 387	6.8	37.8	10	1	AX805906	ACCESSION:AX805906
C 315	7.4	38.9	10	1	AX152589	ACCESSION:AX152589	C 388	6.8	37.8	10	1	BD007876	ACCESSION:BD007876
C 316	7.4	38.9	10	1	AX152897	ACCESSION:AX152897	C 389	6.8	37.8	10	1	BD007963	ACCESSION:BD007963
C 317	7.4	38.9	10	1	AX239914	ACCESSION:AX239914	C 390	6.8	37.8	10	1	BD065179	ACCESSION:BD065179
C 318	7.4	38.9	10	1	AX453771	ACCESSION:AX453771	C 391	6.8	37.8	10	1	BD083205	ACCESSION:BD083205
C 319	7.4	38.9	10	1	AX510716	ACCESSION:AX510716	C 392	6.8	37.8	10	1	BD091155	ACCESSION:BD091155
C 320	7.4	38.9	10	1	BD003379	ACCESSION:BD003379	C 393	6.8	37.8	10	1	BD161411	ACCESSION:BD161411
C 321	7.4	38.9	10	1	BD003381	ACCESSION:BD003381	C 394	6.8	37.8	10	1	BD161422	ACCESSION:BD161422
C 322	7.4	38.9	10	1	BD007822	ACCESSION:BD007822	C 395	6.8	37.8	10	1	BD225319	ACCESSION:BD225319
C 323	7.4	38.9	10	1	BD007830	ACCESSION:BD007830	C 396	6.8	37.8	10	1	AJ593726	ACCESSION:AJ593726
C 324	7.4	38.9	10	1	BD083239	ACCESSION:BD083239							
C 325	7.4	38.9	10	1	BD083345	ACCESSION:BD083345							

ALIGNMENTS		FEATURES	
RESULT 1		source	
AR033668/c	AR033668	Location/Qualifiers	
LOCUS	Sequence 434 from patent US 5869253.	1. .15	
DEFINITION	15 bp DNA	/organism="unknown"	
ACCESSION	AR033668	/mol_type="unassigned DNA"	
VERSION	AR033668.1 GI:5949273	Query Match	
KEYWORDS	Unknown.	Best Local Similarity 68.9%; Score 12.4; DB 1; Length 15;	
SOURCE	Unknown.	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
ORGANISM	Unknown.	QY 1 GTGAGCGACTTCAT 14	
REFERENCE	1 (bases 1 to 15)		
AUTHORS	Draper,K.G.	Db 14 GTGAGCGACTTTAT 1	
TITLE	Method and reagent for inhibiting hepatitis C virus replication	RESULT 4	
JOURNAL	Patent: US 5869253-A 434 09-FEB-1999;	BD207401/c	
FEATURES	Location/Qualifiers	LOCUS	
source	1. .15	DEFINITION	
	/organism="unknown"	Enzymatic nucleic acid treatment of diseases or conditions related	
	/mol_type="unassigned DNA"	to hepatitis C virus infection.	
Query Match	68.9%; Score 12.4; DB 1; Length 15;	ACCESSION	
Best Local Similarity 92.9%; Pred. No. 14;	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	BD207401	
QY 1 GTGAGCGACTTCAT 14		VERSION	
Db 14 GTGAGCGACTTTAT 1		KEYWORDS	
RESULT 2	AR113490	SOURCE	
LOCUS	Sequence 434 from patent US 6132966.	ORGANISM	
DEFINITION	15 bp DNA	unidentified	
ACCESSION	AR113490	unclassified.	
VERSION	AR113490.1 GI:14093812	REFERENCE	
KEYWORDS	Unknown.	1 (bases 1 to 15)	
SOURCE	Unknown.	AUTHORS	
REFERENCE	1 (bases 1 to 15)	Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.	
AUTHORS	Draper,K.G.	Enzymatic nucleic acid treatment of diseases or conditions related	
TITLE	Method and reagent for inhibiting hepatitis C virus replication	to hepatitis C virus infection	
JOURNAL	Patent: US 6132966-A 434 17-OCT-2000;	Patent: JP 2002512791-A 991 08-MAY-2002;	
FEATURES	Location/Qualifiers	RIBOZYME PHARMACEUTICALS INC	
source	1. .15	OS Hepatitis virus (hepatitis C virus)	
	/organism="unknown"	PN JP 2002512791-A/991	
	/mol_type="unassigned DNA"	PD 08-MAY-2002	
Query Match	68.9%; Score 12.4; DB 1; Length 15;	PF 26-APR-1999 JP 2000545991	
Best Local Similarity 92.9%; Pred. No. 14;	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR	
QY 1 GTGAGCGACTTCAT 14		25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI	
Db 14 GTGAGCGACTTTAT 1		LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI	
RESULT 3	I57897/c	PAVCO,	
LOCUS	Sequence 434 from patent US 5610054.	PI DENNIS MACEJAK	
DEFINITION	15 bp DNA	PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,	
ACCESSION	I57897	PC A61K37/66,	
VERSION	I57897.1 GI:2482961	PC C12N15/00	
KEYWORDS	Unknown.	CC Enzymatic nucleic acid treatment of diseases or conditions	
SOURCE	Unknown.	related to	
ORGANISM	Unknown.	CC hepatitis C virus infection.	
REFERENCE	1 (bases 1 to 15)	FH Key	
AUTHORS	Draper,K.G.	Location/Qualifiers	
TITLE	Enzymatic RNA molecule targeted against Hepatitis C virus	FT source	
JOURNAL	Patent: US 5610054-A 434 11-MAR-1997;	1. .15	
FEATURES	Location/Qualifiers	/organism='Hepatitis virus (hepatitis C FT	
source	1. .15	virus)'	
	/organism="unknown"	Location/Qualifiers	
	/mol_type="unassigned DNA"	1. .15	
Query Match	68.9%; Score 12.4; DB 1; Length 15;	/organism="unidentified"	
Best Local Similarity 92.9%; Pred. No. 14;	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	/mol_type="genomic RNA"	
QY 1 GTGAGCGACTTCAT 14		/db_xref="taxon:32644"	
Db 14 GTGAGCGACTTTAT 1		Query Match	
RESULT 4	I57897/c	Best Local Similarity 68.9%; Score 12.4; DB 1; Length 15;	
LOCUS	Sequence 434 from patent US 5610054.	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DEFINITION	15 bp DNA	QY 1 GTGAGCGACTTCAT 14	
ACCESSION	I57897		
VERSION	I57897.1 GI:2482961	Db 14 GTGAGCGACTTTAT 1	
KEYWORDS	Unknown.	RESULT 5	
SOURCE	Unknown.	AX139142	
ORGANISM	Unknown.	LOCUS	
REFERENCE	1 (bases 1 to 15)	DEFINITION	
AUTHORS	Draper,K.G.	Sequence 18 from Patent EP1085093.	
TITLE	Enzymatic RNA molecule targeted against Hepatitis C virus	AX139142	
JOURNAL	Patent: US 5610054-A 434 11-MAR-1997;	ACCESSION	
FEATURES	Location/Qualifiers	AX139142	
source	1. .15	VERSION	
	/organism="unknown"	AX139142.1 GI:14274818	
	/mol_type="unassigned DNA"	KEYWORDS	
Query Match	68.9%; Score 12.4; DB 1; Length 15;	Homo sapiens (human)	
Best Local Similarity 92.9%; Pred. No. 14;	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	SOURCE	
QY 1 GTGAGCGACTTCAT 14			
Db 14 GTGAGCGACTTTAT 1			


```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Blumenberg, M. and Gazel, A. M.
TITLE Genes and polynucleotides associated with ultraviolet
radiation-mediated skin damage and uses thereof
JOURNAL NEW YORK UNIVERSITY (US)
PATENT: EP 1085093-A 18 21-MAR-2001;
FEATURES
Location/Qualifiers
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCATCCT 17
Db 1 GAGTGACTCCATCCT 15

RESULT 6
BD014758
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Gene and polynucleotide relating to skin disturbance via
ultraviolet irradiation and utilization thereof.
ACCESSION BD014758
VERSION BD014758.1 GI:22555541
KEYWORDS JP 2001157590-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 17)
AUTHORS Blumenberg, M. and Gazel, A. M.
TITLE Gene and polynucleotide relating to skin disturbance via
ultraviolet irradiation and utilization thereof
JOURNAL Patent: JP 2001157590-A 12 12-JUN-2001;
NEW YORK UNIVERSITY
COMMENT OS Homo sapiens (human)
PN JP 2001157590-A/12
PD 12-JUN-2001
PF 20-SEP-2000 JP 2000284980
PR 20-SEP-1999 US 60/155029
PI MILOSLAV BLUMENBERG, ALI M GAZEL
PC C12N15/09, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/
PC 12, C12Q1/68,
PC G01N33/15, G01N33/50, C12N15/00, C12N5/00
CC Gene and polynucleotide relating to skin disturbance via CC
ultraviolet
irradiation and utilization thereof
FH Key Location/Qualifiers
FT source 1. .17
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCATCCT 17
Db 1 GAGTGACTCCATCCT 15

RESULT 7

```

```

AX139154
LOCUS 17 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 2 from Patent EP1076099.
ACCESSION AX139154
VERSION AX139154.1 GI:14274827
KEYWORDS Mycobacterium tuberculosis
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE
1
AUTHORS Suzuki, Y., Nishida, M. and Takenishi, S.
TITLE Kit for diagnosis of tubercle bacilli
JOURNAL Patent: EP 1076099-A 2 14-FEB-2001;
NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
(JP)
FEATURES
Location/Qualifiers
source
1. .17
/organism="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
/db_xref="taxon:1773"
/note="capture"
Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCGAATTCAT 15

RESULT 8
BD013438
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Diagnosis kit of tubercle bacillus.
ACCESSION BD013438
VERSION BD013438.1 GI:22553752
KEYWORDS JP 2001103981-A/2
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE
1 (bases 1 to 17)
AUTHORS Suzuki, S., Nishida, M. and Takenishi, S.
TITLE Diagnosis kit of tubercle bacillus
JOURNAL Patent: JP 2001103981-A 2 17-APR-2001;
NISSHINBO IND INC, SYSTEM RESEARCH CO LTD
COMMENT OS Mycobacterium tuberculosis
PN JP 2001103981-A/2
PD 17-APR-2001
PF 26-JUL-2000 JP 2000225985
PI SADAHIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/09, C12Q1/68, C12Q1/68, C12R1:32), PC
(C12Q1/68, C12R1:325), (C12Q1/68, C12R1:33), C12N15/00, C12N15/00 CC
capture
FH Key Location/Qualifiers
FT source 1. .17
/organism="Mycobacterium tuberculosis"
/db_xref="taxon:1773"
FEATURES
source
1. .17
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14

```

```

Db      3  TGAGCGAATTCAT 15

RESULT 9
AX727596
LOCUS      AX727596          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 5283 from Patent WO03025176.
ACCESSION  AX727596
VERSION     AX727596.1  GI:30506939
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS     Telerman,A., Anson,R. and Tuijinder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 5283 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES
source      1. .17
            /organism="Mus musculus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10090"

Query Match      62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2; Pred. No. 32;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  GAGCGACTTCATCCTT 18
Db      1  GATCACTTCATGCTT 16

RESULT 10
A35654
LOCUS      A35654          14 bp      DNA      linear      PAT 02-DEC-1996
DEFINITION Synthetic human IFN-alpha 2 gene oligo.
ACCESSION  A35654
VERSION     A35654.1  GI:1927036
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
AUTHORS     Camble,R. and Edge,M.D.
TITLE       Analogous interferon polypeptides, process for their preparation
            and pharmaceutical compositions containing them
JOURNAL     Patent: EP 0194006-A 9 10-SEP-1986;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source      1. .14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      61.1%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7  GACTTCATCCT 17
Db      3  GACTTCATCCT 13

RESULT 11
AR180366/c
LOCUS      AR180366          15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 434 from patent US 6333152.
ACCESSION  AR180366
VERSION     AR180366.1  GI:20222399

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1  (bases 1 to 15)
AUTHORS     Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE       Gene expression profiles in normal and cancer cells
JOURNAL     Patent: US 6333152-A 434 25-DEC-2001;
FEATURES
source      1. .15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GTGCGCGCTCAT 14
Db      15 GTGCGCGCTCATCAT 2

RESULT 12
BD239875/c
LOCUS      BD239875          10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239875
VERSION     BD239875.1  GI:33049645
KEYWORDS   JP 2002534056-A/1293.
SOURCE      Homo sapiens
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS     Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL     Patent: JP 2002534056-A 1293 15-OCT-2002;
            GENZYME CORP

COMMENT
OS      Homo sapiens (human)
PN      JP 2002534056-A/1293
PD      15-OCT-2002
PF      18-JUN-1999  JP 2000554749
PR      19-JUN-1998  US 60/090039,19-JUN-1998  US 60/090040 PR
            19-JUN-1998  US 60/090041,19-JUN-1998  US 60/089853 PR
            19-JUN-1998  US 60/089997,19-JUN-1998  US 60/090079 PR
            19-JUN-1998  US 60/090035,19-JUN-1998  US 60/089993 PR
            19-JUN-1998  US 60/089992,19-JUN-1998  US 60/090072 PR
            19-JUN-1998  US 60/089878,19-JUN-1998  US 60/089991 PR
            19-JUN-1998  US 60/090000,19-JUN-1998  US 60/090048 PR
            19-JUN-1998  US 60/089999,19-JUN-1998  US 60/090043 PR
            19-JUN-1998  US 60/090042,19-JUN-1998  US 60/090036 PR
            19-JUN-1998  US 60/090044,19-JUN-1998  US 60/089844 PR
            19-JUN-1998  US 60/090080,19-JUN-1998  US 60/089833 PR
            19-JUN-1998  US 60/089994,19-JUN-1998  US 60/090077 PR
            19-JUN-1998  US 60/090078,19-JUN-1998  US 60/090047 PR
            08-DEC-1998  US 60/111715
PI      BRUCE L. ROBERTS, SRINIVAS SHANKARA
PC      C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            G01N33/53,G01N33/50,G01N33/53,G01N33/566, PC
            G01N37/00,
PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key      Location/Qualifiers
FT      source      1. .10
            /organism="Homo sapiens (human)".
            Location/Qualifiers
            1. .10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

```

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
| | | | |
Db 10 TGAGCGACTT 1

RESULT 13
I46929/c
LOCUS I46929 14 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 22 from patent US 5639655.
ACCESSION I46929
VERSION I46929.1 GI:2470894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE PML-RARA targeted ribozymes
JOURNAL Patent: US 5639655-A 22 17-JUN-1997;
FEATURES Location/Qualifiers
1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
| | | | |
Db 10 ACTTCATCCT 1

RESULT 14
AR033669/c
LOCUS AR033669 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 435 from patent US 5869253.
ACCESSION AR033669
VERSION AR033669.1 GI:5949274
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 435 09-FEB-1999;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
| | | | |
Db 10 GTGAGCGACT 1

RESULT 15
AR113491/c
LOCUS AR113491 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 435 from patent US 6132966.
ACCESSION AR113491
VERSION AR113491.1 GI:14093813
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 435 17-OCT-2000;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
| | | | |
Db 10 GTGAGCGACT 1

RESULT 16
I57898/c
LOCUS I57898 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 435 from patent US 5610054.
ACCESSION I57898
VERSION I57898.1 GI:2482962
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 435 11-MAR-1997;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
| | | | |
Db 10 GTGAGCGACT 1

RESULT 17
BD207402/c
LOCUS BD207402 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207402
VERSION BD207402.1 GI:33017172
KEYWORDS JP 2002512791-A/992.
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 992 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/992
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO.

```

PI DENNIS MACBJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
   related to
FH Key Location/Qualifiers
FT source 1..15
FT virus)'.
   /organism='Hepatitis virus (hepatitis C FT
   Location/Qualifiers
FEATURES
   source
     1..15
     /organism="unidentified"
     /mol_type="genomic RNA"
     /db_xref="taxon:32644"

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
   |||||
Db 10 GTGAGCGACT 1

RESULT 18
A42517/c
LOCUS A42517 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 33 from Patent WO9502051.
ACCESSION A42517
VERSION A42517.1 GI:2297966
KEYWORDS
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 33 19-JAN-1995;
COMMENT BIOGOSTIK GES FUER BIOMOLEKUL (DE)
Other publication AU 7345694 950206.
FEATURES
   source
     1..14
     /organism="unidentified"
     /mol_type="unassigned DNA"
     /db_xref="taxon:32644"

Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATCC 16
   ||| |||||
Db 13 AGCAACTTCAACC 1

RESULT 19
A88709/c
LOCUS A88709 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 857 from Patent WO9833904.
ACCESSION A88709
VERSION A88709.1 GI:6737279
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

```

```

JOURNAL Patent: WO 9833904-A 857 06-AUG-1998;
FEATURES BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
   source
     1..14
     Location/Qualifiers
     /organism="unidentified"
     /mol_type="unassigned DNA"
     /db_xref="taxon:32644"

Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATCC 16
   ||| |||||
Db 13 AGCAACTTCAACC 1

RESULT 20
BD066222/c
LOCUS BD066222 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066222
VERSION BD066222.1 GI:22611825
KEYWORDS JP 2001511000-A/857.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 857 07-AUG-2001;
COMMENT BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/857
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
   Location/Qualifiers
   source
     1..14
     /organism='Unknown'.
     Location/Qualifiers
FEATURES
   source
     1..14
     /organism="unidentified"
     /mol_type="genomic DNA"
     /db_xref="taxon:32644"

Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATCC 16
   ||| |||||
Db 13 AGCAACTTCAACC 1

RESULT 21
AR033495
LOCUS AR033495 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 261 from patent US 5869253.
ACCESSION AR033495
VERSION AR033495.1 GI:5949100
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 261 09-FEB-1999;
FEATURES Location/Qualifiers

```

```
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|||||
Db 3 GTGATCGACTGCA 15

RESULT 22
AR113317
LOCUS AR113317 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 261 from patent US 6132966.
ACCESSION AR113317
VERSION AR113317.1 GI:14093639
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 261 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|||||
Db 3 GTGATCGACTGCA 15

RESULT 23
157724
LOCUS 157724 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 261 from patent US 5610054.
ACCESSION 157724
VERSION 157724.1 GI:2482788
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 261 11-MAR-1997;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|||||
Db 3 GTGATCGACTGCA 15

RESULT 24
AR180531/c
LOCUS AR180531 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 599 from patent US 6333152.

ACCESSION AR180531 GI:20222564
VERSION AR180531.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L., and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 599 25-DEC-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
|||||
Db 14 TGAGAGACTGCAT 2

RESULT 25
BD207228
LOCUS BD207228 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207228
VERSION BD207228.1 GI:33016998
KEYWORDS JP 2002512791-A/818.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 818 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/818
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1. .15
/organism="Hepatitis virus (hepatitis C virus)"
/locus="BD207228"
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 56;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|||||
Db 3 GTGATCGACTGCA 15
```

RESULT 26
BD174826/c
LOCUS BD174826 12 bp DNA linear PAT 18-MAR-2003
DEFINITION Antibody-producing transgenic plant.
ACCESSION BD174826
VERSION BD174826.1 GI:29120518
KEYWORDS JP 2002253262-A/12.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Matsumura, T., Yoshida, N., Ito, K., Kato, M., Sugimoto, C., Ueda, I.,
Ohashi, K. and Li, C.
TITLE Antibody-producing transgenic plant
JOURNAL Patent: JP 2002253262-A 12 10-SEP-2002;
KK SCIENCE TANAKA, HOKKAIDO GREEN BIO INSTITUTE, CHIHIO
SUGIMOTO, ICHIRO UEDA
COMMENT OS Unknown
PN JP 2002253262-A/12
PD 10-SEP-2002
PF 05-MAR-2001 JP 2001060462
PI TAKESHI MATSUMURA, NORIKO YOHODA, KEIZO ITO, MIHOKO KATO, CHIHIO
PI SUGIMOTO,
PI ICHIRO UEDA, KAZUHIKO OHASHI, CHENGYI LI
PC C12N15/09, A01H5/00, C07K16/08, C12N5/10, C12Q1/70, G01N33/569, PC
G01N33/577//
CC C12P21/08, C12N15/00, C12N5/00
PC Description of Unknown Organism: KDEL signal
FH Key
FT source 1..12
FT Location/Qualifiers
FEATURES
source
1..12
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
| | | | | | | | | | | | | | | | | |
Db 11 AGTTCACTCTT 1

RESULT 27
A35614
LOCUS A35614 14 bp DNA linear PAT 02-DEC-1996
DEFINITION Synthetic human IFN-alpha 2 gene oligo.
ACCESSION A35614
VERSION A35614.1 GI:1926996
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Camble, R. and Edge, M.D.
TITLE Analogous interferon polypeptides, process for their preparation
and pharmaceutical compositions containing them
JOURNAL Patent: EP 0194006-A 59 10-SEP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 52.2%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 63;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
| | | | | | | | | | | | | | | | | |
Db 3 GACTCCATCCT 13

RESULT 28
AR107783
LOCUS AR107783 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 29 from patent US 6110667.
ACCESSION AR107783
VERSION AR107783.1 GI:12823270
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo. and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 29 29-AUG-2000;
FEATURES
source
1..10
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | | | | | | | | | | | | | | |
Db 2 CTTTCATCCT 10

RESULT 29
AR107805
LOCUS AR107805 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 51 from patent US 6110667.
ACCESSION AR107805
VERSION AR107805.1 GI:12823292
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo. and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 51 29-AUG-2000;
FEATURES
source
1..10
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | | | | | | | | | | | | | | |
Db 1 CTTTCATCCT 9

RESULT 30
AR107806
LOCUS AR107806 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 52 from patent US 6110667.
ACCESSION AR107806
VERSION AR107806.1 GI:12823293
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

```

Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 52 29-AUG-2000;
FEATURES
    LOCATION/Qualifiers
    1..10
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTTCATCCT 9

RESULT 31
AX394637
LOCUS AX394637 11 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 7 from Patent WO0218639.
ACCESSION AX394637
VERSION AX394637.1 GI:21065750
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Anderson,M.K., Lewander,T. and Oliasson,E.
TITLE Detection of cyb2c19 polymorphisms
JOURNAL Patent: WO 0218639-A 7 07-MAR-2002;
Geminl Genomics PLC (GB)
FEATURES
    LOCATION/Qualifiers
    1..11
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Oligonucleotide of polymorphic site 1060"

Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 2 ACTTCATCC 10

RESULT 32
AX394655/c
LOCUS AX394655 11 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 25 from Patent WO0218639.
ACCESSION AX394655
VERSION AX394655.1 GI:21065768
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Anderson,M.K., Lewander,T. and Oliasson,E.
TITLE Detection of cyb2c19 polymorphisms
JOURNAL Patent: WO 0218639-A 25 07-MAR-2002;
Geminl Genomics PLC (GB)
FEATURES
    LOCATION/Qualifiers
    1..11
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Oligonucleotide of polymorphic site 1060"

Unclassified.
Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACTTCATCC 2

RESULT 33
AX625339
LOCUS AX625339 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2380 from Patent WO02053774.
ACCESSION AX625339
VERSION AX625339.1 GI:28453280
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2380 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
    LOCATION/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 34
AX632760
LOCUS AX632760 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9802 from Patent WO02053774.
ACCESSION AX632760
VERSION AX632760.1 GI:28468375
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9802 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
    LOCATION/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 35
AJ599093

```

```

LOCUS      AJ599093                12 bp  DNA      linear  PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
480D05.
ACCESSION  AJ599093
VERSION    AJ599093.1  GI:37948721
KEYWORDS   right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1
AUTHORS    Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Leclarny,A.
TITLE      T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL    EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE    22363535
PUBMED     12446565
REFERENCE  2 (bases 1 to 12)
AUTHORS    Balzergue,S.
TITLE      Direct Submission
JOURNAL    Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT    PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment (s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.inbio.gen.fr).
FEATURES   source
            1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassiliewskij"
            /db_xref="taxon:3702"
            /clone="480D05"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            misc_feature
            1..12
            /note="T-DNA flanking sequence
            right border"
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
    |||||
Db 4 CTTTCATCCT 12

RESULT 36
AR100991/c
LOCUS      AR100991                12 bp  DNA      linear  PAT 14-FEB-2001
DEFINITION Sequence 79 from patent US 6083693.
ACCESSION  AR100991
VERSION    AR100991.1  GI:12811789
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
            1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS    Nandabalan,K. and Rothberg,J.Marc.
TITLE      Identification and comparison of protein-protein interactions that
            occur in populations
JOURNAL    Patent: US 6083693-A 79 04-JUL-2000;
            Location/Qualifiers
FEATURES   source
            1..12
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
    |||||
Db 1 GCCTTCATCC 10

RESULT 39

```

```

source
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGCACTTCA 13
    |||||
Db 12 TCAGCGCACTGCA 1

RESULT 37
AR371424/c
LOCUS      AR371424                12 bp  DNA      linear  PAT 12-SEP-2003
DEFINITION Sequence 79 from patent US 6395478.
ACCESSION  AR371424
VERSION    AR371424.1  GI:34608358
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
            1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS    Nandabalan,K. and Rothberg,J.M.
TITLE      Identification and comparison of protein-protein interactions that
            occur in populations and identification of inhibitors of these
            interactors
JOURNAL    Patent: US 6395478-A 79 28-MAY-2002;
            Location/Qualifiers
FEATURES   source
            1..12
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGCACTTCA 13
    |||||
Db 12 TCAGCGCACTGCA 1

RESULT 38
AR107819
LOCUS      AR107819                10 bp  DNA      linear  PAT 14-FEB-2001
DEFINITION Sequence 65 from patent US 6110667.
ACCESSION  AR107819
VERSION    AR107819.1  GI:12823306
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
            1 (bases 1 to 10)
REFERENCE  1 (bases 1 to 10)
AUTHORS    Lopez-Nieto,C.Eduardo. and Nigan,S.Kumar.
TITLE      Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
JOURNAL    Patent: US 6110667-A 65 29-AUG-2000;
            Location/Qualifiers
FEATURES   source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
    |||||
Db 1 GCCTTCATCC 10

RESULT 39

```



```

BD239322      BD239322      10 bp      DNA      linear      PAT 17-JUL-2003
LOCUS          Preparation and use of superior vaccines.
DEFINITION
ACCESSION      BD239322
VERSION        BD239322.1 GI:33049092
KEYWORDS       JP 2002534056-A/740.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Roberts,B.L. and Shankara,S.
TITLE          Preparation and use of superior vaccines
JOURNAL        Patent: JP 2002534056-A 740 15-OCT-2002;
               GENZYME CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002534056-A/740
               PD 15-OCT-2002
               PF 18-JUN-1999 JP 2000554749
               PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
               19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
               19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
               19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089893 PR
               19-JUN-1998 US 60/089932,19-JUN-1998 US 60/090072 PR
               19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
               19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
               19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
               19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
               19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
               19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
               19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
               19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
               19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
               08-DEC-1998 US 60/111715
               PI BRUCE L ROBERTS, SRINIVAS SHANKARA
               PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
               C12N1/19,
               PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
               G01N37/00,
               PC C12N15/00,C12N5/00,C12N15/00
               CC Preparation and use of superior vaccines
               FH Key Location/Qualifiers
               FT source 1..10
               /organism='Homo sapiens (human)'
               /location/Qualifiers
               1..10
               /organism='Homo sapiens'
               /mol_type='genomic DNA'
               /db_xref='taxon:9606'
               Query Match 46.7%; Score 8.4; DB 1; Length 10;
               Best Local Similarity 90.0%; Pred. No. 66;
               Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
               Qy 8 ACTTCATCCT 17
               Db 1 ACTTCCTCCT 10
               RESULT 40
               E04663/c
               LOCUS          Synthetic nucleotide with (GACGTC)/structure, having immunomodulation
               DEFINITION      activities.
               ACCESSION      E04663
               VERSION        E04663.1 GI:2172859
               KEYWORDS       JP 1992352724-A/20.
               SOURCE         synthetic construct
               ORGANISM       synthetic construct
               REFERENCE      1 (bases 1 to 10)
               AUTHORS        Tokunaga,T., Kataoka,T., Yamamoto,S., Kuramoto,E., Yano,O.,
               Makino,T. and Shimada,S.

```

```

IMMUNOMODULATION TYPE THERAPEUTIC AGENT
Patent: JP 1992352724-A 20 07-DEC-1992;
MITSU TOATSU CHEM INC
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992352724-A/20
PD 07-DEC-1992
PF 18-JUL-1991 JP 1991178058
PI 27-JUL-1990 JP 90P 197778
PI TOKUNAGA TORU, KATAOKA TETSURO, YAMAMOTO SABURO, PI KURAMOTO
ETSURO,
PI YANO OSAMU, MAKINO TADASHI, SHIMADA SHIZUO
PC A61K31/70,A61K31/70,A61K31/70//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Key Location/Qualifiers
FH Key
FT misc feature 1..10
/note='synthetic nucleotide with(GACGTC)/structure'.
FT Location/Qualifiers
1..10
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCGACTTCAT 14
Db 10 GCGAGTCAT 1
RESULT 41
AR029409
LOCUS          AR029409 11 bp DNA linear PAT 29-SEP-1999
DEFINITION      Sequence 10 from patent US 5859233.
ACCESSION      AR029409
VERSION        AR029409.1 GI:5941382
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
               Nelson,J.S. and Schultz,R.G.
TITLE          Synthesis for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL        Patent: US 5859233-A 10 12-JAN-1999;
FEATURES
source 1..11
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCTT 10
RESULT 42
AR030100/c
LOCUS          AR030100 11 bp DNA linear PAT 29-SEP-1999
DEFINITION      Sequence 289 from patent US 5861244.
ACCESSION      AR030100
VERSION        AR030100.1 GI:5943314
KEYWORDS

```

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Wang, C.-G. and Hepburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 289 19-JAN-1999;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
        |||||
Db      1 CTTTCATCCTT 10

RESULT 45
AR058873
LOCUS      AR058873
DEFINITION Sequence 5 from patent US 5837835.
ACCESSION  AR058873
VERSION     AR058873.1 GI:5984450
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Gryaznov, S.M., Schultz, R.G. and Chen, J.-k.
TITLE        Oligonucleotide N3'-p5' phosphoramidates: hybridization and
              nuclease resistance properties
JOURNAL      Patent: US 5837835-A 5 17-NOV-1998;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
        |||||
Db      1 CTTTCATCCTT 10

RESULT 46
AR058874
LOCUS      AR058874
DEFINITION Sequence 6 from patent US 5837835.
ACCESSION  AR058874
VERSION     AR058874.1 GI:5984451
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Gryaznov, S.M., Schultz, R.G. and Chen, J.-k.
TITLE        Oligonucleotide N3'-p5' phosphoramidates: hybridization and
              nuclease resistance properties
JOURNAL      Patent: US 5837835-A 6 17-NOV-1998;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
        |||||
Db      1 CTTTCATCCTT 10

RESULT 47
AR079577
LOCUS      AR079577
DEFINITION Sequence 4 from patent US 5965720.
ACCESSION  AR079577
VERSION     AR079577.1 GI:10006321
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.

```

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Wang, C.-G. and Hepburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 289 19-JAN-1999;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
        |||||
Db      11 CTTTCCTCCTT 2

RESULT 43
AR049977
LOCUS      AR049977
DEFINITION Sequence 10 from patent US 5824793.
ACCESSION  AR049977
VERSION     AR049977.1 GI:5971969
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Hirschbein, B.L., Fearon, K.L., Gryaznov, S.M., McCurdy, S.N.,
              Nelson, J.S. and Schultz, R.G.
TITLE        Solid phase synthesis of oligonucleotide N3'-p5' phosphoramidates
JOURNAL      Patent: US 5824793-A 10 20-OCT-1998;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
        |||||
Db      1 CTTTCCTCCTT 10

RESULT 44
AR058872
LOCUS      AR058872
DEFINITION Sequence 4 from patent US 5837835.
ACCESSION  AR058872
VERSION     AR058872.1 GI:5984449
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Gryaznov, S.M., Schultz, R.G. and Chen, J.-k.
TITLE        Oligonucleotide N3'-p5' phosphoramidates: hybridization and
              nuclease resistance properties
JOURNAL      Patent: US 5837835-A 4 17-NOV-1998;
FEATURES     Location/Qualifiers
             source
             1. .11
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates
JOURNAL Patent: US 5965720-A 4 12-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 48
AR079578
LOCUS 11 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5965720.
ACCESSION AR079578
VERSION AR079578.1 GI:10006322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates
JOURNAL Patent: US 5965720-A 5 12-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 49
AR079579
LOCUS 11 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 6 from patent US 5965720.
ACCESSION AR079579
VERSION AR079579.1 GI:10006323
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates
JOURNAL Patent: US 5965720-A 6 12-OCT-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 50
AR123286
LOCUS 11 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6169170.
ACCESSION AR123286
VERSION AR123286.1 GI:14108252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.N5'Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 4 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 51
AR123287
LOCUS 11 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169170.
ACCESSION AR123287
VERSION AR123287.1 GI:14108253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.N5'Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 52
AR123288
LOCUS 11 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6169170.
ACCESSION AR123288
VERSION AR123288.1 GI:14108254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.N5'Phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 6 02-JAN-2001;
FEATURES Location/Qualifiers
```

source 1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCCT 10

RESULT 53
I03846
LOCUS 11 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent EP 0068693.
ACCESSION I03846
VERSION I03846.1 GI:591985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kleid,D.G. and Yansura,D.G.
TITLE Production of foot and mouth disease vaccine from microbially expressed antigens
JOURNAL Patent: EP 0068693-A2 3 05-JAN-1983;
FEATURES Location/Qualifiers
source 1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACTTCCTCCT 10

RESULT 54
I03847
LOCUS 11 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 4 from Patent EP 0068693.
ACCESSION I03847
VERSION I03847.1 GI:591986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kleid,D.G. and Yansura,D.G.
TITLE Production of foot and mouth disease vaccine from microbially expressed antigens
JOURNAL Patent: EP 0068693-A2 4 05-JAN-1983;
FEATURES Location/Qualifiers
source 1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACTTCCTCCT 10

RESULT 55
I03849

LOCUS I03249 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5591607.
ACCESSION I03249
VERSION I03249.1 GI:1824040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.Ps' phosphoramidates: triplex DNA formation
JOURNAL Patent: US 5591607-A 4 07-JAN-1997;
FEATURES Location/Qualifiers
source 1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCCT 10

RESULT 56
I03250
LOCUS 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5591607.
ACCESSION I03250
VERSION I03250.1 GI:1824041
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.Ps' phosphoramidates: triplex DNA formation
JOURNAL Patent: US 5591607-A 5 07-JAN-1997;
FEATURES Location/Qualifiers
source 1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCCT 10

RESULT 57
I03251
LOCUS 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5591607.
ACCESSION I03251
VERSION I03251.1 GI:1824042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.Ps' phosphoramidates: triplex DNA formation
JOURNAL Patent: US 5591607-A 6 07-JAN-1997;
FEATURES Location/Qualifiers
source 1. .11

```

/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTCTTCCTT 10

RESULT 58
LOCUS I35514 11 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5599922.
ACCESSION I35514
VERSION I35514.1 GI:2088482
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5599922-A 4 04-FEB-1997;
FEATURES
    source
        1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTCTTCCTT 10

RESULT 59
LOCUS I35515 11 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 5 from patent US 5599922.
ACCESSION I35515
VERSION I35515.1 GI:2088483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5599922-A 5 04-FEB-1997;
FEATURES
    source
        1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTCTTCCTT 10

RESULT 60
LOCUS I35516 11 bp DNA linear PAT 13-MAY-1997
```

```

DEFINITION Sequence 6 from patent US 5599922.
ACCESSION I35516
VERSION I35516.1 GI:2088484
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5599922-A 6 04-FEB-1997;
FEATURES
    source
        1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTCTTCCTT 10

RESULT 61
LOCUS I43124 11 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 4 from patent US 5631135.
ACCESSION I43124
VERSION I43124.1 GI:2468368
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5631135-A 4 20-MAY-1997;
FEATURES
    source
        1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTCTTCCTT 10

RESULT 62
LOCUS I43125 11 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 5 from patent US 5631135.
ACCESSION I43125
VERSION I43125.1 GI:2468369
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5631135-A 5 20-MAY-1997;
FEATURES
    source
        1..11
            /organism="unknown"
```

```
/mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 63
I43126
LOCUS      I43126      11 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5631135.
ACCESSION  I43126
VERSION    I43126.1 GI:2468370
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE      Oligonucleotide N3'.fwdarw.P5'.phosphoramidates: hybridization and
           nuclease resistance properties
JOURNAL    Patent: US 5631135-A 6 20-MAY-1997;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 64
I72583
LOCUS      I72583      11 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 2 from patent US 5684143.
ACCESSION  I72583
VERSION    I72583.1 GI:3008722
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Gryaznov,S. and Schultz,R.G.
TITLE      Oligo-2'-fluoronucleotide N3'->P5'.phosphoramidates
JOURNAL    Patent: US 5684143-A 2 04-NOV-1997;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 65
I92002
LOCUS      I92002      11 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 4 from patent US 5726297.
ACCESSION  I92002
```

```
VERSION      192002.1 GI:3936472
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE        Oligodeoxyribonucleotide N3' P5' phosphoramidates
JOURNAL      Patent: US 5726297-A 4 10-MAR-1998;
FEATURES     Location/Qualifiers
              source
              1..11
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 66
I92003
LOCUS      I92003      11 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 5 from patent US 5726297.
ACCESSION  I92003
VERSION    I92003.1 GI:3936473
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE      Oligodeoxyribonucleotide N3' P5' phosphoramidates
JOURNAL    Patent: US 5726297-A 5 10-MAR-1998;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 67
I92004
LOCUS      I92004      11 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 6 from patent US 5726297.
ACCESSION  I92004
VERSION    I92004.1 GI:3936474
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE      Oligodeoxyribonucleotide N3' P5' phosphoramidates
JOURNAL    Patent: US 5726297-A 6 10-MAR-1998;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 9 CTTTCATCCTT 18
    |||||
Db 1 CTTTCATCCTT 10

RESULT 69
AX471440/c
LOCUS AX471440 linear DNA 11 bp PAT 09-AUG-2002
DEFINITION Sequence 1017 from Patent WO02053773.
ACCESSION AX471440
VERSION AX471440.1 GI:22206565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
    |||||
Db 11 ACTTCACCT 2

RESULT 69
AX624519/c
LOCUS AX624519 linear DNA 11 bp PAT 21-FEB-2003
DEFINITION Sequence 1560 from Patent WO02053774.
ACCESSION AX624519
VERSION AX624519.1 GI:28452460
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1560 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
    |||||
Db 11 ACTTCACCT 2

RESULT 70
AX625438
LOCUS AX625438 linear DNA 11 bp PAT 21-FEB-2003
DEFINITION Sequence 2479 from Patent WO02053774.
ACCESSION AX625438
```

```
VERSION AX625438.1 GI:28453379
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2479 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
    |||||
Db 2 GTGAGCTACT 11

RESULT 71
AX626466/c
LOCUS AX626466 linear DNA 11 bp PAT 21-FEB-2003
DEFINITION Sequence 3507 from Patent WO02053774.
ACCESSION AX626466
VERSION AX626466.1 GI:28454504
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3507 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
    |||||
Db 10 GACATCATCC 1

RESULT 72
AX626687/c
LOCUS AX626687 linear DNA 11 bp PAT 21-FEB-2003
DEFINITION Sequence 3728 from Patent WO02053774.
ACCESSION AX626687
VERSION AX626687.1 GI:28454725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3728 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
```

```

FEATURES
  source
    Location/Qualifiers
      1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 10 GACTTGATCC 1

RESULT 73
LOCUS AX626736 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3777 from Patent WO02053774.
ACCESSION AX626736
VERSION AX626736.1 GI:28454774
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
  Method for determining homeostasis of the skin
JOURNAL
  Patent: WO 02053774-A 3777 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
      1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 2 ACTTCCTCCT 11

RESULT 74
LOCUS AX631940/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8982 from Patent WO02053774.
ACCESSION AX631940
VERSION AX631940.1 GI:28467555
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
  Method for determining homeostasis of the skin
JOURNAL
  Patent: WO 02053774-A 8982 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
      1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 2 ACTTCCTCCT 11

RESULT 75
LOCUS BD188888 11 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound; hybridization and nuclease tolerant characteristics.
ACCESSION BD188888
VERSION BD188888.1 GI:32998627
KEYWORDS JP 2003012688-A/4.
SOURCE unclassified
ORGANISM unclassified
REFERENCE
  1 (bases 1 to 11)
  Gryaznov,S.M., Schultz,R.G. and Chen,J.
  Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
  hybridization and nuclease tolerant characteristics
  Patent: JP 2003012688-A 4 15-JAN-2003;
  LYNX THERAPEUTICS INC
  OS Unidentified
  PN JP 2003012688-A/4
  PD 15-JAN-2003
  PF 12-JUN-2002 JP 2002171743
  PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
  SRSGRI M GRVZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
  C07H19/16/C12Q1/02, C12Q1/68
  CC Strandedness: Single;
  CC Topology: Linear;
  CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC
  compound;
  CC hybridization and nuclease tolerant characteristics PH Key
  FT source
    Location/Qualifiers
      1. .11
        /organism="Unidentified".
        /organism="Unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 1 CTTCCTCCTT 10

RESULT 76
LOCUS BD188889 11 bp RNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound; hybridization and nuclease tolerant characteristics.
ACCESSION BD188889
VERSION BD188889.1 GI:32998628
KEYWORDS JP 2003012688-A/5.
SOURCE unclassified
ORGANISM unclassified
REFERENCE
  1 (bases 1 to 11)
  Gryaznov,S.M., Schultz,R.G. and Chen,J.
  Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
  hybridization and nuclease tolerant characteristics
  Patent: JP 2003012688-A 5 15-JAN-2003;
  LYNX THERAPEUTICS INC
  OS Unidentified
  PN JP 2003012688-A/5
  PD 15-JAN-2003
  PF 12-JUN-2002 JP 2002171743
  PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI

```



```

SERGEI M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02.C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC
compound;
CC hybridization and nuclease tolerant characteristics FH Key
FT source Location/Qualifiers
FT source 1..11 /organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1..11 /organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCTT 10
RESULT 77
LOCUS BD188890 11 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
hybridization and nuclease tolerant characteristics.
ACCESSION BD188890
VERSION BD188890.1 GI:32998629
KEYWORDS JP 2003012688-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
hybridization and nuclease tolerant characteristics
JOURNAL Patent: JP 2003012688-A 6 15-JAN-2003;
LYNX THERAPEUTICS INC
COMMENT OS Unidentified
PN JP 2003012688-A/6
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505.18-MAR-1994 US 08/214599 PI
SERGEI M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02.C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /note='where the intersubunit bonds are 'np'' FH Key
CC Location/Qualifiers
FT misc feature 1..11.
FT source Location/Qualifiers
FT source 1..11 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCTT 10
RESULT 78
A36017/c 12 bp DNA linear PAT 04-MAR-1997
LOCUS
DEFINITION Sequence 16 from Patent EP0564801.

```

```

ACCESSION A36017
VERSION A36017.1 GI:2293645
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Sommergruber,W.D., Auer,H., Blaas,D.D., Frasel,L., Hartmuth,K.D.,
Kuechler,E.P., Kowalski,H., Liebig,H.D., Skern,T.D. and
Ziegler,G.S.
TITLE Analysis of host cell shut-off
JOURNAL Patent: EP 0564801-A 16 13-OCT-1993;
BOEHRINGER INGELHEIM INT (DE)
COMMENT Other publication DE 4206769 930909
Other publication JP 6197799 940719
Other publication CA 2090834 930905
Other publication DE 4217929 931202.
FEATURES
source
Location/Qualifiers
1..12 /organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 12 CTTTCATCAT 3
RESULT 79
AR034985/c 12 bp DNA linear PAT 29-SEP-1999
LOCUS AR034985
DEFINITION Sequence 27 from patent US 5871697.
ACCESSION AR034985
VERSION AR034985.1 GI:5951653
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 5871697-A 27 16-FEB-1999;
FEATURES
source
Location/Qualifiers
1..12 /organism='unknown'
/mol_type='unassigned DNA'
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCAGCGCACT 10
Db 10 GTCAGCGCACT 1
RESULT 80
AR036371/c 12 bp DNA linear PAT 29-SEP-1999
LOCUS AR036371
DEFINITION Sequence 34 from patent US 5872105.
ACCESSION AR036371
VERSION AR036371.1 GI:5953039
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.

```

TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5972105-A 34 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
| | | | |
Db 12 CTTTCCTCTT 3

RESULT 81
AR082069/c
LOCUS AR082069 12 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 27 from patent US 5972693.
ACCESSION AR082069
VERSION AR082069.1 GI:10008795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Apparatus for identifying, classifying, or quantifying DNA sequences in a sample without sequencing
JOURNAL Patent: US 5972693-A 27 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACT 10
| | | | |
Db 10 GTCAGCGCACT 1

RESULT 82
AR100996
LOCUS AR100996 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 84 from patent US 6083693.
ACCESSION AR100996
VERSION AR100996.1 GI:12811794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.Marc.
TITLE Identification and comparison of protein-protein interactions that occur in populations
JOURNAL Patent: US 6083693-A 84 04-JUL-2000;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
| | | | |
Db 2 GCGCTTCAT 11

RESULT 83
AR101011
LOCUS AR101011 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 99 from patent US 6083693.
ACCESSION AR101011
VERSION AR101011.1 GI:12811809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.Marc.
TITLE Identification and comparison of protein-protein interactions that occur in populations
JOURNAL Patent: US 6083693-A 99 04-JUL-2000;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
| | | | |
Db 2 GCGCTTCAT 11

RESULT 84
AR118460/c
LOCUS AR118460 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 27 from patent US 6141657.
ACCESSION AR118460
VERSION AR118460.1 GI:14099366
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying classifying or quantifying DNA sequences in a sample without sequencing
JOURNAL Patent: US 6141657-A 27 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACT 10
| | | | |
Db 10 GTCAGCGCACT 1

RESULT 85
AR151028/c
LOCUS AR151028 12 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 27 from patent US 6231812.
ACCESSION AR151028
VERSION AR151028.1 GI:15117078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for indentifying, classifying, or quantifying protein sequences in a sample without sequencing

JOURNAL Patent: US 6231812-A 27 15-MAY-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 86
172119/c
LOCUS 172119 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 34 from patent US 5683874.
ACCESSION I72119
VERSION I72119.1 GI:3008258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a
triplex with a target sequence
JOURNAL Patent: US 5683874-A 34 04-NOV-1997;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 12 CTTTCCTT 3

RESULT 87
188202
LOCUS 188202 12 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 11 from patent US 5717085.
ACCESSION I88202
VERSION I88202.1 GI:3408142
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Lyttle,M.H. and Kauvar,L.M.
TITLE Process for preparing codon amides
JOURNAL Patent: US 5717085-A 11 10-FEB-1998;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 3 CATCATCCTT 12

RESULT 88
188205
LOCUS 188205 12 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 14 from patent US 5717085.
ACCESSION I88205
VERSION I88205.1 GI:3408145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Lyttle,M.H. and Kauvar,L.M.
TITLE Process for preparing codon amides
JOURNAL Patent: US 5717085-A 14 10-FEB-1998;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 3 CATCATCCTT 12

RESULT 89
AR199175/c
LOCUS AR199175 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 31 from patent US 6355423.
ACCESSION AR199175
VERSION AR199175.1 GI:20249249
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 31 12-MAR-2002;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 90
AR218184/c
LOCUS AR218184 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 27 from patent US 6418382.
ACCESSION AR218184
VERSION AR218184.1 GI:23318630
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
DNA sequences in a sample without sequencing
JOURNAL Patent: US 6418382-A 27 09-JUL-2002;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"

```
/mol_type="genomic DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACT 10
Db 10 GTCAGCGCACT 1

RESULT 91
AR222624/c
LOCUS AR222624 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 27 from patent US 6432361.
ACCESSION AR222624
VERSION AR222624.1 GI:23330255
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6432361-A 27 13-AUG-2002;
FEATURES
source
Location/Qualifiers
1..12
/mol_type="genomic DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACT 10
Db 10 GTCAGCGCACT 1

RESULT 92
AR231662/c
LOCUS AR231662 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6453245.
ACCESSION AR231662
VERSION AR231662.1 GI:27272819
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6453245-A 27 17-SEP-2002;
FEATURES
source
Location/Qualifiers
1..12
/mol_type="genomic DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACT 10
Db 10 GTCAGCGCACT 1

RESULT 93
AR371429
LOCUS AR371429 12 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 84 from patent US 6395478.

/mol_type="genomic DNA"

ACCESSION AR371429
VERSION AR371429.1 GI:34608363
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.M.
TITLE Identification and comparison of protein-protein interactions that
occur in populations and identification of inhibitors of these
interactors
JOURNAL Patent: US 6395478-A 84 28-MAY-2002;
FEATURES
source
Location/Qualifiers
1..12
/mol_type="genomic DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 94
AR371444
LOCUS AR371444 12 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 99 from patent US 6395478.
ACCESSION AR371444
VERSION AR371444.1 GI:34608378
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.M.
TITLE Identification and comparison of protein-protein interactions that
occur in populations and identification of inhibitors of these
interactors
JOURNAL Patent: US 6395478-A 99 28-MAY-2002;
FEATURES
source
Location/Qualifiers
1..12
/mol_type="genomic DNA"

Query Match
Best Local Similarity 46.7%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 95
AR107845
LOCUS AR107845 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 91 from patent US 6110667.
ACCESSION AR107845
VERSION AR107845.1 GI:12823332
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 91 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..10
```

```
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
Db 3 CTTTCATCC 10

RESULT 96
ARI94807/c
LOCUS      ARI94807
DEFINITION Sequence 29 from patent US 6350447.
ACCESSION  ARI94807
VERSION     ARI94807.1 GI:20244244
KEYWORDS    .
ORGANISM    Unknown.
REFERENCE    1 Unclassified.
AUTHORS      Chadwick,B.Paul. and Frischauf,A.-M.
TITLE        Methods and compositions relating to CD39-like polypeptides and
              nucleic acids
JOURNAL      Patent: US 6350447-A 29 26-FEB-2002;
FEATURES     Location/Qualifiers
              source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 10 TCATCCTT 3

RESULT 97
AX377225/c
LOCUS      AX377225
DEFINITION Sequence 26 from Patent WO0212497.
ACCESSION  AX377225
VERSION     AX377225.1 GI:19573514
KEYWORDS    .
ORGANISM    Homo sapiens (human)
REFERENCE    1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Choi,J.Y., Kazemi,A. and Koshy,B.
              Haplotypes of the nfkbib gene
              Patent: WO 0212497-A 26 14-FEB-2002;
              Genaisance Pharmaceuticals, Inc. (US)
FEATURES     Location/Qualifiers
              source
                1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8
Db 8 GTGAGCGA 1

RESULT 98
AX085322/c
LOCUS      AX085322
DEFINITION Sequence 8 from Patent WO0112856.
ACCESSION  AX085322
VERSION     AX085322.1 GI:13275378
KEYWORDS    .
ORGANISM    synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE    1 Lizardi,P.M. and Latimer,D.R.
              Analysis of sequence tags with hairpin primers
              Patent: WO 0112856-A 8 22-FEB-2001;
              YALE UNIVERSITY (US)
FEATURES     Location/Qualifiers
              source
                1..12
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="hairpin primer"

Query Match      44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACTT 11
Db 8 AGCGACTT 1

RESULT 99
I38925/c
LOCUS      I38925
DEFINITION Sequence 35 from patent US 5616483.
ACCESSION  I38925
VERSION     I38925.1 GI:2083403
KEYWORDS    .
ORGANISM    Unknown.
REFERENCE    1 Unclassified.
              1 (bases 1 to 11)
              Bjursell,K.G., Carlsson,P.N.I., Enerback,C.S.M., Hansson,S.L.,
              Lidberg,U.F.P., Nilsson,J.A. and Tornell,J.B.F.
              Genomic DNA sequences encoding human BSSL/CEL
              Patent: US 5616483-A 35 01-APR-1997;
              Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTCCTTCTT 1

RESULT 100
I87956/c
LOCUS      I87956
DEFINITION Sequence 35 from patent US 5716817.
ACCESSION  I87956
VERSION     I87956.1 GI:3407896
KEYWORDS    .
ORGANISM    Unknown.
REFERENCE    1 Unclassified.
              1 (bases 1 to 11)
              Tornell,J.Birger.Fredrik.
              Transgenic non-human mammals that express human BSSL/CEL
              Patent: US 5716817-A 35 10-FEB-1998;
```

```
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTCCTTCTT 1

RESULT 101
LOCUS AX099095 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 158 from Patent WO0120026.
ACCESSION AX099095
VERSION AX099095.1 GI:13538305
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wojnowski,L. and Huetert,E.
TITLE Polymorphisms in the human hpxr gene and their use in diagnostic
JOURNAL and therapeutic applications
JOURNAL Patent: WO 0120026-A 158 22-MAR-2001;
Epidaurus Biotechnologie AG (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="artificial sequence"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 1 TGAGCGGCTGC 11

RESULT 102
LOCUS AX099096/c 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 159 from Patent WO0120026.
ACCESSION AX099096
VERSION AX099096.1 GI:13538306
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wojnowski,L. and Huetert,E.
TITLE Polymorphisms in the human hpxr gene and their use in diagnostic
JOURNAL and therapeutic applications
JOURNAL Patent: WO 0120026-A 159 22-MAR-2001;
Epidaurus Biotechnologie AG (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="artificial sequence"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 1 TGAGCGGCTGC 11

RESULT 103
LOCUS AX470540 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 117 from Patent WO02053773.
ACCESSION AX470540
VERSION AX470540.1 GI:22205665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 117 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 1 TGTCGGGCTTC 11

RESULT 104
LOCUS AX623013 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 54 from Patent WO02053774.
ACCESSION AX623013
VERSION AX623013.1 GI:28450954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 54 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 1 TGTCGGGCTTC 11

RESULT 105
LOCUS AX623846/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 887 from Patent WO02053774.
ACCESSION AX623846
VERSION AX623846.1 GI:28451787
```

```
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 887 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GACTTCATCCT 17
Db 11 GAGTTATCCT 1
RESULT 106
AX623941
LOCUS AX623941 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 982 from Patent WO02053774.
ACCESSION AX623941
VERSION AX623941.1 GI:28451882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 982 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGGACTTTAT 11
RESULT 107
AX624355/c
LOCUS AX624355 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1396 from Patent WO02053774.
ACCESSION AX624355
VERSION AX624355.1 GI:28452296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1396 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
          Location/Qualifiers
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
```

```
source
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 11 ACTTGCTCCTT 1
RESULT 108
AX626174
LOCUS AX626174 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3215 from Patent WO02053774.
ACCESSION AX626174
VERSION AX626174.1 GI:28454212
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3215 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGCCACTGCAT 11
RESULT 109
AX626909
LOCUS AX626909 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3950 from Patent WO02053774.
ACCESSION AX626909
VERSION AX626909.1 GI:28454947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3950 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACCGACTTC 12
          Location/Qualifiers
          1..11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
```



```
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 1 ACTCGCTCCTT 11

RESULT 115
AX630434
LOCUS      AX630434                11 bp  DNA
DEFINITION Sequence 7475 from Patent WO02053774.
ACCESSION  AX630434
VERSION     AX630434.1 GI:28458472
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7475 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   .
            Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 1 TGTGGGCTTC 11

RESULT 116
AX631267/c
LOCUS      AX631267                11 bp  DNA
DEFINITION Sequence 8309 from Patent WO02053774.
ACCESSION  AX631267
VERSION     AX631267.1 GI:28459313
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8309 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   .
            Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
Db 11 GAGTTTATCCT 11

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 1 ACTCGCTCCTT 11

RESULT 117
AX631362
LOCUS      AX631362                11 bp  DNA
DEFINITION Sequence 8404 from Patent WO02053774.
ACCESSION  AX631362
VERSION     AX631362.1 GI:28459408
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8404 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   .
            Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 1 AGGACTTTAT 11

RESULT 118
AX631776/c
LOCUS      AX631776                11 bp  DNA
DEFINITION Sequence 8818 from Patent WO02053774.
ACCESSION  AX631776
VERSION     AX631776.1 GI:28459883
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8818 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   .
            Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTGCTCCTT 11

RESULT 119
AX632856/c
LOCUS      AX632856                11 bp  DNA
DEFINITION Sequence 9898 from Patent WO02053774.
ACCESSION  AX632856
VERSION     AX632856.1 GI:28468471
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

REFERENCE 1
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Petersohn, D., Conradt, M. and Hofmann, K.
JOURNAL Method for determining homeostasis of the skin
        Patent: WO 02053774-A 9898 11-JUL-2002;
        Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source 1. .11
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
  Query Match 43.3%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 11 AGCGACTTCCT 1

RESULT 120
S83243/c
LOCUS 11 bp DNA linear PRI 07-MAY-1993
DEFINITION CF transmembrane conductance regulator {precedes exon 21} [human,
ACCESSION S83243.1 GI:245829
VERSION S83243.1
KEYWORDS Genomic Mutant, 11 nt].
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 11)
AUTHORS Dork, T., Neumann, T., Wulbrand, U., Wulf, B., Kalin, N., Maass, G.,
        Krawczak, M., Guillemit, H., Ferec, C., Horn, G. et al.
TITLE Intra- and extragenic marker haplotypes of CFTR mutations in cystic
        fibrosis families
JOURNAL Hum. Genet. 88 (4), 417-425 (1992)
MEDLINE 92155692
PUBMED 1371263
REMARK GenBank staff at the National Library of Medicine created this
        entry [NCBI gibseq 83243] from the original journal article.
        This sequence comes from Figure 4.a.
FEATURES
  source 1. .11
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"
  gene 1. .11
        /gene="CF transmembrane conductance regulator"
  Query Match 43.3%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 11 AACGACATCAT 1

RESULT 121
A13913/c
LOCUS 12 bp DNA linear PAT 04-OCT-1994
DEFINITION Nucleotide sequence 20 from patent number EP0321201.
ACCESSION A13913
VERSION A13913.1 GI:640712
KEYWORDS unidentified
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Gerlach, W.L., Haseloff, J.P., Jennings, P.A. and Cameron, F.H.

```

```

TITLE Ribozymes
JOURNAL Patent: EP 0321201-A 20 21-JUN-1989;
        GENE SHEARS PTY. LIMITED
FEATURES
  source 1. .12
          Location/Qualifiers
          /organism="unidentified"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32644"
  Query Match 43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 1.2e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 122
AR005058/c
LOCUS 12 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 31 from patent US 5747335.
ACCESSION AR005058
VERSION AR005058.1 GI:3965937
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Haseloff, J., Phillip, J., Gerlach, W. Lyle., Jennings, P. Anthony. and
        Cameron, F. Helen.
TITLE Ribozymes
JOURNAL Patent: US 5747335-A 31 05-MAY-1998;
        Location/Qualifiers
FEATURES
  source 1. .12
          /organism="unknown"
          /mol_type="unassigned DNA"
  Query Match 43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 1.2e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 123
AR034968
LOCUS 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5871697.
ACCESSION AR034968
VERSION AR034968.1 GI:5951636
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg, J. Marc., Deem, M. W. and Simpson, J. W.
TITLE Method and apparatus for identifying, classifying, or quantifying
        DNA sequences in a sample without sequencing
JOURNAL Patent: US 5871697-A 10 16-FEB-1999;
        Location/Qualifiers
FEATURES
  source 1. .12
          /organism="unknown"
          /mol_type="unassigned DNA"
  Query Match 43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. No. 1.2e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14

```

```
Db 1 AGTGGCTTCAT 11

RESULT 124
LOCUS AR060874 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 31 from patent US 5840874.
ACCESSION AR060874
VERSION AR060874.1 GI:5987324
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Haseloff,J.Phillip., Gerlach,W.Lyle., Jennings,P.Anthony. and
TITLE Hammerhand ribozymes
JOURNAL Patent: US 5840874-A 31 24-NOV-1998;
FEATURES Location/Qualifiers
source 1..12
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 125
LOCUS AR082052 12 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 10 from patent US 5972693.
ACCESSION AR082052
VERSION AR082052.1 GI:10008778
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Apparatus for identifying, classifying, or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 5972693-A 10 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..12
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11

RESULT 126
LOCUS AR101008 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 96 from patent US 6083693.
ACCESSION AR101008
VERSION AR101008.1 GI:12811806
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.Marc.

TITLE Identification and comparison of protein-protein interactions that
occur in populations
JOURNAL Patent: US 6083693-A 96 04-JUL-2000;
FEATURES Location/Qualifiers
source 1..12
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11

RESULT 127
LOCUS AR110808 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 31 from patent US 6127114.
ACCESSION AR110808
VERSION AR110808.1 GI:12827656
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Haseloff,J.Phillip., Gerlach,W.Lyle., Jennings,P.Anthony. and
TITLE Ribozymes
JOURNAL Patent: US 6127114-A 31 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..12
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 128
LOCUS AR118443 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6141657.
ACCESSION AR118443
VERSION AR118443.1 GI:14099349
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying classifying or quantifying DNA
sequences in a sample without sequencing
JOURNAL Patent: US 6141657-A 10 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..12
/mol_type="unassigned DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11
```

```
RESULT 129
AR151011
LOCUS AR151011 12 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6231812.
ACCESSION AR151011
VERSION AR151011.1 GI:15117061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for indentifying, classifying, or quantifying
protein sequences in a sample without sequencing
JOURNAL Patent: US 6231812-A 10 15-MAY-2001;
FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11

RESULT 130
AR162278
LOCUS AR162278 12 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 13 from patent US 6258585.
ACCESSION AR162278
VERSION AR162278.1 GI:16229434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting influenza virus replication
JOURNAL Patent: US 6258585-A 13 10-JUL-2001;
FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGCACTT 11
Db 1 GTGTGCCACTT 11

RESULT 131
AR167736/c
LOCUS AR167736 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 100 from patent US 6287769.
ACCESSION AR167736
VERSION AR167736.1 GI:17903536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,T.
TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA
fragment, method of assaying microorganisms, method of analyzing
```

```
microorganisms and method of assaying contaminant
Patent: US 6287769-A 100 11-SEP-2001;
FEATURES
source Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GACTTCATCCT 17
Db 12 GACTTCGGCCT 2

RESULT 132
E29620/c
LOCUS E29620 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, method for estimating state of
microorganism existing and method for estimating state of waste.
ACCESSION E29620
VERSION E29620.1 GI:13021123
KEYWORDS JP 1999276176-A/100.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi,I.
TITLE Method for amplifying DNA fragment, method for estimating state of
microorganism existing and method for estimating state of waste
JOURNAL Patent: JP 1999276176-A 100 12-OCT-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 1999276176-A/100
PD 12-OCT-1999
PF 31-MAR-1998 JP 1998087652
PR
PI KOICHI INOUE
PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH Key Location/Qualifiers
FT source 1..12
/organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..12
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GACTTCATCCT 17
Db 12 GACTTCGGCCT 2

RESULT 133
E38726/c
LOCUS E38726 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION E38726
VERSION E38726.1 GI:18621388
KEYWORDS JP 2000270867-A/100.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
```

JOURNAL Patent: JP 2000270867-A 100 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT Unidentified
OS JP 2000270867-A/100
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
/organism='Unidentified'.
Location/Qualifiers
1..12

FEATURES source
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
|||||
Db 12 GACTTCGGCCT 2

RESULT 134
E64152/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.

ACCESSION E64152
VERSION E64152.1 GI:13019556
KEYWORDS JP 1999341989-A/100.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi, I.

TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance

JOURNAL Patent: JP 1999341989-A 100 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES

COMMENT OS Artificial Sequence
PN JP 1999341989-A/100
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694

PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..12
/organism='Artificial Sequence'.
Location/Qualifiers
1..12

FEATURES source
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
|||||
Db 12 GACTTCGGCCT 2

RESULT 135
107917/c

LOCUS 12 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 29 from Patent EP 0159123.
ACCESSION I07917
VERSION I07917.1 GI:589370
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
TITLE Vectors for expressing bovine growth hormone derivatives
JOURNAL Patent: EP 0159123-A2 29 23-OCT-1985;
FEATURES Location/Qualifiers
source 1..12
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 11 ACTTCCTTCTT 1

RESULT 136
118287/c

LOCUS 12 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 33 from patent US 5494814.
ACCESSION I18287
VERSION I18287.1 GI:1598642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Haseloff,J.P., Gerlach,W.L., Jennings,P.A. and Cameron,F.H.
TITLE Ribozymes
JOURNAL Patent: US 5494814-A 33 27-FEB-1996;
FEATURES Location/Qualifiers
source 1..12
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
|||||
Db 11 TGAAGGACTTC 1

RESULT 137
124500/c

LOCUS 12 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 31 from patent US 5543508.
ACCESSION I24500
VERSION I24500.1 GI:1604370
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Haseloff,J.P., Gerlach,W.L., Jennings,P.A. and Cameron,F.H.

/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| |||||
Db 1 AGTGGCTTCAT 11

RESULT 143
AR222607
LOCUS AR222607 Sequence 10 from patent US 6432361. 12 bp DNA linear PAT 26-SEP-2002
DEFINITION AR222607
ACCESSION AR222607
VERSION AR222607.1 GI:23330238
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying protein sequences in a sample without sequencing
JOURNAL Patent: US 6432361-A 10 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| |||||
Db 1 AGTGGCTTCAT 11

RESULT 144
AR231645
LOCUS AR231645 Sequence 10 from patent US 6453245. 12 bp DNA linear PAT 20-DEC-2002
DEFINITION AR231645
ACCESSION AR231645
VERSION AR231645.1 GI:27272802
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Rothberg,J.M., Deem,M.W. and Simpson,J.W.
TITLE Method and apparatus for identifying, classifying, or quantifying protein sequences in a sample without sequencing
JOURNAL Patent: US 6453245-A 10 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| |||||
Db 1 AGTGGCTTCAT 11

RESULT 145
AR277890
LOCUS AR277890 Sequence 13 from patent US 6511808. 12 bp DNA linear PAT 18-DEC-2003
DEFINITION AR277890
ACCESSION AR277890.1 GI:29711814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Wolfe,A., Urnov,F., Guschin,D., Collingwood,T., Li,X.-Y. and Johnstone,B.
TITLE Methods for designing exogenous regulatory molecules
JOURNAL Patent: US 6511808-A 13 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Sequence 13 from patent US 6511808.
AR277890
AR277890.1 GI:29711814
Unknown.
Unclassified.
1 (bases 1 to 12)
Wolfe,A., Urnov,F., Guschin,D., Collingwood,T., Li,X.-Y. and Johnstone,B.
Methods for designing exogenous regulatory molecules
Patent: US 6511808-A 13 28-JAN-2003;
Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| |||||
Db 1 GATCGAATTCAT 11

RESULT 146
AR371441
LOCUS AR371441 Sequence 96 from patent US 6395478. 12 bp DNA linear PAT 12-SEP-2003
DEFINITION AR371441
ACCESSION AR371441
VERSION AR371441.1 GI:34608375
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Nandabalan,K. and Rothberg,J.M.
TITLE Identification and comparison of protein-protein interactions that occur in populations and indentification of inhibitors of these interactors
JOURNAL Patent: US 6395478-A 96 28-MAY-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| |||||
Db 1 AGTGGCTTCAT 11

RESULT 147
AR382247
LOCUS AR382247 Sequence 13 from patent US 6610489. 12 bp DNA linear PAT 18-DEC-2003
DEFINITION AR382247
ACCESSION AR382247
VERSION AR382247.1 GI:40090659
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Wolfe,A., Urnov,F., Guschin,D., Collingwood,T., Li,X.-Y. and Johnstone,B.
TITLE Pharmacogenomics and identification of drug targets by reconstruction of signal transduction pathways based on sequences of accessible regions
JOURNAL Patent: US 6610489-A 13 26-AUG-2003;

```

FEATURES
  source
    Location/Qualifiers
      1..12
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

RESULT 148
AR408045/c
LOCUS
  DEFINITION
    Sequence 138 from patent US 6632057.
  ACCESSION
    AR408045
  VERSION
    AR408045.1 GI:40158032
  KEYWORDS
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 12)
  AUTHORS
    Fauchet, C.R.J.
  TITLE
    Fixing unit with an end imprint in a threaded terminal portion
  JOURNAL
    Patent: US 6632057-A 138 14-OCT-2003;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="unknown"
          /mol_type="unassigned RNA"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
    |||||
Db 11 GAATCATCCT 1

RESULT 149
AX319642
LOCUS
  DEFINITION
    Sequence 13 from Patent WO0183732.
  ACCESSION
    AX319642
  VERSION
    AX319642.1 GI:17901313
  KEYWORDS
    synthetic construct
  ORGANISM
    synthetic construct
  SOURCE
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Wolffe, A., Urnov, F., Guschin, D., Collingwood, T., Li, X.Y. and
    Johnstone, B.
  TITLE
    Databases of regulatory sequences; methods of making and using same
  JOURNAL
    Patent: WO 0183732-A 13 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="adapter oligonucleotide containing a Sau
          3AI-compatible end"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

RESULT 149
AX710994
LOCUS
  DEFINITION
    Sequence 13 from Patent WO0183819.
  ACCESSION
    AX710994
  VERSION
    AX710994.1 GI:18616184
  KEYWORDS
    synthetic construct
  ORGANISM
    synthetic construct
  SOURCE
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Wolffe, A., Urnov, F., Guschin, D., Collingwood, T., Li, X.Y. and
    Johnstone, B.
  TITLE
    Methods for designing exogenous regulatory molecules
  JOURNAL
    Patent: WO 0183819-A 13 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="adapter oligonucleotide containing a Sau
          3AI-compatible end"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

RESULT 150
AX319823
LOCUS
  DEFINITION
    Sequence 13 from Patent WO0184148.
  ACCESSION
    AX319823
  VERSION
    AX319823.1 GI:17901413
  KEYWORDS
    synthetic construct
  ORGANISM
    synthetic construct
  SOURCE
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Wolffe, A., Urnov, F., Guschin, D., Collingwood, T., Li, X.Y. and
    Johnstone, B.
  TITLE
    Pharmacogenomics and identification of drug targets by
    reconstruction of signal transduction pathways based on sequences
    of accessible regions
  JOURNAL
    Patent: WO 0184148-A 13 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="adapter oligonucleotide containing a Sau
          3AI-compatible end"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

RESULT 151
AX350611
LOCUS
  DEFINITION
    Sequence 13 from Patent WO0183819.
  ACCESSION
    AX350611
  VERSION
    AX350611.1 GI:18616184
  KEYWORDS
    synthetic construct
  ORGANISM
    synthetic construct
  SOURCE
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Wolffe, A., Urnov, F., Guschin, D., Collingwood, T., Li, X.Y. and
    Johnstone, B.
  TITLE
    Methods for designing exogenous regulatory molecules
  JOURNAL
    Patent: WO 0183819-A 13 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="adapter oligonucleotide containing a Sau
          3AI-compatible end"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

RESULT 152
AX710994
LOCUS
  DEFINITION
    Sequence 13 from Patent WO0183819.
  ACCESSION
    AX710994
  VERSION
    AX710994.1 GI:18616184
  KEYWORDS
    synthetic construct
  ORGANISM
    synthetic construct
  SOURCE
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Wolffe, A., Urnov, F., Guschin, D., Collingwood, T., Li, X.Y. and
    Johnstone, B.
  TITLE
    Methods for designing exogenous regulatory molecules
  JOURNAL
    Patent: WO 0183819-A 13 08-NOV-2001;
  FEATURES
    source
      Location/Qualifiers
        1..12
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="adapter oligonucleotide containing a Sau
          3AI-compatible end"

Query Match
  Best Local Similarity 43.3%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    |||||
Db 1 GATCGAATTCA 11

```



```

DEFINITION Sequence 294 from Patent EP1288296.
ACCESSION AX710994
VERSION AX710994.1 GI:29787375
SOURCE Influenza virus
ORGANISM Influenza virus
REFERENCE Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
AUTHORS unclassified Orthomyxoviridae.
1
TITLE Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
JOURNAL Macejak,D.G. and Mamone,A.J.
METHOD Method and reagent for inhibiting HBV viral replication
PATENT Patent: EP 1288296-A 294 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1. .12
/organism="Influenza virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11309"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
| | | | |
Db 1 GTGTGCCACTT 11

RESULT 153
BD001135
LOCUS
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001135
VERSION BD001135.1 GI:18625694
KEYWORDS JP 2000342285-A/295.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 12)
REFERENCE Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 295 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342285-A/295
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884331 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN,PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00,C12N9/22,C12N5/10,C12R1/91, PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1/91)
CC
FH Key Location/Qualifiers
FT source 1. .12
/organism="Artificial Sequence".

RESULT 154
BD001564
LOCUS
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001564
VERSION BD001564.1 GI:18626123
KEYWORDS JP 2000342286-A/295.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 12)
REFERENCE Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
AUTHORS Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 295 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/295
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884331 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN,PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00,C12N9/22,C12N5/10,C12R1/91, PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1/91)
CC
FH Key Location/Qualifiers
FT source 1. .12
/organism="Artificial Sequence".

FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
| | | | |
Db 1 GTGTGCCACTT 11

FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GTGAGCGACTT 11
    |||||
Db 1 GTGTGCCACTT 11

RESULT 155
BD143760
LOCUS
DEFINITION BZIP transcription factor controlling the expression of rice
storage protein.
ACCESSION BD143760
VERSION BD143760.1 GI:27849518
KEYWORDS JP 2002119282-A/7.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Takaiwa,F. and Onodera,Y.
BZIP transcription factor controlling the expression of rice
storage protein
Patent: JP 2002119282-A 7 23-APR-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES
MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, BIO ORIENTED
TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION
OS Oryza sativa (rice)
PN JP 2002119282-A/7
PD 23-APR-2002
PF 11-OCT-2000 JP 2000311295
PI FUMIO TAKAIWA,YASUYUKI ONODERA
PC C12N15/09,A01H5/00,C07K14/415,C07K16/16,C12N1/15,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12N5/10,C12N9/22,C12P21/02,C12P21/08//C12Q1/02,PC
(C12N15/09,C12R1:91),(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),PC
C12N15/00,
PC C12N5/00,C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91)CC
BZIP transcription factor controlling the expression of rice
storage
CC protein
FH Key
FT source
FT Location/Qualifiers
1..12
/organism="Oryza sativa (rice)".
FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
    |||||
Db 2 GTGAGTCACCTT 12

RESULT 157
A41388/c
LOCUS
DEFINITION Sequence 14 from Patent WO9426928.
ACCESSION A41388
VERSION A41388.1 GI:2297107
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
Strauss,M. and Bauer,D.
COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
Patent: WO 9426928-A 14 24-NOV-1994;
MAX PLANCK GESELLSCHAFT (DE)
Other publication DE 4317414 940421.
FEATURES
source
1..10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
    |||||
Db 9 GACTTGATC 1

RESULT 158
A52292/c
LOCUS
DEFINITION Sequence 82 from Patent EP0705842.
ACCESSION A52292
VERSION A52292.1 GI:2852021
KEYWORDS

```

```

TITLE BZIP type transcriptional factor regulating the expression of rice
reserve protein
JOURNAL Patent: WO 0231154-A 7 18-APR-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES, BIO ORIENTED
TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION, FUMIO TAKAIWA,
YASUYUKI ONODERA
COMMENT OS Oryza sativa (rice)
PN WO 0231154-A/7
PD 18-APR-2002
PF 11-OCT-2001 WO 2001JP008936
PR 11-OCT-2000 JP 00P 311295
PI FUMIO TAKAIWA,YASUYUKI ONODERA
PC C12N15/29,C12N5/14,C07K14/415,A01H5/00
CC BZIP type transcriptional factor regulating the expression of
rice reserve
CC protein
FH Key
FT source
FT Location/Qualifiers
1..12
/organism="Oryza sativa (rice)".
FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
    |||||
Db 2 GTGAGTCACCTT 12

RESULT 157
A41388/c
LOCUS
DEFINITION Sequence 14 from Patent WO9426928.
ACCESSION A41388
VERSION A41388.1 GI:2297107
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
Strauss,M. and Bauer,D.
COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
Patent: WO 9426928-A 14 24-NOV-1994;
MAX PLANCK GESELLSCHAFT (DE)
Other publication DE 4317414 940421.
FEATURES
source
1..10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
    |||||
Db 9 GACTTGATC 1

RESULT 158
A52292/c
LOCUS
DEFINITION Sequence 82 from Patent EP0705842.
ACCESSION A52292
VERSION A52292.1 GI:2852021
KEYWORDS

```

SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bartnik,E.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 82 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES Location/Qualifiers
source
1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 9 GACTTGATC 1

RESULT 159
AR018730/c
LOCUS AR018730 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5783182.
ACCESSION AR018730
VERSION AR018730.1 GI:3973844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Thompson,T.C.
TITLE Method for identifying metastatic sequences
JOURNAL Patent: US 5783182-A 12 21-JUL-1998;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 9 GACTTGATC 1

RESULT 160
AR030114/c
LOCUS AR030114 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 303 from patent US 5861244.
ACCESSION AR030114
VERSION AR030114.1 GI:5943328
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 303 19-JAN-1999;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bartnik,E.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 82 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES Location/Qualifiers
source
1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 9 GACTTGATC 1

RESULT 159
AR018730/c
LOCUS AR018730 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 12 from patent US 5783182.
ACCESSION AR018730
VERSION AR018730.1 GI:3973844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Thompson,T.C.
TITLE Method for identifying metastatic sequences
JOURNAL Patent: US 5783182-A 12 21-JUL-1998;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 9 GACTTGATC 1

RESULT 160
AR030114/c
LOCUS AR030114 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 303 from patent US 5861244.
ACCESSION AR030114
VERSION AR030114.1 GI:5943328
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 303 19-JAN-1999;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 9 CTTCTCCTCT 1

RESULT 161
AR036561
LOCUS AR036561 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5872235.
ACCESSION AR036561
VERSION AR036561.1 GI:5953229
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Chen,L.Bo., Bao,S. and Liu,Y.
TITLE Nucleic acids encoding tumor marker
JOURNAL Patent: US 5872235-A 14 16-FEB-1999;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 1 TGAGCTACT 9

RESULT 162
AR092691
LOCUS AR092691 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 3 from patent US 5998193.
ACCESSION AR092691
VERSION AR092691.1 GI:10019443
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, trna
JOURNAL Patent: US 5998193-A 3 07-DEC-1999;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
|||||
Db 2 GTGAGCGGC 10

RESULT 163
AR106675
LOCUS AR106675 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107078.
ACCESSION AR106675
VERSION AR106675.1 GI:12821205

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 3 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
| | | | | | | |
Db 2 GTGAGCGC 10
| | | | | | | |
RESULT 164
ARI07804
LOCUS ARI07804 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 50 from patent US 6110667.
ACCESSION ARI07804
VERSION ARI07804.1 GI:12823291
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 50 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
| | | | | | | | | |
Db 1 CTTTCATCAT 9
| | | | | | | | | |
RESULT 165
ARI07807
LOCUS ARI07807 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 53 from patent US 6110667.
ACCESSION ARI07807
VERSION ARI07807.1 GI:12823294
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 53 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
| | | | | | | |
Db 1 CTTTCATCGT 9
| | | | | | | |
RESULT 166
ARI07818
LOCUS ARI07818 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 64 from patent US 6110667.
ACCESSION ARI07818
VERSION ARI07818.1 GI:12823305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 64 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
| | | | | | | |
Db 1 GCCTTCATC 9
| | | | | | | |
RESULT 167
ARI07829
LOCUS ARI07829 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 75 from patent US 6110667.
ACCESSION ARI07829
VERSION ARI07829.1 GI:12823316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 75 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
| | | | | | | |
Db 2 GCCTTCATC 10
| | | | | | | |
RESULT 168
ARI24891/c
LOCUS ARI24891 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6172212.
ACCESSION ARI24891
VERSION ARI24891.1 GI:14110252
KEYWORDS

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Hung,M.-C. and King,X.
TITLE        Pea3 is a tumor suppressor
JOURNAL      Patent: US 6172212-A 5 09-JAN-2001;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACTTCATCC 16
Db      10 ACTTCCTCC 2

RESULT 169
ARI124892/c
LOCUS      ARI124892
DEFINITION Sequence 6 from patent US 6172212.
ACCESSION  ARI124892
VERSION     ARI124892.1 GI:14110253
KEYWORDS    Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Hung,M.-C. and King,X.
TITLE        Pea3 is a tumor suppressor
JOURNAL      Patent: US 6172212-A 6 09-JAN-2001;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 ACTTCCTCC 2
Db      8 ACTTCATCC 16

RESULT 170
ARI147934/c
LOCUS      ARI147934
DEFINITION Sequence 103 from patent US 6225054.
ACCESSION  ARI147934
VERSION     ARI147934.1 GI:15112024
KEYWORDS    Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Frudakis,T.N., Smith,J.M. and Reed,S.G.
TITLE        Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL      Patent: US 6225054-A 103 01-MAY-2001;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 TTCCTCCTT 18
Db      10 TTCATCCTT 18

RESULT 171
BD237032
LOCUS      BD237032
DEFINITION Compounds for remedy and diagnosis of lung cancer and method for using the same.
ACCESSION  BD237032
VERSION     BD237032.1 GI:33046802
KEYWORDS    JP 2002516659-A/33.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Reed,S.G., Lodes,M.J., Frudakis,T.N. and Mohanath,R.
TITLE        Compounds for remedy and diagnosis of lung cancer and method for using the same
JOURNAL      Patent: JP 2002516659-A 33 11-JUN-2002;
CORIXA CORP
OS          Homo sapiens (human)
PN          JP 2002516659-A/33
PD          11-JUN-2002
PF          26-JAN-1998 JP 2000529432
PR          28-JAN-1998 US 09/015029,28-JAN-1998 US 09/015022 PR
18-MAR-1998 US 09/040828,18-MAR-1998 US 09/040831 PR
23-JUL-1998 US 09/122192,23-JUL-1998 US 09/122191 PR
22-DEC-1998 US 09/219245
PI          STEVEN G REED,MICHAEL J LODES,TONY N FRUDAKIS,RAODOH MOHAMATH
PC          C12N15/09,A61K35/14,A61K39/00,A61K39/39,A61K39/395,
PC          A61K39/395,
PC          A61P11/00,A61P35/00,C07K14/47,C07K16/18,C07K19/00,C12N1/19, PC
C12N1/21,
PC          C12N5/10,C12P21/08,C12Q1/69,G01N33/53,G01N33/574,G01N33/577//
PC          (C12N1/21,C12R1:19),C12N15/00,A61K37/02,C12N5/00 CC
Compounds for remedy and diagnosis of lung cancer and method CC
for using the

CC          same
FH          Key
FT          Location/Qualifiers
              1..10
              /organism="Homo sapiens (human)".
              Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTCATCCTT 17
Db      1 CTCACCT 9

RESULT 172
BD238639/c
LOCUS      BD238639
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238639
VERSION     BD238639.1 GI:33048409
KEYWORDS    JP 2002534056-A/57.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Roberts,B.L. and Shankara,S.
TITLE        Preparation and use of superior vaccines

```

```
JOURNAL Patent: JP 2002534056-A 57 15-OCT-2002;
COMMENT GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/57
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCCTCT 17
|||||
Db 10 CTTTCCTCT 2

RESULT 173
BD238706/c LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238706
VERSION BD238706.1 GI:33048476
KEYWORDS JP 2002534056-A/124.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 124 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/124
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTCATCCTT 18
|||||
Db 10 TTCATCCTT 2

RESULT 174
BD239080 LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239080
VERSION BD239080.1 GI:33048850
KEYWORDS JP 2002534056-A/498.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 498 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/498
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTCATCCTT 18
|||||
Db 10 TTCATCCTT 2

RESULT 175
BD239080 LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239080
VERSION BD239080.1 GI:33048850
KEYWORDS JP 2002534056-A/498.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 498 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/498
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTCATCCTT 18
|||||
Db 10 TTCATCCTT 2
```

```
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
    source
        Location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCCAC 9
Db 2 GTGAGCCAC 10
RESULT 175
BD239761/c
LOCUS BD239761 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239761
VERSION BD239761.1 GI:33049531
KEYWORDS JP 2002534056-A/1179.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (Bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 1179 15-OCT-2002;
  GENZYME CORP
  OS Homo sapiens (human)
  PN JP 2002534056-A/1179
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
  19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
  19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
  19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
  19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
  19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
  19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
  19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
  19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
  19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
  19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
  19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
  19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
  19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
  08-DEC-1998 US 60/111715
  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
  PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
  C12N1/19,
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
  G01N37/00,
  PC C12N15/00,C12N5/00,C12N15/00
  CC Preparation and use of superior vaccines
  FH Key Location/Qualifiers
  FT source 1..10
  FT /organism='Homo sapiens (human)'.
FEATURES
    source
        Location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCGACTTCA 13
Db 2 GTGACTTCA 10
RESULT 177
BD248504/c
LOCUS BD248504 10 bp DNA linear PAT 17-JUL-2003
DEFINITION T cells specific for target antigens and methods and vaccines based thereon.
ACCESSION BD248504
```

```
VERSION BD248504.1 GI:33058274
KEYWORDS JP 2002529082-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 10)
AUTHORS Zauderer,M.
TITLE T cells specific for target antigens and methods and vaccines based
JOURNAL thereon
COMMENT Patent: JP 2002529082-A 18 10-SEP-2002;
UNIVERSITY OF ROCHESTER
OS Artificial Sequence
PN JP 2002529082-A/18
PD 10-SEP-2002
PF 10-NOV-1998 JP 2000581183
PI MAURICE ZAUDERER
PC C12N15/09,A01K67/027,A61K35/76,A61K39/00,A61K39/04,A61K39/12,
PC A61K39/395,
PC A61K39/395,A61P31/04,A61P31/10,A61P31/12,A61P35/00,C12N5/10,
PC C1201/02,
PC G01N33/574,C12N15/00,C12N5/00
CC MR14
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..10
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
Db 9 GACTTGATC 1
RESULT 178
E16894/c
LOCUS Brevibacterium flavum.
DEFINITION DNA sequence required for efficient protein transcription in
Brevibacterium flavum.
ACCESSION E16894
VERSION E16894.1 GI:5711577
KEYWORDS JP 1998229881-A/35.
SOURCE Corynebacterium glutamicum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 10)
Kobayashi,M., Man,T. and Yugawa,H.
DNA HAVING SEQUENCE CAPABLE OF EFFICIENTLY TRANSLATING PROTEIN IN
CORYNEFORM BACTERIA
Patent: JP 1998229881-A 35 02-SEP-1998;
JOURNAL MITSUBISHI CHEM CORP
COMMENT OS Brevibacterium flavum
PN JP 1998229881-A/35
PD 02-SEP-1998
PF 19-FEB-1997 JP 1997035338
PI KOBAYASHI MIKI, MAN TOMOKO, YUGAWA HIDEAKI
PC C12N15/09,C07H21/04,C12N1/21//C12N9/38,C12Q1/68,(C12N15/09, PC
C12R1:19),
PC (C12N1/21,C12R1:13),(C12N9/38,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..10
```

```
FT /organism='Brevibacterium flavum' FT
FEATURES
source
Location/Qualifiers
1..10
/organism='Corynebacterium glutamicum'
/mol_type='genomic DNA'
/db_xref='taxon:1718'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTCATCCTT 18
Db 10 TTCCTCCTT 2
RESULT 179
E39572
LOCUS Genes with human dendritic cell expression.
DEFINITION E39572
ACCESSION E39572
VERSION E39572.1 GI:18621663
KEYWORDS JP 2000279181-A/105.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Hashimoto,S., Matsushima,K. and Suzuki,T.
AUTHORS Genes with human dendritic cell expression
TITLE Patent: JP 2000279181-A 105 10-OCT-2000;
JOURNAL SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/105
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCCAC 9
Db 2 GTGAGCCAC 10
RESULT 180
E39654/c
LOCUS Genes with human dendritic cell expression.
DEFINITION E39654
ACCESSION E39654
VERSION E39654.1 GI:18621745
KEYWORDS JP 2000279181-A/187.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Hashimoto,S., Matsushima,K. and Suzuki,T.
AUTHORS Genes with human dendritic cell expression
TITLE
```


JOURNAL Patent: JP 2000279181-A 187 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/187
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR SHINTCHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC
C12N15/09, C07K14/475, C07K16/18, C12N15/00
CC
FH Key 1. .10 Location/Qualifiers
FT source
PT Location/Qualifiers
FEATURES source
1. .10 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
| | | | |
Db 10 CGTCATCCT 2
RESULT 181
190236 I90236 10 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 17 from patent US 5723598.
DEFINITION I90236
ACCESSION I90236
VERSION I90236.1 GI:3410176
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lerner, R., Janda, K. and Brenner, S.
TITLE Encoded combinatorial chemical libraries
JOURNAL Patent: US 5723598-A 17 03-MAR-1998;
FEATURES Location/Qualifiers
source 1. .10 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 AGCGACTTC 12
| | | | |
Db 1 AGCTACTTC 9
RESULT 182
AR219658 AR219658 10 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 103 from patent US 6423496.
DEFINITION AR219658
ACCESSION AR219658
VERSION AR219658.1 GI:23323836
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Frudakis, T.N., Smith, J.M. and Reed, S.G.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6423496-A 103 23-JUL-2002;
FEATURES Location/Qualifiers
source 1. .10

/organism="unknown"
/mol_type="genomic DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
| | | | |
Db 1 CTTCAACCT 9
RESULT 183
AR225432 AR225432 10 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 48 from patent US 6444425.
DEFINITION AR225432
ACCESSION AR225432
VERSION AR225432.1 GI:27263378
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Reed, S.G., Lodes, M.J., Mohamath, R. and Secrist, H.
TITLE Compounds for therapy and diagnosis of lung cancer and methods for their use
JOURNAL Patent: US 6444425-A 48 03-SEP-2002;
FEATURES Location/Qualifiers
source 1. .10 /organism="unknown"
/mol_type="genomic DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
| | | | |
Db 1 CTTCAACCT 9
RESULT 184
AR241699 AR241699 10 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 6 from patent US 6472153.
DEFINITION AR241699
ACCESSION AR241699
VERSION AR241699.1 GI:27287511
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dempcy, R.O., Afonina, I.A. and Vermeulen, N.M.J.
TITLE Hybridization-triggered fluorescent detection of nucleic acids
JOURNAL Patent: US 6472153-A 6 29-OCT-2002;
FEATURES Location/Qualifiers
source 1. .10 /organism="unknown"
/mol_type="genomic DNA"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 AGCGACTTC 12
| | | | |
Db 9 AGCAACTTC 1
RESULT 185
AR303338 AR303338 10 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 63 from patent US 6544736.
DEFINITION

ACCESSION AR303338
VERSION AR303338.1 GI:31692114
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 63 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
| | | | | | | |
Db 10 GACTTCACC 2

RESULT 186
AR303662
LOCUS AR303662 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 387 from patent US 6544736.
ACCESSION AR303662
VERSION AR303662.1 GI:31692438
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 387 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
| | | | | | | |
Db 2 AGCGATTTC 10

RESULT 187
AR303664/c
LOCUS AR303664 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 389 from patent US 6544736.
ACCESSION AR303664
VERSION AR303664.1 GI:31692440
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 389 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
| | | | | | | |
Db 9 AGCGATTTC 1

RESULT 188
AR344453/c
LOCUS AR344453 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 7 from patent US 6582725.
ACCESSION AR344453
VERSION AR344453.1 GI:33740499
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Xing,X. and Hung,M.-C.
TITLE Human PEA3 is a tumor suppressor for cancer cells
JOURNAL Patent: US 6582725-A 7 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
| | | | | | | |
Db 10 ACTTCCTCC 2

RESULT 189
AR344454/c
LOCUS AR344454 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 8 from patent US 6582725.
ACCESSION AR344454
VERSION AR344454.1 GI:33740500
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Xing,X. and Hung,M.-C.
TITLE Human PEA3 is a tumor suppressor for cancer cells
JOURNAL Patent: US 6582725-A 8 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
| | | | | | | |
Db 9 TTCCTCCTT 1

RESULT 190
AR350756
LOCUS AR350756 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 103 from patent US 6586570.
ACCESSION AR350756
VERSION AR350756.1 GI:33752396
KEYWORDS


```

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
    ||| |||||
Db 1 TTTCCTCCTT 9

RESULT 200
AX301574
LOCUS AX301574 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 288 from Patent WO0185941.
ACCESSION AX301574
VERSION AX301574.1 GI:17382657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 288 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
    ||| |||||
Db 1 TTTCCTCCTT 9

RESULT 201
AX301623/c
LOCUS AX301623 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 337 from Patent WO0185941.
ACCESSION AX301623
VERSION AX301623.1 GI:17382706
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 337 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
    ||||| |||||
Db 10 TGAGAGACT 2

RESULT 202
AX302568/c
LOCUS AX302568 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 86 from Patent WO0175177.

```

```

ACCESSION AX302568
VERSION AX302568.1 GI:17383095
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 86 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
    ||||| |||||
Db 10 CTTCTTCCT 2

RESULT 203
AX316766
LOCUS AX316766 10 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 103 from Patent WO0190152.
ACCESSION AX316766
VERSION AX316766.1 GI:17899857
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0190152-A 103 29-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for amplification from breast tumor cDNA"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
    ||||| |||||
Db 1 CTTCAACCT 9

RESULT 204
AX321517
LOCUS AX321517 10 bp DNA linear PAT 15-DEC-2001
DEFINITION Sequence 48 from Patent WO0172295.
ACCESSION AX321517
VERSION AX321517.1 GI:17905579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Reed,S.G., Lodes,M.J., Mohamath,R., Secrist,H., Benson,D.R.,

```

Indirias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elliot,M.,
Mannion,J. and Kalos,M.D.
Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0172295-A 48 04-OCT-2001;
CORIXA CORPORATION (US)

FEATURES

source

1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCACTCCT 17

|||||
1 CTTCAACT 9

RESULT 205
AX351118/c
LOCUS AX351118 10 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 70 from Patent WO0194600.
ACCESSION AX351118
VERSION AX351118.1 GI:18616472
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: WO 0194600-A 70 13-DEC-2001;
GENELABS TECHNOLOGIES, INC. (US)

FEATURES

source

1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16

|||||
9 ACTTCATC 1

RESULT 206
AX510722/c
LOCUS AX510722 10 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 10 from Patent WO227027.
ACCESSION AX510722
VERSION AX510722.1 GI:23391959
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
AUTHORS Zauderer,M.
TITLE Method of screening for therapeutics for infectious diseases
JOURNAL Patent: WO 0227027-A 10 04-APR-2002;
THE UNIVERSITY OF ROCHESTER (US)

FEATURES

source

1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15

|||||
9 GACTTGATC 1

RESULT 207
BD065288
LOCUS BD065288 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065288
VERSION BD065288.1 GI:22610891
KEYWORDS JP 2001509017-A/224.
SOURCE Saccharomyces cerevisiae (baker's yeast)

ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 224 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

COMMENT OS Saccharomyces cerevisiae (yeast)

PN JP 2001509017-A/224

PD 10-JUL-2001

PF 22-JAN-1998 JP 1998532117

PI 23-JAN-1997 US 60/035917

PI VICTOR E VELCULESCU BERT VOGELSTEIN KENNETH W KINZLER PC

C12N15/10; C12N15/31; C07K14/395; C12Q1/68; C12Q1/02 CC

Characterization of the yeast transcriptome

FH Key Location/Qualifiers

FT source 1. .10

FT /organism='Saccharomyces cerevisiae (yeast)'.
Location/Qualifiers

FEATURES

source

1. .10
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGCGACTT 11

|||||
2 GAGCGAATT 10

RESULT 208
BD083377/c
LOCUS BD083377 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083377
VERSION BD083377.1 GI:22628987
KEYWORDS JP 2001327293-A/298.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Matsushina,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 298 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001327293-A/298

PD 27-NOV-2001

```

PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTCATCCTT 18
Db 10 TTCATCCAT 2

RESULT 209
LOCUS BD084309 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Compositions and methods for the treatment and diagnosis of breast
cancer.
ACCESSION BD084309
VERSION BD084309.1 GI:22629919
KEYWORDS JP 2001521384-A/102.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Frudakis,T.N., Smith,J.M. and Read,S.G.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: JP 2001521384-A 102 06-NOV-2001;
CORIXA CORP
COMMENT OS Unidentified
PN JP 2001521384-A/102
PD 06-NOV-2001
PF 09-APR-1998 JP 1998543059
PR 09-APR-1997 US 08/938762,11-DEC-1997 US 08/991789 PI
TONY N FRUDAKIS,JOHN M SMITH,STEVEN G REED
PC C07K14/47,C07K14/82,C07K14/15,C12Q1/68,G01N33/574,A61K38/17,
A61K39/00
CC Strandedness: Single;
CC Topology: Linear;
CC Compositions and methods for the treatment and diagnosis of
breast cancer
FH Key Location/Qualifiers
FT source 1..10
/organism="Unidentified".
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
Db 1 CTTCAACCT 9

RESULT 210
LOCUS BD161423 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161423

```

```

VERSION BD161423.1 GI:27867181
KEYWORDS JP 2002186482-A/245.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 245 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/245
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1..10
FT source /organism="Homo sapiens (human)".
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
Db 10 CTTCTCTCT 2

RESULT 211
LOCUS BD166941 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166941
VERSION BD166941.1 GI:27872753
KEYWORDS JP 2002209591-A/486.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 486 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/486
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 9 CTTATCCT 17
Db 1 CTTATCCT 9

RESULT 212
AR001155
LOCUS AR001155 11 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 19 from patent US 5738990.
ACCESSION AR001155
VERSION AR001155.1 GI:3963222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Edwards, C.A., Fry, K.E., Cantor, C.R. and Andrews, B.M.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5738990-A 19 14-APR-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

RESULT 213
AR003033
LOCUS AR003033 11 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 19 from patent US 5744131.
ACCESSION AR003033
VERSION AR003033.1 GI:3964292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Edwards, C.A., Fry, K.E., Cantor, C.R. and Andrews, B.M.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5744131-A 19 28-APR-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

RESULT 214
AR007243/c
LOCUS AR007243 11 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 20 from patent US 5750375.
ACCESSION AR007243
VERSION AR007243.1 GI:3966727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)

AUTHORS Sledziewski, A.Z., Bell, L. Anne. and Kindsvogel, W.R.
TITLE Methods of producing secreted receptor analogs and biologically active dimerized polypeptide fusions
JOURNAL Patent: US 5750375-A 20 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 11 TGAGCGTCT 3

RESULT 215
AR030101
LOCUS AR030101 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 290 from patent US 5861244.
ACCESSION AR030101
VERSION AR030101.1 GI:5943315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 290 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 2 TTCCTCCTT 10

RESULT 216
AR033007
LOCUS AR033007 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 619 from patent US 5869241.
ACCESSION AR033007
VERSION AR033007.1 GI:5948612
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 619 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

FEATURES	source	Location/Qualifiers	
		1. .11	
		/organism="unknown"	
		/mol_type="unassigned DNA"	
Query Match		41.1%; Score 7.4; DB 1; Length 11;	
Best Local Similarity		88.9%; Pred. No. 1.3e+02;	
Matches	8; Conservative	0; Mismatches 1; Indels	0; Gaps 0;
Qy	2 TGAGCGGACT 10		
Db	11 TGAGCGTCT 3		
RESULT 220			
AR170456/c			
LOCUS	AR170456	11 bp DNA linear	PAT 17-DEC-2001
DEFINITION	Sequence 20 from patent US 6291646.		
ACCESSION	AR170456		
VERSION	AR170456.1 GI:17908415		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Siedziewski,A.Z., Bell,L.Anne. and Kindsvogel,W.R.		
TITLE	Dimerized polypeptide fusions		
JOURNAL	Patent: US 6291646-A 20 18-SEP-2001;		
FEATURES	Location/Qualifiers		
	1. .11		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match		41.1%; Score 7.4; DB 1; Length 11;	
Best Local Similarity		88.9%; Pred. No. 1.3e+02;	
Matches	8; Conservative	0; Mismatches 1; Indels	0; Gaps 0;
Qy	2 TGAGCGGACT 10		
Db	11 TGAGCGTCT 3		
RESULT 221			
I06332/c			
LOCUS	I06332	11 bp DNA linear	PAT 02-DEC-1994
DEFINITION	Sequence 17 from Patent EP 0325224.		
ACCESSION	I06332		
VERSION	I06332.1 GI:590140		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Siedziewski,A.Z., Bell,L.A. and Kindsvogel,W.R.		
TITLE	Methods of producing secreted receptor analogs and biologically active peptide dimers		
JOURNAL	Patent: EP 0325224-A2 17 26-JUL-1989;		
FEATURES	Location/Qualifiers		
	1. .11		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match		41.1%; Score 7.4; DB 1; Length 11;	
Best Local Similarity		88.9%; Pred. No. 1.3e+02;	
Matches	8; Conservative	0; Mismatches 1; Indels	0; Gaps 0;
Qy	2 TGAGCGGACT 10		
Db	11 TGAGCGTCT 3		
RESULT 222			
I22733/c			

```
LOCUS I27733 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5567584.
ACCESSION I27733
VERSION I27733.1 GI:1818509
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sledziewski,A.Z., Bell,L.A. and Kindevoegel,W.R.
TITLE Methods of using biologically active dimerized polypeptide fusions
to detect PDGF
JOURNAL Patent: US 5567584-A 20 22-OCT-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGTCT 3

RESULT 223
LOCUS I28614 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 22 from patent US 5573905.
ACCESSION I28614
VERSION I28614.1 GI:1819390
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Lerner,R., Janda,K. and Brenner,S.
TITLE Encoded combinatorial chemical libraries
JOURNAL Patent: US 5573905-A 22 12-NOV-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
|||||
Db 1 AGCTACTTC 9

RESULT 224
LOCUS I29747 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 619 from patent US 5578444.
ACCESSION I29747
VERSION I29747.1 GI:1820538
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 619 26-NOV-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

LOCUS I27733 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5567584.
ACCESSION I27733
VERSION I27733.1 GI:1818509
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sledziewski,A.Z., Bell,L.A. and Kindevoegel,W.R.
TITLE Methods of using biologically active dimerized polypeptide fusions
to detect PDGF
JOURNAL Patent: US 5567584-A 20 22-OCT-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGTCT 3

RESULT 223
LOCUS I28614 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 22 from patent US 5573905.
ACCESSION I28614
VERSION I28614.1 GI:1819390
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Lerner,R., Janda,K. and Brenner,S.
TITLE Encoded combinatorial chemical libraries
JOURNAL Patent: US 5573905-A 22 12-NOV-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
|||||
Db 1 AGCTACTTC 9

RESULT 224
LOCUS I29747 11 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 619 from patent US 5578444.
ACCESSION I29747
VERSION I29747.1 GI:1820538
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 619 26-NOV-1996;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
|||||
Db 1 TTCCTCCTT 9

RESULT 225
LOCUS I38544/c 11 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 24 from patent US 5614398.
ACCESSION I38544
VERSION I38544.1 GI:2084598
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS O'Brochta,D., Warren,W. and Atkinson,P.
TITLE Gene transfer system for insects
JOURNAL Patent: US 5614398-A 24 25-MAR-1997;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
|||||
Db 10 TTCATCCTT 2

RESULT 226
LOCUS I38545 11 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 25 from patent US 5614398.
ACCESSION I38545
VERSION I38545.1 GI:2084599
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS O'Brochta,D., Warren,W. and Atkinson,P.
TITLE Gene transfer system for insects
JOURNAL Patent: US 5614398-A 25 25-MAR-1997;
FEATURES Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
|||||
Db 2 TTCATCCTT 10

RESULT 227
LOCUS I38546/c 11 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 26 from patent US 5614398.
ACCESSION I38546
VERSION I38546.1 GI:2084600
KEYWORDS Unknown.
```

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      O'Brochta,D., Warren,W. and Atkinson,P.
TITLE        Gene transfer system for insects
JOURNAL      Patent: US 5614398-A 26 25-MAR-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      10 TTCATCCTT 2

RESULT 228
LOCUS      I38547      11 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 27 from patent US 5614398.
ACCESSION  I38547
VERSION     I38547.1 GI:2084601
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      O'Brochta,D., Warren,W. and Atkinson,P.
TITLE        Gene transfer system for insects
JOURNAL      Patent: US 5614398-A 27 25-MAR-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      2 TTCATCCTT 10

RESULT 229
LOCUS      I38549      11 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 29 from patent US 5614398.
ACCESSION  I38549
VERSION     I38549.1 GI:2084603
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      O'Brochta,D., Warren,W. and Atkinson,P.
TITLE        Gene transfer system for insects
JOURNAL      Patent: US 5614398-A 29 25-MAR-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      2 TTCATCCTT 10

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      O'Brochta,D., Warren,W. and Atkinson,P.
TITLE        Gene transfer system for insects
JOURNAL      Patent: US 5614398-A 26 25-MAR-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      10 TTCATCCTT 2

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Edwards,C.A., Fry,K.E., Cantor,C.R. and Andrews,B.M.
TITLE        Method of ordering sequence binding preferences of a DNA-binding molecule
JOURNAL      Patent: US 5693463-A 19 02-DEC-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      1 TTCATCCTT 9

RESULT 230
LOCUS      I76877      11 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 19 from patent US 5693463.
ACCESSION  I76877
VERSION     I76877.1 GI:3013031
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Edwards,C.A., Fry,K.E., Cantor,C.R. and Andrews,B.M.
TITLE        Method of ordering sequence binding preferences of a DNA-binding molecule
JOURNAL      Patent: US 5693463-A 19 02-DEC-1997;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      1 TTCATCCTT 9

RESULT 231
LOCUS      I87829      11 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION Sequence 19 from patent US 5716780.
ACCESSION  I87829
VERSION     I87829.1 GI:3407769
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Edwards,C.A., Fry,K.E., Cantor,C.R. and Andrews,B.M.
TITLE        Method of constructing sequence-specific DNA-binding molecules
JOURNAL      Patent: US 5716780-A 19 10-FEB-1998;
FEATURES     Location/Qualifiers
              source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      1 TTCATCCTT 9

RESULT 232
LOCUS      I90241      11 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION Sequence 22 from patent US 5723598.
ACCESSION  I90241
VERSION     I90241.1 GI:3410181
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Lerner,R., Janda,K. and Brenner,S.
```

```
TITLE      Encoded combinatorial chemical libraries
JOURNAL    Patent: US 5723598-A 22 03-MAR-1998;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 AGCGACTTC 12
       |||||
Db      1 AGCTACTTC 9

RESULT 233
191421
LOCUS      I91421      11 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 619 from patent US 5726014.
ACCESSION  I91421
VERSION     I91421.1 GI:3935891
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
TITLE     Screening assay for the detection of DNA-binding molecules
JOURNAL   Patent: US 5726014-A 619 10-MAR-1998;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
       |||||
Db      1 TTCCTCCTT 9

RESULT 234
AR209671
LOCUS      AR209671      11 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 619 from patent US 6384208.
ACCESSION  AR209671
VERSION     AR209671.1 GI:21511156
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE     Sequence directed DNA binding molecules compositions and methods
JOURNAL   Patent: US 6384208-A 619 07-MAY-2002;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
       |||||
Db      1 TTCCTCCTT 9

RESULT 235
AR262556/c
LOCUS      AR262556      11 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION Sequence 20 from patent US 6323323.
ACCESSION  AR262556
VERSION     AR262556.1 GI:28074067
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Sledziewski,A.Z., Bell,L.A. and Kindsvogel,W.R.
TITLE     Ligand-binding, dimerized polypeptide fusions
JOURNAL   Patent: US 6323323-A 20 27-NOV-2001;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 TGAGCGACT 10
       |||||
Db      11 TGAGCGTCT 3

RESULT 236
AR301423/c
LOCUS      AR301423      11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 4 from patent US 6538173.
ACCESSION  AR301423
VERSION     AR301423.1 GI:31689225
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Heber-Katz,E.
TITLE     Compositions and methods for wound healing
JOURNAL   Patent: US 6538173-A 4 25-MAR-2003;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GTGAGCGAC 9
       |||||
Db      9 GTGAGCCAC 1

RESULT 237
AR301582/c
LOCUS      AR301582      11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 163 from patent US 6538173.
ACCESSION  AR301582
VERSION     AR301582.1 GI:31689384
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Heber-Katz,E.
TITLE     Compositions and methods for wound healing
JOURNAL   Patent: US 6538173-A 163 25-MAR-2003;
FEATURES   Location/Qualifiers
source     1..11
           /organism="unknown"
           /mol_type="genomic DNA"
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 238
AR301686/c AR301686 11 bp DNA linear PAT 12-JUN-2003
LOCUS AR301686 Sequence 267 from patent US 6538173.
DEFINITION AR301686
ACCESSION AR301686
VERSION AR301686.1 GI:31689488
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 267 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..11
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

RESULT 239
AR301736/c AR301736 11 bp DNA linear PAT 12-JUN-2003
LOCUS AR301736 Sequence 317 from patent US 6538173.
DEFINITION AR301736
ACCESSION AR301736
VERSION AR301736.1 GI:31689538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 317 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..11
/mol_type="genomic DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

RESULT 240
AR369671/c AR369671 11 bp DNA linear PAT 12-SEP-2003
LOCUS AR369671 Sequence 20 from patent US 6300099.
DEFINITION AR369671
ACCESSION AR369671
VERSION AR369671.1 GI:34605941
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sledziewski,A.Z.; Bell,L.A. and Kindavogel,W.R.
TITLE Methods for producing secreted ligand-binding fusion proteins
JOURNAL Patent: US 6300099-A 20 09-OCT-2001;
FEATURES Location/Qualifiers
source 1..11
/mol_type="unassigned DNA"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 11 TGAGCGTCT 3

RESULT 241
AX394634 AX394634 11 bp DNA linear PAT 18-MAY-2002
LOCUS AX394634 Sequence 4 from Patent WO0218639.
DEFINITION AX394634
ACCESSION AX394634
VERSION AX394634.1 GI:21065747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger,C.; Andersson,M.K.; Lewander,T. and Oliasson,E.
TITLE Detection of cyp2c19 polymorphisms
JOURNAL Patent: WO 0218639-A 4 07-MAR-2002;
FEATURES Location/Qualifiers
source 1..11
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide of polymorphic site 1060"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 2 ACTTTATCC 10

RESULT 242
AX394654/c AX394654 11 bp DNA linear PAT 18-MAY-2002
LOCUS AX394654 Sequence 24 from Patent WO0218639.
DEFINITION AX394654
ACCESSION AX394654
VERSION AX394654.1 GI:21065767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger,C.; Andersson,M.K.; Lewander,T. and Oliasson,E.
TITLE Detection of cyp2c19 polymorphisms
JOURNAL Patent: WO 0218639-A 24 07-MAR-2002;
FEATURES Location/Qualifiers
source 1..11
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide of polymorphic site 1060"
```

```

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
   ||||| |||||
Db 10 ACTTATCC 2

RESULT 243
LOCUS      AX470521/c
DEFINITION Sequence 98 from Patent WO02053773.
ACCESSION  AX470521
VERSION     AX470521.1 GI:22205646
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 98 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES
  source    Location/Qualifiers
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
   ||||| |||||
Db 9 AGCGACTTC 1

RESULT 244
LOCUS      AX470565/c
DEFINITION Sequence 142 from Patent WO02053773.
ACCESSION  AX470565
VERSION     AX470565.1 GI:22205690
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 142 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES
  source    Location/Qualifiers
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
   ||||| |||||
Db 11 GACTTCAC 3

RESULT 245
LOCUS      AX470673
DEFINITION Sequence 250 from Patent WO02053773.
ACCESSION  AX470673
VERSION     AX470673.1 GI:22205798
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 250 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES
  source    Location/Qualifiers
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
   ||||| |||||
Db 2 CTTTCCTCCT 10

RESULT 246
LOCUS      AX471180/c
DEFINITION Sequence 757 from Patent WO02053773.
ACCESSION  AX471180
VERSION     AX471180.1 GI:22206305
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 757 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES
  source    Location/Qualifiers
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCA 13
   ||||| |||||
Db 11 GCGCCTTCA 3

RESULT 247
LOCUS      AX471634
DEFINITION Sequence 1211 from Patent WO02053773.
ACCESSION  AX471634
VERSION     AX471634.1 GI:22206759
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
```

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 1211 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGCGACT 10
 |||||
 Db 3 TGAGCAACT 11

RESULT 248
 AX471749/c
 LOCUS AX471749 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 1326 from Patent WO02053773.
 ACCESSION AX471749
 VERSION AX471749.1 GI:22206874
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 1326 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TTCATCCTT 18
 |||||
 Db 10 TTCATCAT 2

RESULT 249
 AX622982
 LOCUS AX622982 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 23 from Patent WO02053774.
 ACCESSION AX622982
 VERSION AX622982.1 GI:28450923
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 23 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GACTTCATC 15
 |||||
 Db 2 GGCITCATC 10

RESULT 250
 AX623272/c
 LOCUS AX623272 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 313 from Patent WO02053774.
 ACCESSION AX623272
 VERSION AX623272.1 GI:28451213
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 313 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
 |||||
 Db 11 CTTTCATCTT 3

RESULT 251
 AX623334/c
 LOCUS AX623334 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 375 from Patent WO02053774.
 ACCESSION AX623334
 VERSION AX623334.1 GI:28451275
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 375 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
 source
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TTCATCCTT 18
 |||||
 Db 11 TTCATCTTT 3

RESULT 252
 AX623425
 LOCUS AX623425 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 466 from Patent WO02053774.
ACCESSION AX623425
VERSION AX623425.1 GI:28451366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 466 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTCTCCT 17
|||||
Db 2 CTTCTCCT 10
RESULT 253
AX624155/c
LOCUS AX624155 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1196 from Patent WO02053774.
ACCESSION AX624155
VERSION AX624155.1 GI:28452096
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1196 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
|||||
Db 9 GTGAGCCAC 1
RESULT 254
AX624862/c
LOCUS AX624862 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1903 from Patent WO02053774.
ACCESSION AX624862
VERSION AX624862.1 GI:28452803
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1903 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

JOURNAL Patent: WO 02053774-A 1903 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
|||||
Db 9 GTGAGCCAC 1
RESULT 255
AX624990/c
LOCUS AX624990 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2031 from Patent WO02053774.
ACCESSION AX624990
VERSION AX624990.1 GI:28452931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2031 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
|||||
Db 9 GTGAGCCAC 1
RESULT 256
AX625292
LOCUS AX625292 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2333 from Patent WO02053774.
ACCESSION AX625292
VERSION AX625292.1 GI:28453233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2333 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
|||||
Db 9 GTGAGCCAC 1
RESULT 257
AX625292
LOCUS AX625292 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2333 from Patent WO02053774.
ACCESSION AX625292
VERSION AX625292.1 GI:28453233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2333 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"


```

QY      8 ACTTCATCC 16
Db      2 ACTTCACCC 10

RESULT 257
AX625529/c
LOCUS   AX625529          11 bp      DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 2570 from Patent WO02053774.
ACCESSION AX625529
VERSION   AX625529.1  GI:28453470
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 2570 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
          Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCGACTTCA 13
Db      10 GCAACTTCA 2

RESULT 258
AX626124
LOCUS   AX626124          11 bp      DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3165 from Patent WO02053774.
ACCESSION AX626124
VERSION   AX626124.1  GI:28454162
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3165 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
          Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTTCATCCT 17
Db      1 CTTAATCCT 9

RESULT 259
AX626351/c
LOCUS   AX626351          11 bp      DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3392 from Patent WO02053774.
ACCESSION AX626351

```

```

VERSION   AX626351.1  GI:28454389
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3392 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
          Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTTCATCCT 17
Db      10 CTTCATCCT 2

RESULT 260
AX626497/c
LOCUS   AX626497          11 bp      DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3538 from Patent WO02053774.
ACCESSION AX626497
VERSION   AX626497.1  GI:28454535
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3538 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
          Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGAGCGACT 10
Db      11 TGAGCCACT 3

RESULT 261
AX626864/c
LOCUS   AX626864          11 bp      DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 3905 from Patent WO02053774.
ACCESSION AX626864
VERSION   AX626864.1  GI:28454902
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3905 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)

```

```
FEATURES
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 11 GAATTCATC 3

RESULT 262
AX627293/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 11 CTTACCTCCT 3

RESULT 263
AX627788
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 11 CTTACCTCCT 3

RESULT 264
AX627937
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 2 ACCTCATCC 10

RESULT 265
AX628236
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 2 CGTCATCCT 10

RESULT 266
AX628722
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 2 CGTCATCCT 10

RESULT 267
AX628722
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 2 CGTCATCCT 10

RESULT 268
AX628722
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
source
  Location/Qualifiers
  1..11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 2 CGTCATCCT 10
```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5763 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred.No.1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          2 TGAGCGGACT 10
           |||||
Db          3 TGAGCGGCT 11

RESULT 267
AX628820
LOCUS       AX628820                11 bp    DNA        linear    PAT 21-FEB-2003
DEFINITION Sequence 5861 from Patent WO02053774.
ACCESSION  AX628820
VERSION     AX628820.1 GI:28456858
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5861 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred.No.1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          3 GAGCGGACTT 11
           |||||
Db          1 GAGGGGACTT 9

RESULT 268
AX629012/c
LOCUS       AX629012                11 bp    DNA        linear    PAT 21-FEB-2003
DEFINITION Sequence 6053 from Patent WO02053774.
ACCESSION  AX629012
VERSION     AX629012.1 GI:28457050
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6053 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
             source          1..11

```

```
RESULT 271
AX629138/c
LOCUS AX629138 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6179 from Patent WO02053774.
ACCESSION AX629138
VERSION AX629138.1 GI:28457176
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6179 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 10 TGAGAGACT 2

RESULT 272
AX629363/c
LOCUS AX629363 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6404 from Patent WO02053774.
ACCESSION AX629363
VERSION AX629363.1 GI:28457401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6404 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 10 TGAGAGACT 2

RESULT 273
AX629761/c
LOCUS AX629761 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6802 from Patent WO02053774.
ACCESSION AX629761
VERSION AX629761.1 GI:28457799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6802 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 10 CGTCATCCT 2

RESULT 274
AX630199
LOCUS AX630199 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7240 from Patent WO02053774.
ACCESSION AX630199
VERSION AX630199.1 GI:28458237
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 7240 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 11 GACTTCAAC 3

RESULT 275
AX630199
LOCUS AX630199 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7240 from Patent WO02053774.
ACCESSION AX630199
VERSION AX630199.1 GI:28458237
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 7240 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 11 GACTTCAAC 3
```

```

/db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      3 TTCTCTCTT 11

RESULT 276
AX630295/c
LOCUS      AX630295      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7336 from Patent WO02053774.
ACCESSION  AX630295
VERSION     AX630295.1 GI:28458333
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conrad,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7336 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCT 17
Db      10 CTTCTCTCT 2

RESULT 277
AX630403
LOCUS      AX630403      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7444 from Patent WO02053774.
ACCESSION  AX630403
VERSION     AX630403.1 GI:28458441
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conrad,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7444 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GACTTCATC 15
Db      2 GGCTTCATC 10

RESULT 278
AX630693/c
LOCUS      AX630693      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7734 from Patent WO02053774.
ACCESSION  AX630693
VERSION     AX630693.1 GI:28458731
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conrad,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7734 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCT 17
Db      11 CTTTCATCTT 3

RESULT 279
AX630755/c
LOCUS      AX630755      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7796 from Patent WO02053774.
ACCESSION  AX630755
VERSION     AX630755.1 GI:28458793
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conrad,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7796 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
Db      11 TTCATCTTT 3

RESULT 280
AX630846
LOCUS      AX630846      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7887 from Patent WO02053774.
ACCESSION  AX630846
VERSION     AX630846.1 GI:28458886
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

<hr/>					
Query Match 41.1%; Score 7.4; DB 1; Length 11;					
Best Local Similarity 88.9%; Pred. No. 1.3e+02;					
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
Qy	1 GTGAGGCAC 9				
Db	9 GTGAGCCAC 1				
<hr/>					
RESULT 283					
AX632411/c					
LOCUS 11 bp DNA linear PAT 21-FEB-2003					
DEFINITION Sequence 9453 from Patent WO02053774.					
ACCESSION AX632411					
VERSION AX632411.1 GI:28468026					
KEYWORDS Homo sapiens (human)					
SOURCE Homo sapiens					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
<hr/>					
REFERENCE 1					
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.					
TITLE Method for determining homeostasis of the skin					
JOURNAL Patent: WO 02053774-A 9453 11-JUL-2002;					
Henkel Kommanditgesellschaft auf Aktien (DE)					
<hr/>					
FEATURES					
source Location/Qualifiers					
1..11					
/organism="Homo sapiens"					
/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
<hr/>					
Query Match 41.1%; Score 7.4; DB 1; Length 11;					
Best Local Similarity 88.9%; Pred. No. 1.3e+02;					
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
Qy	1 GTGAGGCAC 9				
Db	9 GTGAGCCAC 1				
<hr/>					
RESULT 284					
AX632713					
LOCUS 11 bp DNA linear PAT 21-FEB-2003					
DEFINITION Sequence 9755 from Patent WO02053774.					
ACCESSION AX632713					
VERSION AX632713.1 GI:28468328					
KEYWORDS Homo sapiens (human)					
SOURCE Homo sapiens					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
<hr/>					
REFERENCE 1					
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.					
TITLE Method for determining homeostasis of the skin					
JOURNAL Patent: WO 02053774-A 9755 11-JUL-2002;					
Henkel Kommanditgesellschaft auf Aktien (DE)					
<hr/>					
FEATURES					
source Location/Qualifiers					
1..11					
/organism="Homo sapiens"					
/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
<hr/>					
Query Match 41.1%; Score 7.4; DB 1; Length 11;					
Best Local Similarity 88.9%; Pred. No. 1.3e+02;					
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
<hr/>					
Qy	8 ACTTCATCC 16				
Db	2 ACTTCACC 10				
<hr/>					
RESULT 285					
AX632798					

```
LOCUS       AX632798               11 bp    DNA             linear       PAT 21-FEB-2003
DEFINITION   Sequence 9840 from Patent WO02053774.
ACCESSION    AX632798
VERSION      AX632798.1   GI:28468413
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 9840 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCGACTTCA 13
        |||||||
Db       2 GCAACTTCA 10

RESULT 286
BD124173/c
LOCUS       BD124173               11 bp    DNA             linear       PAT 18-SEP-2002
DEFINITION   Compositions and method for healing wound.
ACCESSION    BD124173
VERSION      BD124173.1   GI:23219118
KEYWORDS     Mus musculus
SOURCE       Mus musculus
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Katz,E.H.
TITLE        (bases 1 to 11)
JOURNAL      Compositions and method for healing wound
              Patent: JP 2002503460-A 4 05-FEB-2002;
              THE WISTAR INSTITUTE
COMMENT      OS Mus musculus (mouse)
              PN JP 2002503460-A/4
              PD 05-FEB-2002
              PF 12-FEB-1999 JP 2000531545
              PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
              28-SEP-1998 US 60/102051
              PI ELLEN HEBER KATZ
              PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
              CC Compositions and method for healing wound
              FH Key
              FT source
              1..11
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /db_xref="taxon:10090"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTGAGCGAC 9
        |||||||
Db       9 GTGAGCCAC 1

RESULT 287
BD124332/c
LOCUS       BD124332               11 bp    DNA             linear       PAT 18-SEP-2002
DEFINITION   Compositions and method for healing wound.
ACCESSION    BD124332
VERSION      BD124332.1   GI:23219277
KEYWORDS     Mus musculus
SOURCE       Mus musculus
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Katz,E.H.
TITLE        (bases 1 to 11)
JOURNAL      Compositions and method for healing wound
              Patent: JP 2002503460-A 163 05-FEB-2002;
              THE WISTAR INSTITUTE
COMMENT      OS Mus musculus (mouse)
              PN JP 2002503460-A/163
              PD 05-FEB-2002
              PF 12-FEB-1999 JP 2000531545
              PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
              28-SEP-1998 US 60/102051
              PI ELLEN HEBER KATZ
              PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
              CC Compositions and method for healing wound
              FH Key
              FT source
              1..11
               /organism="Mus musculus (mouse)"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTGAGCGAC 9
        |||||||
Db       9 GTGAGCCAC 1

RESULT 288
BD124436/c
LOCUS       BD124436               11 bp    DNA             linear       PAT 18-SEP-2002
DEFINITION   Compositions and method for healing wound.
ACCESSION    BD124436
VERSION      BD124436.1   GI:23219381
KEYWORDS     Mus musculus
SOURCE       Mus musculus
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Katz,E.H.
TITLE        (bases 1 to 11)
JOURNAL      Compositions and method for healing wound
              Patent: JP 2002503460-A 267 05-FEB-2002;
              THE WISTAR INSTITUTE
COMMENT      OS Mus musculus (mouse)
              PN JP 2002503460-A/267
              PD 05-FEB-2002
              PF 12-FEB-1999 JP 2000531545
              PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
              28-SEP-1998 US 60/102051
              PI ELLEN HEBER KATZ
              PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
              CC Compositions and method for healing wound
              FH Key
              FT source
              1..11
               /organism="Mus musculus (mouse)"

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTGAGCGAC 9
        |||||||
Db       9 GTGAGCCAC 1
```

```
FEATURES
source
1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

RESULT 289
BD124486/c
LOCUS BD124486 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124486
VERSION BD124486.1 GI:32219431
KEYWORDS JP 2002503460-A/317.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 317 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/317
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00,PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism="Mus musculus (mouse)".
FEATURES
source
1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match
Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 290
BD244765/c
LOCUS BD244765 9 bp DNA linear PAT 17-JUL-2003
DEFINITION Isolation method of primer extension products by modular
oligonucleotide.
ACCESSION BD244765
VERSION BD244765.1 GI:33054535
KEYWORDS JP 2002525076-A/44.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Lundberg,J. and Uhlen,M.
TITLE Isolation method of primer extension products by modular

JOURNAL Patent: JP 2002525076-A 44 13-AUG-2002;
DYNAL AS
COMMENT OS Artificial Sequence
PN JP 2002525076-A/44
PD 13-AUG-2002
PF 15-SEP-1998 JP 2000570369
PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
JOAKIM LUNDBERG, MATHIAS UHLEN
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: Synthetic oligonucleotide
FH Key H8 Location/Qualifiers
FT source 1. .9
/organism="Artificial Sequence".
FEATURES
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 38.9%; Score 7; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
Db 8 GTGAGCG 2

RESULT 291
AX205264
LOCUS AX205264 9 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 156 from Patent WO0155369.
ACCESSION AX205264
VERSION AX205264.1 GI:15394527
KEYWORDS synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 9)
AUTHORS Mauro,V.P., Edelman,G.M., Chappell,G.M., Owens,G., Pinkstaff,J.K.,
Kruschel,L. and Zhou,W.
TITLE Synthetic internal ribosome entry sites and methods of identifying
same
JOURNAL Patent: WO 0155369-A 156 02-AUG-2001;
The Scripps Research Institute (US) ; The Neurosciences Institute
FEATURES
source
1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="random 9 nt sequence"

Query Match
Best Local Similarity 38.9%; Score 7; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
Db 3 GTGAGCG 9

RESULT 292
AX669023/c
LOCUS AX669023 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2472 from Patent WO0242459.
ACCESSION AX669023
VERSION AX669023.1 GI:29292000
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
ORGANISM synthetic construct
artificial sequences.
```


REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 2472 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source
1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTTCATCC 16
Db 9 TTTCATCC 3
|||||

RESULT 293
LOCUS AX669028 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2477 from Patent WO0242459.
ACCESSION AX669028
VERSION AX669028.1 GI:29292005
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 2477 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source
1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTTCATCC 16
Db 9 TTTCATCC 3
|||||

RESULT 294
LOCUS AR058729 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 306 from patent US 5837832.
ACCESSION AR058729
VERSION AR058729.1 GI:5984306
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 10)
AUTHORS Chee, M., Cronin, M.T., Fodor, S.P.A., Huang, X.X., Hubbell, E.A.,
Lipshutz, R.J., Lohman, P.E., Morris, M.S. and Sheldom, E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 306 17-NOV-1998;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTTCATCC 16
Db 9 TTTCATCC 3
|||||

RESULT 295
LOCUS AR107870 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 116 from patent US 6110667.
ACCESSION AR107870
VERSION AR107870.1 GI:12823357
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C., Eduardo, and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 116 29-AUG-2000;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 17
Db 1 TCATCCTT 7
|||||

RESULT 296
LOCUS AR134572 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6194155.
ACCESSION AR134572
VERSION AR134572.1 GI:14123477
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 10)
AUTHORS Cohen, J.
TITLE Computerized method of identifying and locating resonating,
self-hybridizing nucleic acid elements
JOURNAL Patent: US 6194155-A 21 27-FEB-2001;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCATC 15
Db 4 CTTCATC 10
|||||

RESULT 297
LOCUS AR134573 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6194155.
ACCESSION AR134573

```

VERSION AR134573.1 GI:14123478
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cohen,J.
TITLE Computerized method of identifying and locating resonating,
self-hybridizing nucleic acid elements
JOURNAL Patent: US 6194155-A 22 27-FEB-2001;
FEATURES
    source
        1..10
        /mol_type="unassigned DNA"
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 298
LOCUS AR134582 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6194155.
ACCESSION AR134582
VERSION AR134582.1 GI:14123487
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cohen,J.
TITLE Computerized method of identifying and locating resonating,
self-hybridizing nucleic acid elements
JOURNAL Patent: US 6194155-A 31 27-FEB-2001;
FEATURES
    source
        1..10
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 4 CTTTCATC 10

RESULT 299
LOCUS BD238699/c 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238699
VERSION BD238699.1 GI:33048469
KEYWORDS JP 2002534056-A/117.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 117 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/117
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'

FEATURES
    source
        1..10
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12
Db 7 CGACTTC 1

RESULT 300
LOCUS BD238707 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238707
VERSION BD238707.1 GI:33048477
KEYWORDS JP 2002534056-A/125.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 125 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/125
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

```

```

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 3 CATCCTT 9

RESULT 301
BD239507/c
LOCUS BD239507 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239507
VERSION BD239507.1 GI:33049277
KEYWORDS JP 2002534056-A/925.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 925 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/925
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 10 CTTTCATC 4

```

```

source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 7 CATCCTT 1

RESULT 302
BD239938/c
LOCUS BD239938 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239938
VERSION BD239938.1 GI:33049708
KEYWORDS JP 2002534056-A/1356.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1356 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1356
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 10 CTTTCATC 4

```

```
RESULT 303
BD240530/c
LOCUS      BD240530              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD240530
VERSION    BD240530.1 GI:33050300
KEYWORDS  JP 2002534056-A/1948.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
            Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1948 15-OCT-2002;
GENZYME CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002534056-A/1948
            PD 15-OCT-2002
            PF 18-JUN-1998 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089937,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
            G01N37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            FT Location/Qualifiers
            source 1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 10 CATCCTT 4

RESULT 304
BD248497
LOCUS      BD248497              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION T cells specific for target antigens and methods and vaccines based
            thereon.
ACCESSION  BD248497
VERSION    BD248497.1 GI:33058267
KEYWORDS  JP 2002529082-A/11
SOURCE    synthetic construct
            ORGANISM  artificial construct
            1 (bases 1 to 10)
REFERENCE  1 (bases 1 to 10)

Zauderer,M.
T cells specific for target antigens and methods and vaccines based
thereon
Patent: JP 2002529082-A 11 10-SEP-2002;
UNIVERSITY OF ROCHESTER
OS Artificial Sequence
PN JP 2002529082-A/11
PD 10-SEP-2002
PF 10-NOV-1998 JP 2000581183
PI MAURICE ZAUDERER
PC C12N15/09,A01K67/027,A61K35/76,A61K39/00,A61K39/04,A61K39/12,
PC A61K39/395,
PC A61K39/395,A61P31/04,A61P31/10,A61P35/00,C12N5/10,
PC C12O1/02,
PC G01N33/574,C12N15/00,C12N5/00
CC MR7 Location/Qualifiers
FH Key 1..10
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
Db 4 GACTTCA 10

RESULT 305
E39663/c
LOCUS      E39663              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39663
VERSION    E39663.1 GI:18621754
KEYWORDS  JP 2000279181-A/196.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
            Hashimoto,S., Matsushima,K. and Suzuki,T.
            Genes with human dendritic cell expression
            Patent: JP 2000279181-A 196 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT    OS Homo sapiens (human)
            PN JP 2000279181-A/196
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH Key Location/Qualifiers
            FT source 1..10
            FT Location/Qualifiers
            source 1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12
Db 6 CGACTTC 12
```

Db 7 CGACTTC 1

RESULT 306
AR214814/c
LOCUS AR214814 10 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 32 from patent US 6410226.
ACCESSION AR214814
VERSION AR214814.1 GI:23312745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kmiec.E.B., Holloman,W.K., Rice,M.C., Smith,S.T. and Shu,Z.
TITLE Mammalian and human REC2
JOURNAL Patent: US 6410226-A 32 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
|||||
Db 9 TCATCCT 3

RESULT 307
AR303309/c
LOCUS AR303309 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 34 from patent US 6544736.
ACCESSION AR303309
VERSION AR303309.1 GI:31692085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 34 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
|||||
Db 10 CATCCTT 4

RESULT 308
AR303407/c
LOCUS AR303407 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 132 from patent US 6544736.
ACCESSION AR303407
VERSION AR303407.1 GI:31692183
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.

TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 132 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
|||||
Db 8 TTCATCC 2

RESULT 309
AR303484
LOCUS AR303484 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 209 from patent US 6544736.
ACCESSION AR303484
VERSION AR303484.1 GI:31692260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 209 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
|||||
Db 1 CATCCTT 7

RESULT 310
AR303574
LOCUS AR303574 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 299 from patent US 6544736.
ACCESSION AR303574
VERSION AR303574.1 GI:31692350
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 299 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
|||||
Db 4 GTGAGCG 10

```
RESULT 311
AX152105/c
LOCUS          AX152105          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION     Sequence 20 from Patent WO0138577.
ACCESSION      AX152105
VERSION        AX152105.1  GI:14533756
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 20 31-MAY-2001;
               The Johns Hopkins University (US)
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy             11 TCATCCT 17
Db             9 TCATCCT 3
               |||||
RESULT 312
AX152122
LOCUS          AX152122          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION     Sequence 37 from Patent WO0138577.
ACCESSION      AX152122
VERSION        AX152122.1  GI:14533773
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 37 31-MAY-2001;
               The Johns Hopkins University (US)
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy             11 TCATCCT 17
Db             9 TCATCCT 3
               |||||
RESULT 313
AX152124
LOCUS          AX152124          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION     Sequence 39 from Patent WO0138577.
ACCESSION      AX152124
VERSION        AX152124.1  GI:14533775
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 39 31-MAY-2001;
               The Johns Hopkins University (US)
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy             9 CTTTCATC 15
Db             3 CTTTCATC 9
               |||||
RESULT 314
AX152559/c
LOCUS          AX152559          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION     Sequence 474 from Patent WO0138577.
ACCESSION      AX152559
VERSION        AX152559.1  GI:14534210
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 474 31-MAY-2001;
               The Johns Hopkins University (US)
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.4e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy             2 TGAGCGA 8
Db             9 TGAGCGA 3
               |||||
RESULT 315
AX152589/c
LOCUS          AX152589          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION     Sequence 504 from Patent WO0138577.
ACCESSION      AX152589
VERSION        AX152589.1  GI:14534240
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 504 31-MAY-2001;
               The Johns Hopkins University (US)
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
```

```

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 7 TCATCCT 1

RESULT 316
AX152897
LOCUS AX152897 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 812 from Patent WO0138577.
ACCESSION AX152897
VERSION AX152897.1 GI:14534548
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptsomes
JOURNAL The Johns Hopkins University (US)
FEATURES
    source
    Location/Qualifiers
        1..10
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9

RESULT 317
AX239914
LOCUS AX239914 10 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 41 from Patent WO0164958.
ACCESSION AX239914
VERSION AX239914.1 GI:15797516
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Dempcy,R.O., Gall,A.A., Lohkov,S.G., Afonina,I.A., Singer,M.J.,
TITLE Kutyavin,I.V. and Vermeulen,N.M.
JOURNAL Modified oligonucleotides for mismatch discrimination
    Patent: WO 0164958-A 41 07-SEP-2001;
    Epoch Biosciences, Inc. (US)
FEATURES
    source
    Location/Qualifiers
        1..10
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="duplex complement 6"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
Db 4 AGCGACT 10

RESULT 318
AX453771
LOCUS AX453771 10 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 8 from Patent EP1212941.
ACCESSION AX453771
VERSION AX453771.1 GI:21713443
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Mcneish,J.D., Soeller,W.C. and Thompson,J.P.
TITLE Modulating ramp activity
JOURNAL Patent: EP 1212941-A 8 12-JUN-2002;
Pfizer Products Inc. (US)
FEATURES
    source
    Location/Qualifiers
        1..10
        /organism="Mus musculus"
        /mol_type="unassigned DNA"
        /db_xref="taxon:10090"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 1 CATCCTT 7

RESULT 319
AX510716
LOCUS AX510716 10 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4 from Patent WO0227027.
ACCESSION AX510716
VERSION AX510716.1 GI:23391953
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Zauderer,M.
TITLE Method of screening for therapeutics for infectious diseases
JOURNAL Patent: WO 0227027-A 4 04-APR-2002;
THE UNIVERSITY OF ROCHESTER (US)
FEATURES
    source
    Location/Qualifiers
        1..10
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide primer"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
Db 4 GACTTCA 10

RESULT 320
BD003379/c
LOCUS BD003379 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Mammalian and human REC2.
ACCESSION BD003379
VERSION BD003379.1 GI:18631340
KEYWORDS JP 2001500729-A/29.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
REFERENCE 1
AUTHORS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
TITLE Saccharomycetales; Saccharomycetaceae; Saccharomyces.

```



```

LOCUS      BD167838                      10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Method for examination of allergosis.
ACCESSION  BD167838
VERSION    BD167838.1 GI:27873650
KEYWORDS   WO 0233122-A/5.
SOURCE     synthetic construct
ORGANISM   artificial construct
REFERENCE   1 (bases 1 to 10)
AUTHORS    Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
           and Takahashi,E.
TITLE      Method for examination of allergosis
JOURNAL    Patent: WO 0233122-A 5 25-APR-2002;
           GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
           NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
           HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
           SAITO,EIKI TAKAHASHI
COMMENT    OS Artificial Sequence
           PN WO 0233122-A/5
           PD 25-APR-2002
           PF 11-OCT-2001 WO 2001JP008937
           PR 13-OCT-2000 JP 00P 314093
           PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
           TAKESHI NAGASU,
           PI HIROHISA SAITO,EIKI TAKAHASHI
           PC C1201/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
           A61K39/395,
           PC A01K67/027//C07K16/18,C12N5/10
           CC Description of Artificial Sequence:an artificially synthesized

CC         sequence      primer
FH         sequence      Location/Qualifiers
FT         key           1..10
           /organism='Artificial Sequence'.
FEATURES   source
           1..10
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGAGCGA 8
Db      4 TGAGCGA 10

RESULT 328
LOCUS      BD188967                      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION MODULATING RAMP1 OR RAMP3 ACTIVITY.
ACCESSION  BD188967
VERSION    BD188967.1 GI:32998706
KEYWORDS   JP 200300098-A/8.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Soeller,W.C., Thompson,J.F. and McNeish,J.D.
TITLE      MODULATING RAMP1 OR RAMP3 ACTIVITY
JOURNAL    Patent: JP 200300098-A 8 07-JAN-2003;
           Pfizer Inc,John D McNeish,Walter C Soeller,John F Thompson
COMMENT    OS Mus Musculus
           PN 'JP 200300098-A/8
           PD 07-JAN-2003
           PF 27-NOV-2001 JP 2001360473
           PR 30-NOV-2000 US 60/250965
           PI walter carl soeller,John fenton thompson,John dauglas mcneish
           CC Key           Location/Qualifiers.

```

```

FEATURES   source
           1..10
           /organism="unidentified"
           /mol_type="genomic DNA"
           /db_xref="taxon:32644"

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 CATCCTT 18
Db      1 CATCCTT 7

RESULT 329
LOCUS      A35589/c                      10 bp      DNA      linear      PAT 02-DEC-1996
DEFINITION Synthetic human IFN-alpha 2 gene oligo.
ACCESSION  A35589
VERSION    A35589.1 GI:1926971
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE   1 (bases 1 to 10)
AUTHORS    Camble,R. and Edge,M.D.
TITLE      Analogous interferon polypeptides, process for their preparation
           and pharmaceutical compositions containing them
           Patent: EP 0194006-A 34 10-SEP-1986;
           IMPERIAL CHEMICAL INDUSTRIES PLC
JOURNAL

FEATURES   source
           1..10
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 CTTATCCTT 18
Db      10 CTTATCCTT 1

RESULT 330
LOCUS      A67805                      10 bp      DNA      linear      PAT 05-MAY-1999
DEFINITION Sequence 10 from Patent WO9743427.
ACCESSION  A67805
VERSION    A67805.1 GI:4756631
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1 (bases 1 to 10)
AUTHORS    De,V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F.
TITLE      PRODUCTION OF APOMITIC SEED
JOURNAL    Patent: WO 9743427-A 10 20-NOV-1997;
           Ciba Geigy AG (CH)
FEATURES   source
           1..10
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GACTTCATCC 16
           ||| ||| |||

```

```
Db          1 GACATCGTCC 10

RESULT 331
LOCUS       AR070981               10 bp      DNA          linear      PAT 18-FEB-2000
DEFINITION   Sequence 15 from patent US 5908978.
ACCESSION   AR070981
VERSION     AR070981.1  GI:7221869
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Amerson,H.V., Wilcox,P., Sederoff,R.R., Kuhlman,E.George.,
            O'Malley,D.M. and Grattapaglia,D.
TITLE      Methods for within family selection of disease resistance in woody
            perennials using genetic markers
JOURNAL    Patent: US 5908978-A 15 01-JUN-1999;
FEATURES    Location/Qualifiers
             source
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTGAGCGACT 10
        |||||
Db      10 GGGAGTGACT 1

RESULT 332
LOCUS       AR074451               10 bp      DNA          linear      PAT 28-AUG-2000
DEFINITION   Sequence 23 from patent US 5955075.
ACCESSION   AR074451
VERSION     AR074451.1  GI:10001206
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL    Patent: US 5955075-A 23 21-SEP-1999;
FEATURES    Location/Qualifiers
             source
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTTCATCCTT 18
        ::|||::
Db      1 YYCAYYYY 10

RESULT 333
LOCUS       AR081131               10 bp      DNA          linear      PAT 31-AUG-2000
DEFINITION   Sequence 23 from patent US 5972353.
ACCESSION   AR081131
VERSION     AR081131.1  GI:10007859
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.

Db          1 GACATCGTCC 10

TITLE      MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL    Patent: US 5972353-A 23 26-OCT-1999;
FEATURES    Location/Qualifiers
             source
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTTCATCCTT 18
        ::|||::
Db      1 YYCAYYYY 10

RESULT 334
LOCUS       AR085328               10 bp      DNA          linear      PAT 01-SEP-2000
DEFINITION   Sequence 23 from patent US 5981711.
ACCESSION   AR085328
VERSION     AR085328.1  GI:10012097
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN-specific antibodies and hybridomas
JOURNAL    Patent: US 5981711-A 23 09-NOV-1999;
FEATURES    Location/Qualifiers
             source
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTTCATCCTT 18
        ::|||::
Db      1 YYCAYYYY 10

RESULT 335
LOCUS       AR088076               10 bp      DNA          linear      PAT 07-SEP-2000
DEFINITION   Sequence 23 from patent US 5989838.
ACCESSION   AR088076
VERSION     AR088076.1  GI:10014839
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL    Patent: US 5989838-A 23 23-NOV-1999;
FEATURES    Location/Qualifiers
             source
               1..10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTTCATCCTT 18
        ::|||::
Db      1 YYCAYYYY 10

RESULT 336
LOCUS       AR081131               10 bp      DNA          linear      PAT 31-AUG-2000
DEFINITION   Sequence 23 from patent US 5972353.
ACCESSION   AR081131
VERSION     AR081131.1  GI:10007859
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
```

```
AR104235
LOCUS AR104235 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 23 from patent US 6093548.
ACCESSION AR104235
VERSION AR104235.1 GI:12816943
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Zavada,J., Pastorekova,S. and Pastorek,J.
JOURNAL Detection and quantitation of MN-specific antibodies
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db :::||:::
1 YYCAYVYVY 10
RESULT 337
AR107341/c
LOCUS AR107341 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6109776.
ACCESSION AR107341
VERSION AR107341.1 GI:12822828
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Haas,J.
JOURNAL Method and system for computationally identifying clusters within a
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db |||||
10 CTGCTCCTT 1
RESULT 338
AR107831
LOCUS AR107831 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 77 from patent US 6110667.
ACCESSION AR107831
VERSION AR107831.1 GI:12823318
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
JOURNAL Processes, apparatus and compositions for characterizing nucleotide
FEATURES
source
Location/Qualifiers
1..10
Patent: US 6110667-A 77 29-AUG-2000;
```

```
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCT 17
Db |||||
1 ACTACTTCCT 10
RESULT 339
AR119433/c
LOCUS AR119433 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6153379.
ACCESSION AR119433
VERSION AR119433.1 GI:14102132
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Caskey,C.Thomas., Shumaker,J. and Metspalu,A.
JOURNAL Parallel primer extension approach to nucleic acid sequence
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGGACT 10
Db |||||
10 GTAAGCGGATT 1
RESULT 340
AR124889/c
LOCUS AR124889 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6172212.
ACCESSION AR124889
VERSION AR124889.1 GI:14110250
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Hung,M.-C. and Xing,X.
JOURNAL Pea3 is a tumor suppressor
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCT 17
Db |||||
10 ACTTCCTGCT 1
RESULT 341
AR143499
LOCUS AR143499 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6204370.
```

[illegible]


```

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/56G, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'
FEATURES
source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCCACTTCA 13
||| |||
Db 1 AGCCACTTCA 10

RESULT 349
BD243164
LOCUS BD243164 10 bp DNA linear PAT 17-JUL-2003
DEFINITION MN gene and protein.
ACCESSION BD243164
VERSION BD243164.1 GI:33052934
KEYWORDS JP 2002528085-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Zavada,J., Pastorekova,S. and Pastorek,J.
MN gene and protein
Patent: JP 2002528085-A 13 03-SEP-2002;
INSTITUTE OF VIROLOGY
OS Homo sapiens (human)
PN JP 2002528085-A/13
PD 03-SEP-2002
PF 22-OCT-1998 JP 2000578465
PR 23-OCT-1998 US -09/177776.23-OCT-1998 US 09/178115 PI
JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
C07K14/47,
PC C12Q1/02,G01N33/566/(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
CC MN gene and protein
FH Key Location/Qualifiers
FT misc feature (1)..(10).
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.5e+02;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 YYCAYYYY 10

RESULT 350
BD243165
LOCUS BD243165 10 bp DNA linear PAT 17-JUL-2003
DEFINITION MN gene and protein.
ACCESSION BD243165
VERSION BD243165.1 GI:33052935

```

```

KEYWORDS JP 2002528085-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Zavada,J., Pastorekova,S. and Pastorek,J.
MN gene and protein
Patent: JP 2002528085-A 14 03-SEP-2002;
INSTITUTE OF VIROLOGY
OS Homo sapiens (human)
PN JP 2002528085-A/14
PD 03-SEP-2002
PF 22-OCT-1998 JP 2000578465
PR 23-OCT-1998 US 09/177776.23-OCT-1998 US 09/178115 PI
JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
C07K14/47,
PC C12Q1/02,G01N33/566/(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
CC MN gene and protein
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'
FEATURES
source
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
||| |||
Db 1 TGAGAGACTT 10

RESULT 351
BD248496/c
LOCUS BD248496 10 bp DNA linear PAT 17-JUL-2003
DEFINITION T cells specific for target antigens and methods and vaccines based
thereon.
ACCESSION BD248496
VERSION BD248496.1 GI:33058266
KEYWORDS JP 2002529082-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zauderer,M.
TITLE T cells specific for target antigens and methods and vaccines based
thereon
JOURNAL Patent: JP 2002529082-A 10 10-SEP-2002;
UNIVERSITY OF ROCHESTER
COMMENT OS Artificial Sequence
PN JP 2002529082-A/10
PD 10-SEP-2002
PF 10-NOV-1998 JP 2000581183
PI MAURICE ZAUDERER
PC C12N15/09,A01K67/027,A61K35/76,A61K39/00,A61K39/04,A61K39/12,
A61K39/395,
PC A61K39/395,A61P31/04,A61P31/10,A61P31/12,A61P35/00,C12N5/10,
C12Q1/02,
PC G01N33/574,C12N15/00,C12N5/00
CC MRS
FH Key Location/Qualifiers
FT source 1..10
/organism='Artificial Sequence'
FEATURES
source
1..10
/organism='synthetic construct'
/mol_type='genomic DNA'

```

/db_xref="taxon:32630"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
||| |||
Db 10 GACTTGTCC 1

RESULT 352
E40334
LOCUS E40334 10 bp DNA linear PAT 31-JAN-2002
DEFINITION DNA marker positioned in the vicinity of rice hybrid abortive site,
S-5 site and method for discriminating gene type of the S-5 site
using it.
ACCESSION E40334
VERSION E40334.1 GI:18621912
KEYWORDS JP 2000342267-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Yokozeki.Y.
TITLE DNA marker positioned in the vicinity of rice hybrid abortive site,
S-5 site and method for discriminating gene type of the S-5 site
JOURNAL MITSUI CHEM INC
COMMENT OS Unidentified
PN JP 2000342267-A/11
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999155219
PR YUMI YOKOZEKI
PI C12N15/09,A01H1/00,C12Q1/68,C12N15/00
PC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..10
/organism="Unidentified".

FEATURES
source
1..10
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| |||
Db 1 GAGGAGCTTC 10

RESULT 353
E54721/c
LOCUS E54721 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54721
VERSION E54721.1 GI:22556204
KEYWORDS JP 2001211883-A/73.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yanashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 73 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)

PN JP 2001211883-A/73
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YANASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC

FEATURES
source
FH Key Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||
Db 10 CTTGCTCCTT 1

RESULT 354
I21680/c
LOCUS I21680 10 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 12 from patent US 5523221.
ACCESSION I21680
VERSION I21680.1 GI:1602034
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weiner,M.P.
TITLE Method for the directional cloning of DNA
JOURNAL Patent: US 5523221-A 12 04-JUN-1996;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| |||
Db 10 GAAGGACTTC 1

RESULT 355
I22203/c
LOCUS I22203 10 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 17 from patent US 5527671.
ACCESSION I22203
VERSION I22203.1 GI:1602557
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Li,K., Rouse,D.I. and German,T.L.
TITLE Assay for verticillium dahliae
JOURNAL Patent: US 5527671-A 17 18-JUN-1996;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

Qy 9 CTTATCCTT 18
Db 10 CGTCATCAT 1

RESULT 356
AR201714 LOCUS linear PAT 20-APR-2002
DEFINITION Sequence 46 from patent US 6361937.
ACCESSION AR201714
VERSION AR201714.1 GI:20256253
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACATCACCT 10

RESULT 357
AR212997 LOCUS linear PAT 25-SEP-2002
DEFINITION Sequence 11 from patent US 6403314.
ACCESSION AR212997
VERSION AR212997.1 GI:23309897
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACATCACCT 10

RESULT 358
AR220101 LOCUS linear PAT 26-SEP-2002
DEFINITION Sequence 15 from patent US 6423538.
ACCESSION AR220101
VERSION AR220101.1 GI:23324532
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 1 GGGACTTTAT 10

RESULT 359
AR222980 LOCUS linear PAT 26-SEP-2002
DEFINITION Sequence 33 from patent US 6432640.
ACCESSION AR222980
VERSION AR222980.1 GI:23330818
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
Db 1 GATCGAATTC 10

RESULT 360
AR303352 LOCUS linear PAT 12-JUN-2003
DEFINITION Sequence 77 from patent US 6544736.
ACCESSION AR303352
VERSION AR303352.1 GI:31692128
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
Db 1 AGCCACTGCA 10

RESULT 361
AR303352 LOCUS linear PAT 12-JUN-2003
DEFINITION Sequence 77 from patent US 6544736.
ACCESSION AR303352
VERSION AR303352.1 GI:31692128
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 10 GGCTTCATC 1

```

```
RESULT 361
AR303429
LOCUS          AR303429          10 bp      DNA          linear      PAT 12-JUN-2003
DEFINITION     Sequence 154 from patent US 6544736.
ACCESSION      AR303429
VERSION        AR303429.1 GI:31692205
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
                Watahiki,M.
TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 154 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             6 CGACTTCATC 15
              ||| |||||
Db             1 CGAATTCATC 10

RESULT 362
AR303522/c
LOCUS          AR303522/c        10 bp      DNA          linear      PAT 12-JUN-2003
DEFINITION     Sequence 247 from patent US 6544736.
ACCESSION      AR303522
VERSION        AR303522.1 GI:31692298
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
                Watahiki,M.
TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 247 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             7 GACTTCATCC 16
              ||| |||||
Db             1 GGCTTCATTC 10

RESULT 363
AR303557
LOCUS          AR303557          10 bp      DNA          linear      PAT 12-JUN-2003
DEFINITION     Sequence 282 from patent US 6544736.
ACCESSION      AR303557
VERSION        AR303557.1 GI:31692333
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
                Watahiki,M.

TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 282 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             6 CGACTTCATC 15
              ||| |||||
Db             1 CGAATTCATC 10

TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 282 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             9 CTTCACTCCTT 18
              ||| |||||
Db             10 CTACATCCGT 1

TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 411 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             9 CTTCACTCCTT 18
              ||| |||||
Db             10 CTACATCCGT 1

TITLE          Method for synthesizing cDNA from mRNA sample
JOURNAL        Patent: US 6544736-A 411 08-APR-2003;
FEATURES       Location/Qualifiers
                source
                1..10
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches        8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy             5 GCGACTTCAT 14
              ||| |||||
Db             10 GAGACTCCAT 1
```

```
RESULT 366
AR336855
LOCUS AR336855 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 30 from patent US 6566130.
ACCESSION AR336855
VERSION AR336855.1 GI:33722705
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Srivastava,S.; Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 30 20-MAY-2003;
FEATURES
source
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
| | | | |
Db 1 CAACTTCAAC 10

RESULT 367
AR344451/c
LOCUS AR344451 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6582725.
ACCESSION AR344451
VERSION AR344451.1 GI:33740497
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Xing,X. and Hung,M.-C.
TITLE Human PEA3 is a tumor suppressor for cancer cells
JOURNAL Patent: US 6582725-A 5 24-JUN-2003;
FEATURES
source
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
| | | | |
Db 10 ACTTCCTGCT 1

RESULT 368
AR351726/c
LOCUS AR351726 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1268 from patent US 6588746.
ACCESSION AR351726
VERSION AR351726.1 GI:33753522
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet
JOURNAL Patent: US 6588746-A 1268 08-JUL-2003;
FEATURES
source

RESULT 369
AR351825
LOCUS AR351825 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1630 from patent US 6588746.
ACCESSION AR351825
VERSION AR351825.1 GI:33753621
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet
JOURNAL Patent: US 6588746-A 1630 08-JUL-2003;
FEATURES
source
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
| | | | |
Db 1 GAGGGAGTTC 10

RESULT 370
AR351826
LOCUS AR351826 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1631 from patent US 6588746.
ACCESSION AR351826
VERSION AR351826.1 GI:33753622
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet
JOURNAL Patent: US 6588746-A 1631 08-JUL-2003;
FEATURES
source
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
| | | | |
Db 1 GAGGGAGTTC 10

RESULT 371
AR362545
LOCUS AR362545 10 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1268 from patent US 6588746.
ACCESSION AR362545
VERSION AR362545.1 GI:33753522
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet
JOURNAL Patent: US 6588746-A 1268 08-JUL-2003;
FEATURES
source
```

```

/db_xref="taxon:32630"
/note="synthetic oligomer"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
Db 10 GTAAGCGATT 1

RESULT 374
AX113035/c
LOCUS      AX113035
DEFINITION Sequence 82 from Patent WO0127267.
ACCESSION  AX113035
VERSION     AX113035.1 GI:13939470
KEYWORDS   .
SOURCE     Mus sp.
ORGANISM   Mus sp.
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.;
REFERENCE  1
AUTHORS    Adams,B., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE      Genes differentially expressed in tri cells and their use in the
            manufacture of immunoregulatory compositions
JOURNAL    Patent: WO 0127267-A 82 19-APR-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES   source
            location/Qualifiers
            1..10
            /organism="Mus sp."
            /mol_type="unassigned DNA"
            /db_xref="taxon:10095"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 10 CTTCCACCTT 1

RESULT 375
AX152839
LOCUS      AX152839
DEFINITION Sequence 754 from Patent WO0138577.
ACCESSION  AX152839
VERSION     AX152839.1 GI:14534490
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 754 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   source
            location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
Db 1 GAGCGGCTC 10

```

```
RESULT 376
AX152854/c
LOCUS AX152854 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 769 from Patent W00138577.
ACCESSION AX152854
VERSION AX152854.1 GI:14534505
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 885 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACGGACTT 11
| | | | |
Db 10 TGAATGACTT 1

RESULT 377
AX152855/c
LOCUS AX152855 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 770 from Patent W00138577.
ACCESSION AX152855
VERSION AX152855.1 GI:14534506
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 770 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACGGACTT 11
| | | | |
Db 10 TGAATGACTT 1

RESULT 378
AX152970
LOCUS AX152970 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 885 from Patent W00138577.
ACCESSION AX152970
VERSION AX152970.1 GI:14534621
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 885 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACGGACTT 11
| | | | |
Db 10 TGAATGACTT 1
```

```
RESULT 379
AX153025
LOCUS AX153025 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 940 from Patent W00138577.
ACCESSION AX153025
VERSION AX153025.1 GI:14534676
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 940 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCA 13
| | | | |
Db 1 AGCCACTGCA 10

RESULT 380
AX153430/c
LOCUS AX153430 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1345 from Patent W00138577.
ACCESSION AX153430
VERSION AX153430.1 GI:14535081
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 1345 31-MAY-2001;
The Johns Hopkins University (US)
LOCATION/Qualifiers
1. .10
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGACGGACTT 11
| | | | |
Db 1 TGGCGGCTT 10
```

/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCTT 18
| | | | |
Db 10 CATCTTCCTT 1

RESULT 381
AX189811/c
LOCUS AX189811 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 29 from Patent WO0148247.
ACCESSION AX189811
VERSION AX189811.1 GI:15143182

KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Wang, S.M., Chen, J. and Rowley, J.D.
TITLE Method for generation of longer cdna fragments from sage tags for
Gene identification
JOURNAL Patent: WO 0148247-A 29 05-JUL-2001;
Arch Development Corporation (US)

FEATURES
source
1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
| | | | |
Db 10 GAGCGCTCC 1

RESULT 382
AX510715/c
LOCUS AX510715 10 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 3 from Patent WO0227027.
ACCESSION AX510715
VERSION AX510715.1 GI:23391952

KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Zauderer, M.
TITLE Method of screening for therapeutics for infectious diseases
JOURNAL Patent: WO 0227027-A 3 04-APR-2002;
THE UNIVERSITY OF ROCHESTER (US)

FEATURES
source
1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
| | | | |
Db 10 GACTTGGTCC 1

RESULT 383

AX667819/c
LOCUS AX667819 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1268 from Patent WO0242459.
ACCESSION AX667819
VERSION AX667819.1 GI:29291356

KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1268 30-MAY-2002;
Sangamo Biosciences Inc. (US)

FEATURES
source
1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
| | | | |
Db 10 GCGACTCCTT 1

RESULT 384

AX668181
LOCUS AX668181 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1630 from Patent WO0242459.
ACCESSION AX668181
VERSION AX668181.1 GI:29291460

KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1630 30-MAY-2002;
Sangamo Biosciences Inc. (US)

FEATURES
source
1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
| | | | |
Db 1 GAGGGAGTTC 10

RESULT 385

AX668182
LOCUS AX668182 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1631 from Patent WO0242459.
ACCESSION AX668182
VERSION AX668182.1 GI:29291461

KEYWORDS
SOURCE
synthetic construct

```

ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL     Patent: WO 0242459-A 1631 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
    ||| ||| |||
Db 1 GAGGAGTTC 10

RESULT 386
AX753456/c
LOCUS       AX753456                10 bp      DNA          linear      PAT 23-JUN-2003
DEFINITION Sequence 1 from Patent EP1310556.
ACCESSION  AX753456
VERSION     AX753456.1 GI:32166216
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1
AUTHORS     Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE       Composition and methods for the identification of lung tumor cells
JOURNAL     Patent: EP 1310556-A 1 14-MAY-2003;
            GENZYME CORPORATION (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTGCTCCTT 18
    ||| ||| |||
Db 10 CTTGCTCCTT 1

RESULT 387
AX805906/c
LOCUS       AX805906                10 bp      DNA          linear      PAT 25-NOV-2003
DEFINITION Sequence 52 from Patent WO03060163.
ACCESSION  AX805906
VERSION     AX805906.1 GI:38522817
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1
AUTHORS     van Eijk,M.J. and van Schaik,C.
TITLE       Discrimination and detection of target nucleotide sequences using
            mass spectrometry
JOURNAL     Patent: WO 03060163-A 52 24-JUL-2003;
            Keygene N.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"

```

```

            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="stuffer sequence"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTGCTCCTT 18
    ||| ||| |||
Db 10 CTTGCTCCTT 1

RESULT 388
BD007876
LOCUS       BD007876                10 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007876
VERSION     BD007876.1 GI:18636249
KEYWORDS    JP 2001069993-A/152.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 152 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2001069993-A/152
            PD 21-MAR-2001
            PF 28-APR-2000 JP 2000131079
            PR
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00.
            CC A61P31/00,C12P21/08,C12N15/00
            FH Key
            FT source
            Location/Qualifiers
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
    ||| ||| |||
Db 1 AGCGGCTACA 10

RESULT 389
BD007963
LOCUS       BD007963                10 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007963
VERSION     BD007963.1 GI:18636336
KEYWORDS    JP 2001069993-A/239.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 239 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP

```

```

COMMENT      OS Homo sapiens (human)
PN JP 2001069993-A/239
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00.
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism="Homo sapiens"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:9606"

FEATURES
source
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
|||||
Db 1 GAGCGGCTC 10

RESULT 390
BD065179
LOCUS BD065179 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065179
VERSION BD065179.1 GI:22610782
KEYWORDS JP 2001509017-A/115.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10)
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Characterization of the yeast transcriptome
TITLE Patent: JP 2001509017-A 115 10-JUL-2001;
JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/115
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism="Saccharomyces cerevisiae (yeast)".
FT Location/Qualifiers
source 1..10
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
|||||
Db 1 AGCGTCTCTA 10

RESULT 391
BD083205
LOCUS BD083205 10 bp DNA linear PAT 27-AUG-2002

```

```

DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083205
VERSION BD083205.1 GI:22628815
KEYWORDS JP 2001327293-A/126.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 126 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/126
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
|||||
Db 1 AGCGGCTACA 10

RESULT 392
BD091155
LOCUS BD091155 10 bp DNA linear PAT 27-AUG-2002
DEFINITION P53-induced apoptosis.
ACCESSION BD091155
VERSION BD091155.1 GI:22636765
KEYWORDS JP 2001523441-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE P53-induced apoptosis
JOURNAL Patent: JP 2001523441-A 33 27-NOV-2001;
COMMENT THE JOHNS HOPKINS UNIVERSITY
OS Homo sapiens (human)
PN JP 2001523441-A/33
PD 27-NOV-2001
PF 17-SEP-1998 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC
P53-induced
apoptosis
FH Key Location/Qualifiers
FT source 1..10
FT /organism="Homo sapiens (human)".
FT Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



```

Qy 4 AGGCACTTCA 13
Db 1 AGGCACTGCA 10

RESULT 393
BD161411
LOCUS Human activated Th1 and Th2 cell expression genes. PAT 17-JAN-2003
DEFINITION
ACCESSION BD161411
VERSION BD161411.1 GI:27867169
KEYWORDS JP 2002186482-A/233.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 233 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/233
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
Location/Qualifiers
FT source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
Db 1 TGGGCGCCTT 10

RESULT 394
BD161422
LOCUS Human activated Th1 and Th2 cell expression genes. PAT 17-JAN-2003
DEFINITION
ACCESSION BD161422
VERSION BD161422.1 GI:27867180
KEYWORDS JP 2002186482-A/244.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 244 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/244
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)"

FEATURES
source
1..10
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 1 GAGATCATCC 10

RESULT 395
BD225319
LOCUS Compositions and methods for the identification of lung tumor
DEFINITION cells.
ACCESSION BD225319
VERSION BD225319.1 GI:33035089
KEYWORDS JP 2002509707-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 1 02-APR-2002;
GENZYME CORP
COMMENT OS Artificial Sequence
PN JP 2002509707-A/1
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor CC
cells
FH Key Location/Qualifiers
FT source 1..10
Location/Qualifiers
FT source 1..10
/organism="Artificial Sequence".

FEATURES
source
1..10
Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 10 CTTCCTCCTT 1

RESULT 396
AJ593726
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 386B10.
ACCESSION AJ593726
VERSION AJ593726.1 GI:37943350
KEYWORDS left border: T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

FEATURES
source
1..10
Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTCATCCTT 18
Db 10 CTTCCTCCTT 1

RESULT 396
AJ593726
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 386B10.
ACCESSION AJ593726
VERSION AJ593726.1 GI:37943350
KEYWORDS left border: T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

22363535

12446565

2 (bases 1 to 10)

Direct Submission

Balzergue, S.

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1..10

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassillewskija"

/db_xref="taxon:3702"

/clone="386B10"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature

1..10

/note="T-DNA flanking sequence

left border"

Query Match 37.8%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. NO. 1.5e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11

|||||

Db 1 TGAGAGATT 10

Search completed: September 9, 2004, 11:24:53

Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:27:15 ; Search time 1 Seconds
(without alignments)
0.342 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18
Sequence: 1 gtgagcgacttcattc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 826 seqs, 9501 residues

Total number of hits satisfying chosen parameters: 1652

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 826 summaries

Database : rng32.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	1	AAA08479
2	13.4	74.4	20	1	ABS59760
3	13	72.2	18	1	AAA08480
4	12.4	68.9	15	1	AAZ262823
5	12.4	68.9	15	1	ABX00674
6	12.4	68.9	18	1	AAZ52478
7	11.8	65.6	17	1	AAZ30498
8	11.4	63.3	15	1	AAQ84058
9	11.4	63.3	15	1	ADC33608
10	11.4	63.3	17	1	AAF95009
11	11.2	62.2	17	1	ACC68036
12	11	61.1	13	1	ABF25604
13	11	61.1	13	1	ABF25604
14	10.8	60.0	15	1	AAZ31379
15	10.8	60.0	15	1	ABK81202
16	10.8	60.0	15	1	ABK81201
17	10.8	60.0	15	1	ABK81200
18	10.8	60.0	15	1	ABK81199
19	10.8	60.0	15	1	ABK32333
20	10.8	60.0	15	1	ABQ83715
21	10.8	60.0	15	1	ABQ83716
22	10.4	57.8	15	1	AAF52638
23	10.4	57.8	15	1	AAF52638
24	10.4	57.8	15	1	AAF52636
25	10.4	57.8	15	1	AAF52637
26	10.2	56.7	15	1	AAZ35559
27	10	55.6	10	1	AAZ78865
28	10	55.6	12	1	ABI77129
29	10	55.6	12	1	ABI09824
30	10	55.6	12	1	ABI79247
31	10	55.6	12	1	ABI11598
32	10	55.6	13	1	ABH44338
33	10	55.6	13	1	ABH44339

c	34	10	55.6	13	1	ABH05746	Oligonucleotide SE
c	35	10	55.6	13	1	ABH05747	Oligonucleotide SE
c	36	10	55.6	14	1	AAQ51865	PML mRNA ribozyme
c	37	10	55.6	15	1	AAZ62824	Substrate for HH r
c	38	10	55.6	15	1	ABX00675	Hepatitis C virus
c	39	9.8	54.4	13	1	ABCO1449	Oligonucleotide SE
c	40	9.8	54.4	13	1	ABH13586	Oligonucleotide SE
c	41	9.8	54.4	13	1	ABH13587	Oligonucleotide SE
c	42	9.8	54.4	13	1	ABCO1448	Oligonucleotide SE
c	43	9.8	54.4	14	1	AAQ83299	c-jun antisense ol
c	44	9.8	54.4	15	1	AAZ31544	Tag sequence of a
c	45	9.8	54.4	15	1	AAZ62650	Substrate for HH r
c	46	9.8	54.4	15	1	ABK34498	Human pancreatic c
c	47	9.8	54.4	15	1	ABX00501	Hepatitis C virus
c	48	9.8	54.4	15	1	ABQ84046	Tubercle bacillus
c	49	9.8	54.4	15	1	ACQ73410	Mycobacterium anti
c	50	9.8	54.4	15	1	ACQ73410	M. tuberculosis ol
c	51	9.8	54.4	15	1	ADC33596	Oligonucleotide SE
c	52	9.6	53.3	13	1	ABC71483	Oligonucleotide SE
c	53	9.6	53.3	13	1	ABC71482	Oligonucleotide SE
c	54	9.6	53.3	13	1	ABF42964	Oligonucleotide SE
c	55	9.6	53.3	13	1	ABF42965	Oligonucleotide SE
c	56	9.6	53.3	13	1	ABF42960	Oligonucleotide SE
c	57	9.6	53.3	13	1	ABF42961	Oligonucleotide SE
c	58	9.4	52.2	12	1	AB104554	Oligonucleotide pr
c	59	9.4	52.2	12	1	ABH68283	Oligonucleotide pr
c	60	9.4	52.2	12	1	AB116330	Oligonucleotide pr
c	61	9.4	52.2	12	1	AB140174	Oligonucleotide pr
c	62	9.4	52.2	12	1	ABH90125	Oligonucleotide pr
c	63	9.4	52.2	12	1	AB159049	Oligonucleotide pr
c	64	9.4	52.2	12	1	ABH68729	Oligonucleotide pr
c	65	9.4	52.2	12	1	AB104489	Oligonucleotide pr
c	66	9.4	52.2	12	1	AB151369	Oligonucleotide pr
c	67	9.4	52.2	12	1	AB175389	Oligonucleotide pr
c	68	9.4	52.2	12	1	ABT15850	Anti-human calisv
c	69	9.4	52.2	13	1	ABC43362	Oligonucleotide SE
c	70	9.4	52.2	13	1	ABF73760	Oligonucleotide SE
c	71	9.4	52.2	13	1	ABH40385	Oligonucleotide SE
c	72	9.4	52.2	13	1	ABH56983	Oligonucleotide SE
c	73	9.4	52.2	13	1	ABC78469	Oligonucleotide SE
c	74	9.4	52.2	13	1	ABC63957	Oligonucleotide SE
c	75	9.4	52.2	13	1	ABC67524	Oligonucleotide SE
c	76	9.4	52.2	13	1	ABF25609	Oligonucleotide SE
c	77	9.4	52.2	13	1	ABF73761	Oligonucleotide SE
c	78	9.4	52.2	13	1	ABC63956	Oligonucleotide SE
c	79	9.4	52.2	13	1	ABF25607	Oligonucleotide SE
c	80	9.4	52.2	13	1	ABF25608	Oligonucleotide SE
c	81	9.4	52.2	13	1	ABH02049	Oligonucleotide SE
c	82	9.4	52.2	13	1	ABC67525	Oligonucleotide SE
c	83	9.4	52.2	13	1	ABH56982	Oligonucleotide SE
c	84	9.4	52.2	13	1	ABF34091	Oligonucleotide SE
c	85	9.4	52.2	13	1	ABC67933	Oligonucleotide SE
c	86	9.4	52.2	13	1	ABC83972	Oligonucleotide SE
c	87	9.4	52.2	13	1	ABC72103	Oligonucleotide SE
c	88	9.4	52.2	13	1	ABC99862	Oligonucleotide SE
c	89	9.4	52.2	13	1	ABH40384	Oligonucleotide SE
c	90	9.4	52.2	13	1	ABC67932	Oligonucleotide SE
c	91	9.4	52.2	13	1	ABC72102	Oligonucleotide SE
c	92	9.4	52.2	13	1	ABC83973	Oligonucleotide SE
c	93	9.4	52.2	13	1	ABC44363	Oligonucleotide SE
c	94	9.4	52.2	13	1	ABC99863	Oligonucleotide SE
c	95	9.4	52.2	13	1	ABC78468	Oligonucleotide SE
c	96	9.4	52.2	13	1	ABH12570	Oligonucleotide SE
c	97	9.4	52.2	13	1	ABH12571	Oligonucleotide SE
c	98	9.4	52.2	13	1	ABF25606	Oligonucleotide SE
c	99	9.4	52.2	13	1	ABF34090	Oligonucleotide SE
c	100	9.4	52.2	13	1	ABH02048	Oligonucleotide SE
c	101	9.2	51.1	14	1	AAF77604	Modified transcrip
c	102	9.2	51.1	14	1	AAZ42211	Hansenula wingei U
c	103	9	50.0	10	1	AAT29317	5'-primer for mamm
c	104	9	50.0	10	1	AAT29316	5'-primer for mamm
c	105	9	50.0	10	1	AAT29296	5'-primer for mamm
c	106	9	50.0	10	1	AAZ83547	Metastatic breast

c 107	9	50.0	10	1	AAF35047	Yeast NORF gene SA	180	8.8	48.9	12	1	ABI25036	Oligonucleotide pr
c 108	9	50.0	10	1	AAF41819	Yeast NORF gene SA	181	8.8	48.9	12	1	ABI11045	Oligonucleotide pr
c 109	9	50.0	10	1	AAF39735	Yeast NORF gene SA	c 182	8.8	48.9	12	1	ABI14744	Oligonucleotide pr
c 110	9	50.0	10	1	AAF34938	Yeast NORF gene SA	c 183	8.8	48.9	12	1	ABI78596	Oligonucleotide pr
c 111	9	50.0	10	1	AAF34381	Yeast NORF gene SA	c 184	8.8	48.9	12	1	ABK13228	Self-assembled mon
c 112	9	50.0	10	1	AA595622	Apolipoprotein C-I	c 185	8.8	48.9	12	1	ADJ45523	RC15 linker DNA us
c 113	9	50.0	10	1	ABV64594	Human skin EST 238	c 186	8.8	48.9	12	1	AA142765	Self-assembled mon
c 114	9	50.0	11	1	ABV72015	Human skin EST 980	c 187	8.8	48.9	12	1	AA142766	Self-assembled mon
c 115	9	50.0	11	1	AD34602	Human CYP2C19 gene	c 188	8.8	48.9	12	1	ABC93881	Oligonucleotide SE
c 116	9	50.0	11	1	AD34584	Human CYP2C19 gene	c 189	8.8	48.9	13	1	ABC91635	Oligonucleotide SE
c 117	9	50.0	12	1	AB104356	Oligonucleotide pr	c 190	8.8	48.9	13	1	ABF26209	Oligonucleotide SE
c 118	9	50.0	12	1	AB104356	Oligonucleotide pr	c 191	8.8	48.9	13	1	ABF35407	Oligonucleotide SE
c 119	9	50.0	12	1	AB173201	Oligonucleotide pr	c 192	8.8	48.9	13	1	ABF41254	Oligonucleotide SE
c 120	9	50.0	12	1	AB148663	Oligonucleotide pr	c 193	8.8	48.9	13	1	ABH43891	Oligonucleotide SE
c 121	9	50.0	12	1	AB156153	Oligonucleotide pr	c 194	8.8	48.9	13	1	ABH43891	Oligonucleotide SE
c 122	9	50.0	12	1	AB172894	Oligonucleotide pr	c 195	8.8	48.9	13	1	ABH49687	Oligonucleotide SE
c 123	9	50.0	12	1	ABH74903	Oligonucleotide pr	c 196	8.8	48.9	13	1	ABC69498	Oligonucleotide SE
c 124	9	50.0	12	1	ABH82223	Oligonucleotide pr	c 197	8.8	48.9	13	1	ABC19584	Oligonucleotide SE
c 125	9	50.0	12	1	AB122432	Oligonucleotide pr	c 198	8.8	48.9	13	1	ABC57831	Oligonucleotide SE
c 126	9	50.0	12	1	AB160190	Oligonucleotide pr	c 199	8.8	48.9	13	1	ABF41255	Oligonucleotide SE
c 127	9	50.0	13	1	ABC94001	Oligonucleotide SE	c 200	8.8	48.9	13	1	ABF64319	Oligonucleotide SE
c 128	9	50.0	13	1	ABC95696	Oligonucleotide SE	c 201	8.8	48.9	13	1	ABH57611	Oligonucleotide SE
c 129	9	50.0	13	1	ABF60699	Oligonucleotide SE	c 202	8.8	48.9	13	1	ABC57830	Oligonucleotide SE
c 130	9	50.0	13	1	ABH33314	Oligonucleotide SE	c 203	8.8	48.9	13	1	ABH49686	Oligonucleotide SE
c 131	9	50.0	13	1	ABF86198	Oligonucleotide SE	c 204	8.8	48.9	13	1	ABC69499	Oligonucleotide SE
c 132	9	50.0	13	1	ABF60696	Oligonucleotide SE	c 205	8.8	48.9	13	1	ABF95821	Oligonucleotide SE
c 133	9	50.0	13	1	ABC57255	Oligonucleotide SE	c 206	8.8	48.9	13	1	ABH43890	Oligonucleotide SE
c 134	9	50.0	13	1	ABC62600	Oligonucleotide SE	c 207	8.8	48.9	13	1	ABC19585	Oligonucleotide SE
c 135	9	50.0	13	1	ABH33315	Oligonucleotide SE	c 208	8.8	48.9	13	1	ABF35406	Oligonucleotide SE
c 136	9	50.0	13	1	ABF60697	Oligonucleotide SE	c 209	8.8	48.9	13	1	ABH57612	Oligonucleotide SE
c 137	9	50.0	13	1	ABC25977	Oligonucleotide SE	c 210	8.8	48.9	13	1	ABH57613	Oligonucleotide SE
c 138	9	50.0	13	1	ABF37452	Oligonucleotide SE	c 211	8.8	48.9	13	1	ABF64318	Oligonucleotide SE
c 139	9	50.0	13	1	ABF86199	Oligonucleotide SE	c 212	8.8	48.9	13	1	ABH57610	Oligonucleotide SE
c 140	9	50.0	13	1	ABH50895	Oligonucleotide SE	c 213	8.8	48.9	13	1	ABC91634	Oligonucleotide SE
c 141	9	50.0	13	1	ABH50895	Oligonucleotide SE	c 214	8.8	48.9	13	1	ABC93880	Oligonucleotide SE
c 142	9	50.0	13	1	ABF95510	Oligonucleotide SE	c 215	8.8	48.9	13	1	ABF95820	Oligonucleotide SE
c 143	9	50.0	13	1	ABF24926	Oligonucleotide SE	c 216	8.6	47.8	13	1	ABC97421	Oligonucleotide SE
c 144	9	50.0	13	1	ABF37666	Oligonucleotide SE	c 217	8.6	47.8	13	1	ABC97416	Oligonucleotide SE
c 145	9	50.0	13	1	ABF53607	Oligonucleotide SE	c 218	8.6	47.8	13	1	ABC99714	Oligonucleotide SE
c 146	9	50.0	13	1	ABC25976	Oligonucleotide SE	c 219	8.6	47.8	13	1	ABC97417	Oligonucleotide SE
c 147	9	50.0	13	1	ABF53606	Oligonucleotide SE	c 220	8.6	47.8	13	1	ABC10016	Oligonucleotide SE
c 148	9	50.0	13	1	ABH50894	Oligonucleotide SE	c 221	8.6	47.8	13	1	ABC10017	Oligonucleotide SE
c 149	9	50.0	13	1	ABH65795	Oligonucleotide SE	c 222	8.6	47.8	13	1	ABC97420	Oligonucleotide SE
c 150	9	50.0	13	1	ABC95697	Oligonucleotide SE	c 223	8.6	47.8	13	1	ABC99715	Oligonucleotide SE
c 151	9	50.0	13	1	ABF37667	Oligonucleotide SE	c 224	8.4	46.7	10	1	AAT29329	5'-primer for mamm
c 152	9	50.0	13	1	ABH47184	Oligonucleotide SE	c 225	8.4	46.7	10	1	AAT29329	Human dendritic ce
c 153	9	50.0	13	1	ABH59422	Oligonucleotide SE	c 226	8.4	46.7	10	1	AAT29329	Metastatic breast
c 154	9	50.0	13	1	ABC62601	Oligonucleotide SE	c 227	8.4	46.7	10	1	AAT29329	Metastatic breast
c 155	9	50.0	13	1	ABF23816	Oligonucleotide SE	c 228	8.4	46.7	10	1	AAT29329	Metastatic breast
c 156	9	50.0	13	1	ABH47185	Oligonucleotide SE	c 229	8.4	46.7	10	1	AAF35444	Yeast NORF gene SA
c 157	9	50.0	13	1	ABC96952	Oligonucleotide SE	c 230	8.4	46.7	10	1	AAF42018	Yeast NORF gene SA
c 158	9	50.0	13	1	ABC86371	Oligonucleotide SE	c 231	8.4	46.7	10	1	AAF37674	CBP2 detecting AS
c 159	9	50.0	13	1	ABH65794	Oligonucleotide SE	c 232	8.4	46.7	10	1	AA139530	Modified RNA oligo
c 160	9	50.0	13	1	ABC96953	Oligonucleotide SE	c 233	8.4	46.7	11	1	AA139530	Modified oligonucle
c 161	9	50.0	13	1	ABC86370	Oligonucleotide SE	c 234	8.4	46.7	11	1	AA139530	Modified oligonucle
c 162	9	50.0	13	1	ABF37453	Oligonucleotide SE	c 235	8.4	46.7	11	1	AA139530	Oligonucleotide co
c 163	9	50.0	13	1	ABF24927	Oligonucleotide SE	c 236	8.4	46.7	11	1	AA139530	Oligo-2'-fluoronic
c 164	9	50.0	13	1	ABF60698	Oligonucleotide SE	c 237	8.4	46.7	11	1	AA139530	N3-P5 phosphoramid
c 165	9	50.0	13	1	ABF63942	Oligonucleotide SE	c 238	8.4	46.7	11	1	AA139530	Triple helix formi
c 166	9	50.0	13	1	ABC57254	Oligonucleotide SE	c 239	8.4	46.7	11	1	AA139530	Human skin stress/
c 167	9	50.0	13	1	ABF23817	Oligonucleotide SE	c 240	8.4	46.7	11	1	ABQ87262	Human skin EST 372
c 168	9	50.0	13	1	ABF63943	Oligonucleotide SE	c 241	8.4	46.7	11	1	ABV65942	Human skin EST 898
c 169	9	50.0	13	1	ABH59423	Oligonucleotide SE	c 242	8.4	46.7	11	1	ABV71195	Human skin EST 350
c 170	8.8	48.9	12	1	AA55920	Adapter linker nuc	c 243	8.4	46.7	11	1	ABV65721	Human skin EST 377
c 171	8.8	48.9	12	1	AA73432	Linker RC15. Sacc	c 244	8.4	46.7	11	1	ABV65991	Human skin EST 156
c 172	8.8	48.9	12	1	ABH74215	Oligonucleotide pr	c 245	8.4	46.7	11	1	ABV63774	Human skin EST 247
c 173	8.8	48.9	12	1	AB158053	Oligonucleotide pr	c 246	8.4	46.7	11	1	ABV64693	Human skin EST 247
c 174	8.8	48.9	12	1	AB165792	Oligonucleotide pr	c 247	8.4	46.7	12	1	AA139530	Codon sequence fro
c 175	8.8	48.9	12	1	AB110237	Oligonucleotide pr	c 248	8.4	46.7	12	1	AAT42900	bcr2/abl2 breakpoi
c 176	8.8	48.9	12	1	AB143459	Oligonucleotide pr	c 249	8.4	46.7	12	1	AA55925	Adapter linker nuc
c 177	8.8	48.9	12	1	AB132036	Oligonucleotide pr	c 250	8.4	46.7	12	1	AA55925	Adapter linker nuc
c 178	8.8	48.9	12	1	AB119295	Oligonucleotide pr	c 251	8.4	46.7	12	1	AA55925	Linker JA37. Sacc
c 179	8.8	48.9	12	1	AB108311	Oligonucleotide pr	c 252	8.4	46.7	12	1	AA55925	Linker JC7. Sacc

c 253	8.4	46.7	12	1	AAH233505	Antibacterial pept	c 326	8	44.4	12	1	ABI72079	Oligonucleotide pr
254	8.4	46.7	12	1	ABI38653	Oligonucleotide pr	327	8	44.4	12	1	ABI58718	Oligonucleotide pr
c 255	8.4	46.7	12	1	ABH88708	Oligonucleotide pr	c 328	8	44.4	12	1	ABI24046	Oligonucleotide pr
c 256	8.4	46.7	12	1	ABI40787	Oligonucleotide pr	329	8	44.4	12	1	ABI32606	Oligonucleotide pr
c 257	8.4	46.7	12	1	ABI71673	Oligonucleotide pr	c 330	8	44.4	12	1	ABI58329	Oligonucleotide pr
c 258	8.4	46.7	12	1	ABI77738	Oligonucleotide pr	c 331	8	44.4	12	1	ABH70603	Oligonucleotide pr
c 259	8.4	46.7	12	1	ABI66111	Oligonucleotide pr	c 332	8	44.4	12	1	ABI38408	Oligonucleotide pr
c 260	8.4	46.7	12	1	ABI02919	Oligonucleotide pr	333	8	44.4	12	1	ABI74005	Oligonucleotide pr
261	8.4	46.7	12	1	ABI15957	Oligonucleotide pr	334	8	44.4	12	1	ABH97016	Oligonucleotide pr
262	8.4	46.7	12	1	ABI15994	Oligonucleotide pr	c 335	8	44.4	12	1	ABI12331	Oligonucleotide pr
263	8.4	46.7	12	1	ABI72532	Oligonucleotide pr	c 336	8	44.4	12	1	ABH67749	Oligonucleotide pr
264	8.4	46.7	12	1	ABI63681	Oligonucleotide pr	c 337	8	44.4	12	1	ABH06054	Oligonucleotide pr
c 265	8.4	46.7	12	1	ABI21944	Oligonucleotide pr	338	8	44.4	12	1	ABI08302	Oligonucleotide pr
c 266	8.4	46.7	12	1	ABI10721	Oligonucleotide pr	339	8	44.4	12	1	ABI59006	Oligonucleotide pr
267	8.4	46.7	12	1	ABI112430	Oligonucleotide pr	340	8	44.4	12	1	ABI64861	Oligonucleotide pr
268	8.4	46.7	12	1	ABI42318	Oligonucleotide pr	341	8	44.4	12	1	ABH77981	Oligonucleotide pr
c 269	8.4	46.7	12	1	ABI45284	Oligonucleotide pr	c 342	8	44.4	12	1	ABI29279	Oligonucleotide pr
c 270	8.4	46.7	12	1	ABI46259	Oligonucleotide pr	c 343	8	44.4	12	1	ABI35506	Oligonucleotide pr
271	8.4	46.7	12	1	ABI69695	Oligonucleotide pr	c 344	8	44.4	12	1	ABI13395	Oligonucleotide pr
c 272	8.4	46.7	12	1	ABI80833	Oligonucleotide pr	345	8	44.4	12	1	ABI14542	Oligonucleotide pr
c 273	8.4	46.7	12	1	ABI37248	Oligonucleotide pr	346	8	44.4	12	1	ABI46271	Oligonucleotide pr
274	8.4	46.7	12	1	ABI38368	Oligonucleotide pr	c 347	8	44.4	12	1	ABI62400	Oligonucleotide pr
c 275	8.4	46.7	12	1	ABI58052	Oligonucleotide pr	c 348	8	44.4	12	1	ABI10041	Oligonucleotide pr
c 276	8.4	46.7	12	1	ABI65300	Oligonucleotide pr	c 349	8	44.4	12	1	ABI13456	Oligonucleotide pr
277	8.4	46.7	12	1	ABI24466	Oligonucleotide pr	c 350	8	44.4	12	1	ABI17083	Oligonucleotide pr
c 278	8.4	46.7	12	1	ABH88322	Oligonucleotide pr	351	8	44.4	12	1	ABI45520	Oligonucleotide pr
c 279	8.4	46.7	12	1	ABI40399	Oligonucleotide pr	352	8	44.4	12	1	ABI60787	Oligonucleotide pr
c 280	8.4	46.7	12	1	ABI49646	Oligonucleotide pr	c 353	8	44.4	12	1	ABI19890	Oligonucleotide pr
281	8.4	46.7	12	1	ABI6964	Oligonucleotide pr	354	8	44.4	12	1	ABH72969	Oligonucleotide pr
c 282	8.4	46.7	12	1	ABI61170	Oligonucleotide pr	355	8	44.4	12	1	ABH77014	Oligonucleotide pr
c 283	8.4	46.7	12	1	ABI64864	Oligonucleotide pr	c 356	8	44.4	12	1	ABI49134	Oligonucleotide pr
c 284	8.4	46.7	12	1	ABI19099	Oligonucleotide pr	c 357	8	44.4	12	1	ABI70363	Oligonucleotide pr
c 285	8.4	46.7	12	1	ABI43005	Oligonucleotide pr	c 358	8	44.4	12	1	ABI77059	Oligonucleotide pr
c 286	8.4	46.7	12	1	ABI57031	Oligonucleotide pr	c 359	8	44.4	12	1	ABI81177	Oligonucleotide pr
287	8.4	46.7	12	1	ABI38765	Oligonucleotide pr	360	8	44.4	12	1	ABI03315	Oligonucleotide pr
c 288	8.4	46.7	12	1	ABI22662	Oligonucleotide pr	361	8	44.4	12	1	ABI08303	Oligonucleotide pr
c 289	8.4	46.7	12	1	ABI48147	Oligonucleotide pr	362	8	44.4	12	1	ABI38045	Oligonucleotide pr
c 290	8.4	46.7	12	1	ABI69275	Oligonucleotide pr	c 363	8	44.4	12	1	ABI46960	Oligonucleotide pr
c 291	8.4	46.7	12	1	ABH81267	Oligonucleotide pr	c 364	8	44.4	12	1	ABI66089	Oligonucleotide pr
c 292	8.4	46.7	12	1	ABI43520	Oligonucleotide pr	365	8	44.4	12	1	ABI23145	Oligonucleotide pr
c 293	8.4	46.7	12	1	ABI52994	Oligonucleotide pr	c 366	8	44.4	12	1	ABI02982	Oligonucleotide pr
c 294	8.4	46.7	12	1	ABI10951	Oligonucleotide pr	c 367	8	44.4	12	1	ABI50485	Oligonucleotide pr
c 295	8.4	46.7	12	1	ABI40854	Oligonucleotide pr	c 368	8	44.4	12	1	ABI73137	Oligonucleotide pr
c 296	8.4	46.7	12	1	ABI22663	Oligonucleotide pr	369	8	44.4	12	1	ABI60786	Oligonucleotide pr
c 297	8.4	46.7	12	1	ABI08313	Oligonucleotide pr	370	8	44.4	12	1	ABI62796	Oligonucleotide pr
c 298	8.4	46.7	12	1	ABI22803	Oligonucleotide pr	371	8	44.4	12	1	ABI66538	Oligonucleotide pr
c 299	8.4	46.7	12	1	ABH76196	Oligonucleotide pr	372	8	44.4	12	1	ABI35956	Oligonucleotide pr
c 300	8.4	46.7	12	1	ABI50334	Oligonucleotide pr	373	8	44.4	12	1	ABI32607	Oligonucleotide pr
c 301	8.4	46.7	12	1	ABI64624	Oligonucleotide pr	c 374	8	44.4	12	1	ABI41408	Oligonucleotide pr
c 302	8.4	46.7	12	1	ABI78984	Oligonucleotide pr	c 375	8	44.4	12	1	ABI80535	Oligonucleotide pr
c 303	8.4	46.7	12	1	ABI41311	Oligonucleotide pr	c 376	8	44.4	12	1	ABI23612	Oligonucleotide pr
c 304	8.4	46.7	12	1	AAH45528	JA7 linker DNA use	377	8	44.4	12	1	ABI09120	Oligonucleotide pr
305	8.4	46.7	12	1	AAH45543	JA7 linker DNA use	c 378	8	44.4	12	1	ABI12330	Oligonucleotide pr
c 306	8	44.4	10	1	AAH29361	5'-primer for mamm	379	7.8	43.3	11	1	AAA60137	Human APC gene sca
c 307	8	44.4	10	1	AAH34979	Synthetic Agaricus	c 380	7.8	43.3	11	1	AAH02889	Human pregnane X r
c 308	8	44.4	10	1	AAH282665	Metastatic breast	381	7.8	43.3	11	1	AAH02888	Human skin stress/
c 309	8	44.4	10	1	AAH83780	Metastatic breast	382	7.8	43.3	11	1	ABQ86362	Human skin stress/
c 310	8	44.4	10	1	AAH285774	Metastatic breast	383	7.8	43.3	11	1	ABV66164	Human skin EST 395
c 311	8	44.4	10	1	AAH37636	Yeast NORP gene SA	384	7.8	43.3	11	1	ABV69339	Human skin EST 712
c 312	8	44.4	10	1	AAH34559	Yeast NORP gene SA	385	7.8	43.3	11	1	ABV69008	Human skin EST 679
c 313	8	44.4	10	1	AAH35638	Yeast NORP gene SA	386	7.8	43.3	11	1	ABV70617	Human skin EST 840
c 314	8	44.4	10	1	ABK24272	Retinaldehyde-bind	c 387	7.8	43.3	11	1	ABV70522	Human skin EST 830
c 315	8	44.4	10	1	AAH32203	Human NFkBIB gene	388	7.8	43.3	11	1	ABV62268	Human skin EST 54
c 316	8	44.4	10	1	AAH31708	Human CD39L2 initi	389	7.8	43.3	11	1	ABV63196	Human skin EST 982
c 317	8	44.4	10	1	AAH26873	Human GPR4 gene po	c 390	7.8	43.3	11	1	ABV72111	Human skin EST 989
c 318	8	44.4	12	1	AAH92032	Hairpin primer #2	391	7.8	43.3	11	1	ABV67844	Human skin EST 563
c 319	8	44.4	12	1	ABH72504	Oligonucleotide pr	392	7.8	43.3	11	1	ABV65429	Human skin EST 321
c 320	8	44.4	12	1	ABH99093	Oligonucleotide pr	393	7.8	43.3	11	1	ABV68137	Human skin EST 592
c 321	8	44.4	12	1	ABH81825	Oligonucleotide pr	c 394	7.8	43.3	11	1	ABV63101	Human skin EST 887
c 322	8	44.4	12	1	ABH88008	Oligonucleotide pr	c 395	7.8	43.3	11	1	ABV63610	Human skin EST 139
c 323	8	44.4	12	1	ABI57121	Oligonucleotide pr	c 396	7.8	43.3	11	1	ABV71031	Human skin EST 881
c 324	8	44.4	12	1	ABI02510	Oligonucleotide pr	c 397	7.8	43.3	11	1	ABV68543	Human skin EST 632
c 325	8	44.4	12	1	ABI36184	Oligonucleotide pr	398	7.8	43.3	11	1	ABV69689	Human skin EST 747

399	7.8	43.3	11	1	ABK13229	Self-assembled mon	c 472	7.8	43.3	12	1	ABI19115	Oligonucleotide pr
400	7.8	43.3	11	1	AA42767	Self-assembled mon	c 473	7.8	43.3	12	1	ABI31704	Oligonucleotide pr
c 401	7.8	43.3	11	1	AA42768	Self-assembled mon	c 474	7.8	43.3	12	1	ABI35134	Oligonucleotide pr
402	7.8	43.3	12	1	AAQ5903	Influenza virus ta	c 475	7.8	43.3	12	1	ABI14454	Oligonucleotide pr
c 403	7.8	43.3	12	1	AAQ88175	Endoribonuclease r	c 476	7.8	43.3	12	1	ABI72561	Oligonucleotide pr
404	7.8	43.3	12	1	AAV07774	N3 to P5 oligonucle	c 477	7.8	43.3	12	1	ABI78059	Oligonucleotide pr
c 405	7.8	43.3	12	1	AAZ41739	Organic material d	c 478	7.8	43.3	12	1	ABI79441	Oligonucleotide pr
406	7.8	43.3	12	1	AAZ41523	Microbe detection	c 479	7.8	43.3	12	1	ABH74658	Oligonucleotide pr
c 407	7.8	43.3	12	1	AA55937	Adapter linker nuc	c 480	7.8	43.3	12	1	ABH74660	Oligonucleotide pr
408	7.8	43.3	12	1	AA73449	Linker JC3. Sacch	c 481	7.8	43.3	12	1	ABI29175	Oligonucleotide pr
c 409	7.8	43.3	12	1	AAAC97874	Primer used to ill	c 482	7.8	43.3	12	1	ABI29854	Oligonucleotide pr
410	7.8	43.3	12	1	ABH97306	Oligonucleotide pr	c 483	7.8	43.3	12	1	ABI06143	Oligonucleotide pr
c 411	7.8	43.3	12	1	ABI00329	Oligonucleotide pr	c 484	7.8	43.3	12	1	ABI09863	Oligonucleotide pr
412	7.8	43.3	12	1	ABI04308	Oligonucleotide pr	c 485	7.8	43.3	12	1	ABI139188	Oligonucleotide pr
c 413	7.8	43.3	12	1	ABI35462	Oligonucleotide pr	c 486	7.8	43.3	12	1	ABI13827	Oligonucleotide pr
414	7.8	43.3	12	1	ABI12630	Oligonucleotide pr	c 487	7.8	43.3	12	1	ABH71716	Oligonucleotide pr
c 415	7.8	43.3	12	1	ABI42674	Oligonucleotide pr	c 488	7.8	43.3	12	1	ABH97829	Oligonucleotide pr
416	7.8	43.3	12	1	ABI45454	Oligonucleotide pr	c 489	7.8	43.3	12	1	ABH07180	Oligonucleotide pr
c 417	7.8	43.3	12	1	ABI64359	Oligonucleotide pr	c 490	7.8	43.3	12	1	ABI09108	Oligonucleotide pr
418	7.8	43.3	12	1	ABI19294	Oligonucleotide pr	c 491	7.8	43.3	12	1	ABI76128	Oligonucleotide pr
c 419	7.8	43.3	12	1	ABH72261	Oligonucleotide pr	c 492	7.8	43.3	12	1	ABI77755	Oligonucleotide pr
420	7.8	43.3	12	1	ABI23304	Oligonucleotide pr	c 493	7.8	43.3	12	1	ABH68282	Oligonucleotide pr
c 421	7.8	43.3	12	1	ABH76377	Oligonucleotide pr	c 494	7.8	43.3	12	1	ABH96294	Oligonucleotide pr
422	7.8	43.3	12	1	ABI04717	Oligonucleotide pr	c 495	7.8	43.3	12	1	ABH96483	Oligonucleotide pr
c 423	7.8	43.3	12	1	ABH84394	Oligonucleotide pr	c 496	7.8	43.3	12	1	ABI25488	Oligonucleotide pr
424	7.8	43.3	12	1	ABH86843	Oligonucleotide pr	c 497	7.8	43.3	12	1	ABI51247	Oligonucleotide pr
c 425	7.8	43.3	12	1	ABH87893	Oligonucleotide pr	c 498	7.8	43.3	12	1	ABI51908	Oligonucleotide pr
426	7.8	43.3	12	1	ABI38290	Oligonucleotide pr	c 499	7.8	43.3	12	1	ABI72639	Oligonucleotide pr
c 427	7.8	43.3	12	1	ABH88759	Oligonucleotide pr	c 500	7.8	43.3	12	1	ABI61606	Oligonucleotide pr
428	7.8	43.3	12	1	ABH68518	Oligonucleotide pr	c 501	7.8	43.3	12	1	ABI23319	Oligonucleotide pr
c 429	7.8	43.3	12	1	ABI04718	Oligonucleotide pr	c 502	7.8	43.3	12	1	ABH99757	Oligonucleotide pr
430	7.8	43.3	12	1	ABI33276	Oligonucleotide pr	c 503	7.8	43.3	12	1	ABI09761	Oligonucleotide pr
c 431	7.8	43.3	12	1	ABI14991	Oligonucleotide pr	c 504	7.8	43.3	12	1	ABI10740	Oligonucleotide pr
432	7.8	43.3	12	1	ABI42352	Oligonucleotide pr	c 505	7.8	43.3	12	1	ABI51909	Oligonucleotide pr
c 433	7.8	43.3	12	1	ABI65791	Oligonucleotide pr	c 506	7.8	43.3	12	1	ABI70736	Oligonucleotide pr
434	7.8	43.3	12	1	ABH7796	Oligonucleotide pr	c 507	7.8	43.3	12	1	ABI77347	Oligonucleotide pr
c 435	7.8	43.3	12	1	ABH97842	Oligonucleotide pr	c 508	7.8	43.3	12	1	ABI63539	Oligonucleotide pr
436	7.8	43.3	12	1	ABH76914	Oligonucleotide pr	c 509	7.8	43.3	12	1	ABH76484	Oligonucleotide pr
c 437	7.8	43.3	12	1	ABI37224	Oligonucleotide pr	c 510	7.8	43.3	12	1	ABI02467	Oligonucleotide pr
438	7.8	43.3	12	1	ABI12821	Oligonucleotide pr	c 511	7.8	43.3	12	1	ABI03957	Oligonucleotide pr
c 439	7.8	43.3	12	1	ABI58837	Oligonucleotide pr	c 512	7.8	43.3	12	1	ABI14453	Oligonucleotide pr
440	7.8	43.3	12	1	ABH73759	Oligonucleotide pr	c 513	7.8	43.3	12	1	ABH92247	Oligonucleotide pr
c 441	7.8	43.3	12	1	ABH88077	Oligonucleotide pr	c 514	7.8	43.3	12	1	ABI64455	Oligonucleotide pr
442	7.8	43.3	12	1	ABI15737	Oligonucleotide pr	c 515	7.8	43.3	12	1	ABL59978	Oligonucleotide pr
c 443	7.8	43.3	12	1	ABI44233	Oligonucleotide pr	c 516	7.8	43.3	12	1	AA445540	Adapter oligonucle
444	7.8	43.3	12	1	ABI62270	Oligonucleotide pr	c 517	7.8	43.3	12	1	AAI70640	JC3 linker DNA use
c 445	7.8	43.3	12	1	ABI63212	Oligonucleotide pr	c 518	7.8	43.3	12	1	AAI70640	Adaptor-specific p
446	7.8	43.3	12	1	ABH72760	Oligonucleotide pr	c 519	7.8	43.3	12	1	AAI70659	Rice seed bZIP tra
c 447	7.8	43.3	12	1	ABI11247	Oligonucleotide pr	c 520	7.8	43.3	12	1	ABZ72909	Adaptor-specific o
448	7.8	43.3	12	1	ABI37360	Oligonucleotide pr	c 521	7.8	43.3	12	1	ABZ23896	Rod opsin hammethe
c 449	7.8	43.3	12	1	ABI13665	Oligonucleotide pr	c 522	7.8	43.3	12	1	ABV75305	TERT minimal promo
450	7.8	43.3	12	1	ABI78455	Oligonucleotide pr	c 523	7.8	43.3	12	1	ABV75305	Sequence inserted
c 451	7.8	43.3	12	1	ABH72788	Oligonucleotide pr	c 524	7.4	41.1	10	1	AAH82164	Sequence #22 recog
452	7.8	43.3	12	1	ABI00251	Oligonucleotide pr	c 525	7.4	41.1	10	1	AAQ45103	5'-primer #14 for
c 453	7.8	43.3	12	1	ABH87546	Oligonucleotide pr	c 526	7.4	41.1	10	1	AAQ96589	HIV-1 NL4-3 nef ge
454	7.8	43.3	12	1	ABH87544	Oligonucleotide pr	c 527	7.4	41.1	10	1	AAQ96590	HIV-1 NL4-3 nef ge
c 455	7.8	43.3	12	1	ABI15260	Oligonucleotide pr	c 528	7.4	41.1	10	1	AAQ90123	PCR primer for the
456	7.8	43.3	12	1	ABI46698	Oligonucleotide pr	c 529	7.4	41.1	10	1	AAT29328	5'-primer for mamm
c 457	7.8	43.3	12	1	ABI70658	Oligonucleotide pr	c 530	7.4	41.1	10	1	AAT29318	5'-primer for mamm
458	7.8	43.3	12	1	ABI28344	Oligonucleotide pr	c 531	7.4	41.1	10	1	AAT29339	5'-primer for mamm
c 459	7.8	43.3	12	1	ABI04684	Oligonucleotide pr	c 532	7.4	41.1	10	1	AAT29315	5'-primer for mamm
460	7.8	43.3	12	1	ABI32587	Oligonucleotide pr	c 533	7.4	41.1	10	1	AAT18634	Arbitrary 5' oligo
c 461	7.8	43.3	12	1	ABI12589	Oligonucleotide pr	c 534	7.4	41.1	10	1	AAT69130	Primer (12) for RT
462	7.8	43.3	12	1	ABI73193	Oligonucleotide pr	c 535	7.4	41.1	10	1	AAH83302	Breast cancer tumo
c 463	7.8	43.3	12	1	ABI81939	Oligonucleotide pr	c 536	7.4	41.1	10	1	AAV69061	Human breast tumou
464	7.8	43.3	12	1	ABI07895	Oligonucleotide pr	c 537	7.4	41.1	10	1	AAV50268	Yeast tag for addi
c 465	7.8	43.3	12	1	ABI64698	Oligonucleotide pr	c 538	7.4	41.1	10	1	AAH18617	p53 serial analysi
466	7.8	43.3	12	1	ABI18693	Oligonucleotide pr	c 539	7.4	41.1	10	1	AAH14916	Triple helix formi
c 467	7.8	43.3	12	1	ABH71715	Oligonucleotide pr	c 540	7.4	41.1	10	1	AAZ08327	Human lung tumour
468	7.8	43.3	12	1	ABI56467	Oligonucleotide pr	c 541	7.4	41.1	10	1	AAV45648	Probe for prokaryo
c 469	7.8	43.3	12	1	ABI73121	Oligonucleotide pr	c 542	7.4	41.1	10	1	AAH62777	Differential displ
470	7.8	43.3	12	1	ABI78897	Oligonucleotide pr	c 543	7.4	41.1	10	1	AAH55563	Human dendritic ce
c 471	7.8	43.3	12	1	ABI79114	Oligonucleotide pr	c 544	7.4	41.1	10	1	AAZ79699	Human dendritic ce

c 545	7.4	41.1	10	1	AAZ77629	Human dendritic ce	618	7.4	41.1	10	1	AAS98881	Colony stimulating
c 546	7.4	41.1	10	1	AAZ78070	Human dendritic ce	619	7.4	41.1	10	1	AAS99671	Breast tumour-spec
c 547	7.4	41.1	10	1	AAZ78751	Human dendritic ce	c 620	7.4	41.1	10	1	ABL42924	Human maturation/a
c 548	7.4	41.1	10	1	AAZ83025	Metastatic breast	c 621	7.4	41.1	10	1	ABL60201	Human MUC1 PCR pri
c 549	7.4	41.1	10	1	AAZ86370	Metastatic breast	c 622	7.4	41.1	10	1	AS96188	Human Acetylcholin
c 550	7.4	41.1	10	1	AAZ86589	Metastatic breast	c 623	7.4	41.1	10	1	ABK4715	Human breast tumou
c 551	7.4	41.1	10	1	AAZ82789	Metastatic breast	c 624	7.4	41.1	10	1	ABN80636	Human P450(cytochr
c 552	7.4	41.1	10	1	AAZ80915	Metastatic breast	c 625	7.4	41.1	10	1	ABV78534	Human Th1 cell pre
c 553	7.4	41.1	10	1	AAZ833904	Metastatic breast	c 626	7.4	41.1	10	1	ABV84676	Human amino acid t
c 554	7.4	41.1	10	1	AAZ84679	Metastatic breast	c 627	7.4	41.1	10	1	ABK23661	Transcript tag DNA
c 555	7.4	41.1	10	1	AAZ81733	Metastatic breast	c 628	7.4	41.1	10	1	ABK23547	Transcript tag DNA
c 556	7.4	41.1	10	1	AAZ83460	Metastatic breast	c 629	7.4	41.1	10	1	ABK23602	Transcript tag DNA
c 557	7.4	41.1	10	1	AAZ84920	Metastatic breast	c 630	7.4	41.1	10	1	ABK23710	Transcript tag DNA
c 558	7.4	41.1	10	1	AAZ86569	Metastatic breast	c 631	7.4	41.1	10	1	ABK23658	Transcript tag DNA
c 559	7.4	41.1	10	1	AAZ81164	Metastatic breast	c 632	7.4	41.1	10	1	ABL52033	Human SLC18A2 pref
c 560	7.4	41.1	10	1	AAZ833259	Metastatic breast	c 633	7.4	41.1	10	1	ABK09674	Arteriosclerosis-d
c 561	7.4	41.1	10	1	AAZ84009	Metastatic breast	c 634	7.4	41.1	10	1	ABK68734	Human OR11A1 gene
c 562	7.4	41.1	10	1	AAZ86139	Metastatic breast	c 635	7.4	41.1	10	1	ABN88039	Human SCYB14 prefe
c 563	7.4	41.1	10	1	AAZ86325	Metastatic breast	c 636	7.4	41.1	10	1	ABK14439	ASO Oligo primer #
c 564	7.4	41.1	10	1	AAZ81317	Metastatic breast	c 637	7.4	41.1	10	1	ABL91868	Human LiPG gene pr
c 565	7.4	41.1	10	1	AAZ84870	Metastatic breast	c 638	7.4	41.1	10	1	AAAD31792	MR 14 arbitrary pr
c 566	7.4	41.1	10	1	AAZ86235	Metastatic breast	c 639	7.4	41.1	10	1	ABL45787	Human MMP13 gene a
c 567	7.4	41.1	10	1	AAZ84043	Metastatic breast	c 640	7.4	41.1	10	1	ABK29921	Human epidermal gr
c 568	7.4	41.1	10	1	AAZ74018	Human dendritic ce	c 641	7.4	41.1	10	1	ABL36403	Human lysosomal ac
c 569	7.4	41.1	10	1	AAZ74100	Human dendritic ce	c 642	7.4	41.1	10	1	AAAD51164	Decoder binding si
c 570	7.4	41.1	10	1	AAZ50020	Interleukin 2 enha	c 643	7.4	41.1	10	1	AAAD51168	Decoder probe #3 u
c 571	7.4	41.1	10	1	AAZ50019	Ets-2 promoter for	c 644	7.4	41.1	10	1	ADAL1182	Differential displ
c 572	7.4	41.1	10	1	AAZ80825	Human B18Ag1 cDNA	c 645	7.4	41.1	10	1	ABV76219	Primer for detecti
c 573	7.4	41.1	10	1	AAZ15249	Primer MRL4 for mo	c 646	7.4	41.1	10	1	ACC85187	Human COX1 gene DS
c 574	7.4	41.1	10	1	AAZ34683	D14 randomer used	c 647	7.4	41.1	10	1	ACC85186	Human COX1 gene DS
c 575	7.4	41.1	10	1	AAZ79078	Human lung tumour-	c 648	7.4	41.1	10	1	ADB81028	LINE retro-positio
c 576	7.4	41.1	10	1	AAH44157	Escherichia coli 1	c 649	7.4	41.1	10	1	ADC15155	Human breast tumou
c 577	7.4	41.1	10	1	AAZ30878	Oligonucleotide po	c 650	7.4	41.1	10	1	ADD07264	Mouse differential
c 578	7.4	41.1	10	1	AAH64040	Human ubiquitously	c 651	7.4	41.1	10	1	ADD66356	Human lung tumour-
c 579	7.4	41.1	10	1	AAH64082	Human ubiquitously	c 652	7.4	41.1	10	1	ADE87610	Human lung tumour
c 580	7.4	41.1	10	1	AAH64081	Human ubiquitously	c 653	7.4	41.1	10	1	AAQ69869	Sample distancin
c 581	7.4	41.1	10	1	AAH64326	Human ubiquitously	c 654	7.4	41.1	10	1	AAQ49573	NFAR-1 binding sit
c 582	7.4	41.1	10	1	AAH63895	Human ubiquitously	c 655	7.4	41.1	10	1	AAZ18694	Murine C57BL/6 SAG
c 583	7.4	41.1	10	1	AAZ57303	Human CHRN2 allele	c 656	7.4	41.1	10	1	AAZ19007	Murine MRL SAGE ta
c 584	7.4	41.1	10	1	AAZ23153	Human lung tumour-	c 657	7.4	41.1	10	1	AAZ18957	Murine MRL SAGE ta
c 585	7.4	41.1	10	1	AAZ83126	Tumour rejection a	c 658	7.4	41.1	10	1	AAZ18853	Triple helix third
c 586	7.4	41.1	10	1	AAZ34122	Yeast NORF gene SA	c 659	7.4	41.1	10	1	AAZ14903	Distancin sample
c 587	7.4	41.1	10	1	AAZ42074	Yeast NORF gene SA	c 660	7.4	41.1	10	1	AAZ17619	N11 active EGS 23
c 588	7.4	41.1	10	1	AAZ35238	Yeast NORF gene SA	c 661	7.4	41.1	10	1	AAZ77659	DNA sequence that
c 589	7.4	41.1	10	1	AAZ33485	Yeast NORF gene SA	c 662	7.4	41.1	10	1	AAZ82242	Human skin stress/
c 590	7.4	41.1	10	1	AAZ35943	Yeast NORF gene SA	c 663	7.4	41.1	10	1	ABQ86387	Human skin stress/
c 591	7.4	41.1	10	1	AAZ35079	Yeast NORF gene SA	c 664	7.4	41.1	10	1	ABQ87456	Human skin stress/
c 592	7.4	41.1	10	1	AAZ36262	Yeast NORF gene SA	c 665	7.4	41.1	10	1	ABQ86343	Human skin stress/
c 593	7.4	41.1	10	1	AAZ39042	Yeast NORF gene SA	c 666	7.4	41.1	10	1	ABQ86495	Human skin stress/
c 594	7.4	41.1	10	1	AAZ40204	Yeast NORF gene SA	c 667	7.4	41.1	10	1	ABQ87002	Human skin stress/
c 595	7.4	41.1	10	1	AAZ40585	Yeast NORF gene SA	c 668	7.4	41.1	10	1	ABQ87571	Human skin stress/
c 596	7.4	41.1	10	1	AAZ42897	Yeast NORF gene SA	c 669	7.4	41.1	10	1	ABV65752	Human skin EST 353
c 597	7.4	41.1	10	1	AAZ36542	Yeast NORF gene SA	c 670	7.4	41.1	10	1	ABV67491	Human skin EST 527
c 598	7.4	41.1	10	1	AAZ40379	Yeast NORF gene SA	c 671	7.4	41.1	10	1	ABV68393	Human skin EST 617
c 599	7.4	41.1	10	1	AAZ37254	Yeast NORF gene SA	c 672	7.4	41.1	10	1	ABV70831	Human skin EST 861
c 600	7.4	41.1	10	1	AAZ33972	Yeast NORF gene SA	c 673	7.4	41.1	10	1	ABV71968	Human skin EST 975
c 601	7.4	41.1	10	1	AAZ34658	Yeast NORF gene SA	c 674	7.4	41.1	10	1	ABV64547	Human skin EST 233
c 602	7.4	41.1	10	1	AAZ37149	Yeast NORF gene SA	c 675	7.4	41.1	10	1	ABV68341	Human skin EST 612
c 603	7.4	41.1	10	1	AAZ37919	Yeast NORF gene SA	c 676	7.4	41.1	10	1	ABV69848	Human skin EST 773
c 604	7.4	41.1	10	1	AAZ34682	Yeast NORF gene SA	c 677	7.4	41.1	10	1	ABV71538	Human skin EST 932
c 605	7.4	41.1	10	1	AAZ42044	Yeast NORF gene SA	c 678	7.4	41.1	10	1	ABV66548	Human skin EST 433
c 606	7.4	41.1	10	1	AAZ36972	Yeast NORF gene SA	c 679	7.4	41.1	10	1	ABV69063	Human skin EST 684
c 607	7.4	41.1	10	1	AAZ42155	Yeast NORF gene SA	c 680	7.4	41.1	10	1	ABV62527	Human skin EST 313
c 608	7.4	41.1	10	1	AAZ33706	Yeast NORF gene SA	c 681	7.4	41.1	10	1	ABV67977	Human skin EST 576
c 609	7.4	41.1	10	1	AAZ36501	Yeast NORF gene SA	c 682	7.4	41.1	10	1	ABV64784	Human skin EST 257
c 610	7.4	41.1	10	1	AAZ36973	Yeast NORF gene SA	c 683	7.4	41.1	10	1	ABV68267	Human skin EST 605
c 611	7.4	41.1	10	1	AAZ39329	Yeast NORF gene SA	c 684	7.4	41.1	10	1	ABV69658	Human skin EST 779
c 612	7.4	41.1	10	1	AAZ39819	Yeast NORF gene SA	c 685	7.4	41.1	10	1	ABV70010	Human skin EST 749
c 613	7.4	41.1	10	1	AAZ34234	Yeast NORF gene SA	c 686	7.4	41.1	10	1	ABV62680	Human skin EST 466
c 614	7.4	41.1	10	1	AAZ35014	Yeast NORF gene SA	c 687	7.4	41.1	10	1	ABV66119	Human skin EST 390
c 615	7.4	41.1	10	1	ABL88455	Pain regulated gen	c 688	7.4	41.1	10	1	ABV67043	Human skin EST 482
c 616	7.4	41.1	10	1	AAZ18735	Primer-extension o	c 689	7.4	41.1	10	1	ABV70101	Human skin EST 788
c 617	7.4	41.1	10	1	ABL01193	Human AKR1B1 gene	c 690	7.4	41.1	10	1	ABV62237	Human skin EST 23

C 691	7.4	41.1	11	1	ABV65606	Human skin EST 339	C 764	7	38.9	10	1	AAF41808	Yeast NORF gene SA
C 692	7.4	41.1	11	1	ABV62589	Human skin EST 375	C 765	7	38.9	10	1	AAF35626	Yeast NORF gene SA
C 693	7.4	41.1	11	1	ABV64245	Human skin EST 203	C 766	7	38.9	10	1	AAF36462	Yeast NORF gene SA
C 694	7.4	41.1	11	1	ABV68075	Human skin EST 586	C 767	7	38.9	10	1	AAF38906	Yeast NORF gene SA
C 695	7.4	41.1	11	1	ABV68618	Human skin EST 640	C 768	7	38.9	10	1	AAF36183	Yeast NORF gene SA
C 696	7.4	41.1	11	1	ABV69016	Human skin EST 680	C 769	7	38.9	10	1	AAF40128	Yeast NORF gene SA
C 697	7.4	41.1	11	1	ABV65379	Human skin EST 316	C 770	7	38.9	10	1	AAF40706	Yeast NORF gene SA
C 698	7.4	41.1	11	1	ABV68327	Human skin EST 611	C 771	7	38.9	10	1	AAF34367	Yeast NORF gene SA
C 699	7.4	41.1	11	1	ABV69550	Human skin EST 733	C 772	7	38.9	10	1	AAF36277	Yeast NORF gene SA
C 700	7.4	41.1	11	1	ABV71666	Human skin EST 945	C 773	7	38.9	10	1	AAF37614	Yeast NORF gene SA
C 701	7.4	41.1	11	1	ABV63410	Human skin EST 119	C 774	7	38.9	10	1	AAF40734	Yeast NORF gene SA
C 702	7.4	41.1	11	1	ABV64117	Human skin EST 190	C 775	7	38.9	10	1	AAF42712	Yeast NORF gene SA
C 703	7.4	41.1	11	1	ABV67192	Human skin EST 497	C 776	7	38.9	10	1	AAF38165	Yeast NORF gene SA
C 704	7.4	41.1	11	1	ABV72053	Human skin EST 983	C 777	7	38.9	10	1	AAF42504	Yeast NORF gene SA
C 705	7.4	41.1	11	1	ABV69454	Human skin EST 724	C 778	7	38.9	10	1	AAF42922	Yeast NORF gene SA
C 706	7.4	41.1	11	1	ABK83110	DNA binding molecu	C 779	7	38.9	10	1	AAF35273	Yeast NORF gene SA
C 707	7.4	41.1	11	1	AAD34601	Human CYP2C19 gene	C 780	7	38.9	10	1	AAF43489	Yeast NORF gene SA
C 708	7.4	41.1	11	1	AAD34581	Human CYP2C19 gene	C 781	7	38.9	10	1	AAF35108	Yeast NORF gene SA
C 709	7.4	41.1	11	1	ACC97178	Consensus 16S rRNA	C 782	7	38.9	10	1	AAF35646	Yeast NORF gene SA
C 710	7.4	41.1	11	1	AD80649	Duplex oligonucleo	C 783	7	38.9	10	1	AAF36303	Yeast NORF gene SA
C 711	7	38.9	8	1	AAA81052	A. thaliana primer	C 784	7	38.9	10	1	AAF38071	Yeast NORF gene SA
C 712	7	38.9	8	1	AAA80772	A. thaliana primer	C 785	7	38.9	10	1	AAF39675	Yeast NORF gene SA
C 713	7	38.9	8	1	AAA80798	A. thaliana primer	C 786	7	38.9	10	1	AAF42156	Yeast NORF gene SA
C 714	7	38.9	9	1	AAA28773	Tethered probe CF1	C 787	7	38.9	10	1	AAF38429	Yeast NORF gene SA
C 715	7	38.9	9	1	AAF91646	Breast-cancer asso	C 788	7	38.9	10	1	AAF43238	Yeast NORF gene SA
C 716	7	38.9	9	1	AAD21036	Human CYP2 gene ex	C 789	7	38.9	10	1	AAF36982	Yeast NORF gene SA
C 717	7	38.9	9	1	ABQ72179	Zinc finger protei	C 790	7	38.9	10	1	AAF35394	Yeast NORF gene SA
C 718	7	38.9	9	1	ABQ72174	Zinc finger protei	C 791	7	38.9	10	1	AAF37498	Yeast NORF gene SA
C 719	7	38.9	9	1	AAD44140	PCR primer #5 desi	C 792	7	38.9	10	1	AAF38878	Yeast NORF gene SA
C 720	7	38.9	9	1	ADA64501	Zinc finger target	C 793	7	38.9	10	1	AAF42917	Yeast NORF gene SA
C 721	7	38.9	9	1	ADA64506	Zinc finger target	C 794	7	38.9	10	1	AAF40129	Yeast NORF gene SA
C 722	7	38.9	10	1	AAQ88357	Set of probes for	C 795	7	38.9	10	1	AAF33628	Yeast NORF gene SA
C 723	7	38.9	10	1	AAZ29354	5'-primer for mamm	C 796	7	38.9	10	1	AAF34498	Yeast NORF gene SA
C 724	7	38.9	10	1	AAZ77697	Human dendritic ce	C 797	7	38.9	10	1	AAF35237	Yeast NORF gene SA
C 725	7	38.9	10	1	AAZ79520	Human dendritic ce	C 798	7	38.9	10	1	AAF36405	Yeast NORF gene SA
C 726	7	38.9	10	1	AAZ77689	Human dendritic ce	C 799	7	38.9	10	1	AAF39465	Yeast NORF gene SA
C 727	7	38.9	10	1	AAZ78497	Human dendritic ce	C 800	7	38.9	10	1	AAF33629	Yeast NORF gene SA
C 728	7	38.9	10	1	AAZ78928	Human dendritic ce	C 801	7	38.9	10	1	AAF41221	Yeast NORF gene SA
C 729	7	38.9	10	1	AAZ85072	Human dendritic ce	C 802	7	38.9	10	1	AAZ95353	Human Histamine H2
C 730	7	38.9	10	1	AAZ84663	Metastatic breast	C 803	7	38.9	10	1	AAZ25096	Primer #23 used to
C 731	7	38.9	10	1	AAZ82467	Metastatic breast	C 804	7	38.9	10	1	AAD25317	Human HSD3B1 gene
C 732	7	38.9	10	1	AAZ83044	Metastatic breast	C 805	7	38.9	10	1	ABL01185	Human AKR1B1 gene
C 733	7	38.9	10	1	AAZ86171	Metastatic breast	C 806	7	38.9	10	1	ABL42892	Human maturation/a
C 734	7	38.9	10	1	AAZ82672	Metastatic breast	C 807	7	38.9	10	1	ABL42786	Human maturation/a
C 735	7	38.9	10	1	AAZ882301	Metastatic breast	C 808	7	38.9	10	1	ABK81441	SCYA20 primer exte
C 736	7	38.9	10	1	AAZ83912	Metastatic breast	C 809	7	38.9	10	1	ABK81454	SCYA20 primer exte
C 737	7	38.9	10	1	AAZ84299	Metastatic breast	C 810	7	38.9	10	1	ABL39515	Human E1FB primer-
C 738	7	38.9	10	1	AAZ85672	Metastatic breast	C 811	7	38.9	10	1	ABL39515	Human E1FB primer-
C 739	7	38.9	10	1	AAZ81332	Metastatic breast	C 812	7	38.9	10	1	ABN80655	Human P450 (cytochr
C 740	7	38.9	10	1	AAZ85381	Metastatic breast	C 813	7	38.9	10	1	ABV84329	Mouse receptor-act
C 741	7	38.9	10	1	AAZ82094	Metastatic breast	C 814	7	38.9	10	1	AAZ95616	Human phosphatidic
C 742	7	38.9	10	1	AAZ83333	Metastatic breast	C 815	7	38.9	10	1	ABL45894	Human phosphatidic
C 743	7	38.9	10	1	AAZ84131	Metastatic breast	C 816	7	38.9	10	1	ABL45906	Human EDG6 gene al
C 744	7	38.9	10	1	AAZ85948	Metastatic breast	C 817	7	38.9	10	1	ABL47237	Human EDG6 gene al
C 745	7	38.9	10	1	AAZ86466	Metastatic breast	C 818	7	38.9	10	1	ABL91888	Allergic disease e
C 746	7	38.9	10	1	AAZ82152	Metastatic breast	C 819	7	38.9	10	1	ABL57223	Human L1PG gene pr
C 747	7	38.9	10	1	AAZ85841	Metastatic breast	C 820	7	38.9	10	1	ABL57229	Primer extension o
C 748	7	38.9	10	1	AAZ74109	Human dendritic ce	C 821	7	38.9	10	1	ABL57229	Primer extension o
C 749	7	38.9	10	1	AAZ56456	Human macrophage g	C 822	7	38.9	10	1	AAZ31785	MR 7 arbitrary pri
C 750	7	38.9	10	1	AAZ15242	Primer MR7 for mod	C 823	7	38.9	10	1	ABK96529	Human FLAU gene, p
C 751	7	38.9	10	1	AAF77152	R-structure wing s	C 824	7	38.9	10	1	ACC78757	Normal estrogen re
C 752	7	38.9	10	1	AAF77162	R-structure 5899.	C 825	7	38.9	10	1	ADE14179	Optineurin promote
C 753	7	38.9	10	1	AAF77153	R-structure wing s	C 826	7	38.9	10	1	ADE14178	Optineurin promote
C 754	7	38.9	10	1	AAH63972	Human ubiquitously							Primer #12 of the
C 755	7	38.9	10	1	AAH63664	Human ubiquitously							
C 756	7	38.9	10	1	AAH63197	Human colon epithe							
C 757	7	38.9	10	1	AAH63180	Human colon epithe							
C 758	7	38.9	10	1	AAH63199	Human colon epithe							
C 759	7	38.9	10	1	AAH63634	Human ubiquitously							
C 760	7	38.9	10	1	AAZ57323	Human CHRN2 allele							
C 761	7	38.9	10	1	AAH32725	LPS activated huma							
C 762	7	38.9	10	1	AAH32733	LPS activated huma							
C 763	7	38.9	10	1	AAF36541	Yeast NORF gene SA							

ALIGNMENTS

RESULT 1
AAA08479
ID AAA08479 standard; DNA; 18 BP.
XX
AC AAA08479;


```
XX 17-JUL-2000 (first entry)
XX Human Akt-2 phosphorothioate antisense oligonucleotide SEQ ID NO:32.
XX
XX Human; Akt-2; antisense oligonucleotide; phosphorothioate; inhibition;
XX serine/threonine kinase; antiinflammatory; cytosstatic; antiinfectious;
XX gene therapy; infection; inflammation; tumour; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..18
XX /*tag= a
XX /*note= "phosphorothioate linkages"
XX
XX US6043090-A.
XX
XX 28-MAR-2000.
XX
XX 23-FEB-1999; 99US-00256465.
XX
XX 23-FEB-1999; 99US-00256465.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowsett LM;
XX
XX WPI; 2000-270345/23.
XX
XX Antisense compound for diagnosis and treatment of infection, inflammation
XX and tumor formation is targeted towards the nucleic acid encoding a
XX member of serine/threonine family of kinases.
XX
XX Claim 3; Col 38; 30pp; English.
XX
XX The present invention describes antisense compounds of about 8-30
XX nucleotides in length targeted to the 5' UTR (untranslated region), 3'
XX UTR or coding region of the nucleic acid encoding human Akt-2, which
XX inhibits the expression of human Akt-2. Human Akt-2 is a member of the
XX Akt/PKB family of serine/threonine kinases. The antisense compounds have
XX antiinflammatory, cytostatic and antiinfectious activities, and can be
XX used in gene therapy. They are useful in inhibiting the expression of
XX human Akt-2 by contacting the cells or the tissues in vitro. They can
XX also be used for diagnosis and treatment of infection, inflammation and
XX tumour formation, and for prophylaxis. The present sequence represents a
XX human Akt-2 phosphorothioate antisense oligonucleotide used in the
XX exemplification of the present invention
XX
XX Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Gaps 0;
XX Matches 18; Conservative 0; Indels 0;
XX
XX Qy 1 GTGAGCGACTTCATCCTT 18
XX |||||
XX Db 1 GTGAGCGACTTCATCCTT 18
XX
XX RESULT 2
XX ABS59760/c
XX ID ABS59760 standard; DNA; 20 BP.
XX
XX AC ABS59760;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human damage specific DNA binding protein 1 antisense oligo #52.
XX
XX Antisense; cytostatic; hepatotropic; antiinflammatory; virucide;
XX Damage-specific DNA-binding protein 1; p127; cancer; human; ss;
XX hyperproliferative disorder; haematopoietic cancer; hepatitis.
XX
```

```
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /*mod_base= m5C
XX /*note= "All cytosines are 5-methyl cytosine"
XX
XX modified_base 1..20
XX /*tag= c
XX /*mod_base= OTHER
XX /*note= "OTHER= phosphorothioate backbone"
XX
XX modified_base 1..5
XX /*tag= b
XX /*mod_base= OTHER
XX /*note= "OTHER= 2'-O-methoxyethyl nucleotide"
XX
XX modified_base 16..20
XX /*tag= d
XX /*mod_base= OTHER
XX /*note= "OTHER= 2'-O-methoxyethyl nucleotide"
XX
XX WO200246206-A1.
XX
XX 13-JUN-2002.
XX
XX 04-DEC-2001; 2001WO-US046485.
XX
XX 06-DEC-2000; 2000US-00731457.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Popoff I, Wyatt JR;
XX
XX WPI; 2002-599454/64.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
XX Damage-specific DNA-binding protein 1, p127, useful for treating animal
XX having disease associated with the protein such as liver cancer, or
XX hepatitis.
XX
XX Page 90; Claim 3; 121pp; English.
XX
XX This invention relates to a novel antisense compound 8 to 50 nucleobases
XX in length targeted to nucleic acid molecule encoding Damage-specific DNA-
XX binding protein 1, p127 where the antisense compound specifically
XX hybridises with and inhibits expression of the damage specific DNA
XX binding protein-1 gene. The compounds of the invention may be used in
XX antisense therapy as an inhibitor of expression of Damage-specific DNA-
XX binding protein 1, p127. The antisense compounds of the invention are
XX useful for inhibiting the expression of damage specific DNA binding
XX protein 1, p127 in cells or tissues and are also useful for treating an
XX animal having a disease or condition associated with expression of p127,
XX such as a hyperproliferative disorder (e.g., cancer such as breast, skin,
XX liver, or haematopoietic cancer), or hepatitis, by inhibiting the
XX expression of p127. All antisense oligonucleotides of the invention are
XX chimeric oligonucleotides (gapmers) 20 nucleotides in length, composed of
XX a central gap region consisting of ten 2'-deoxynucleotides, which are
XX flanked on both sides (5' and 3' directions) by five- nucleotide wings.
XX The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The
XX internucleoside (backbone) linkages are phosphorothioate (P=S) throughout
XX the oligonucleotide and all cytidine residues are 5-methylcytidines. The
XX present sequence represents a damage-specific DNA binding protein 1, p127
XX antisense oligonucleotide of the invention
XX
XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 24;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 3 GAGCGACTTCATCCTT 17
XX | |||||
```


KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX Hepatitis C virus.

XX US2002082225-A1.

XX 27-JUN-2002.

XX 23-MAR-1999; 99US-00274553.

XX 23-MAR-1999; 99US-00274553.

XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX (ROBE/) ROBERTS B.
 XX (PAVC/) PAVCO P A.
 XX (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
 XX WPI; 2002-617759/66.

XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 XX replication and are useful to treat hepatitis C virus infections and
 XX cirrhosis, liver failure or hepatocellular carcinoma.

XX Claim 1; Page 34; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
 XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
 XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 XX (HP) motif where the binding arms comprise sequences complementary to one
 XX of the substrate sequences defined in the specification. The HCV
 XX ribozymes are useful for modulating the expression and/or replication of
 XX HCV. They can be used to treat cirrhosis, liver failure and/or
 XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 XX a condition associated with HCV infection in conjunction with one or more
 XX other drug therapies, particularly type I interferon, especially
 XX interferon alpha, beta or gamma or consensus interferon. The present
 XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 XX Some of the sequence data for this patent did not form part of the
 XX printed specification. The complete sequence data for this patent was
 XX obtained in electronic format directly from the USPTO web site at
 XX seqdata.uspto.gov/psipdIDentry.html

XX Sequence 15 BP; 5 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 68.9%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 33;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
 Db 14 GTGAGCGACTTTAT 1

RESULT 6

AAD52478
 ID AAD52478 standard; DNA; 18 BP.

XX AAD52478;

XX 02-MAY-2003 (first entry)

XX Lolium perenne lPLEAa cDNA sequencing forward primer.

XX Abscisic acid-inducible and stress responsive protein; ASR; A22; PKABA;
 KW stress-inducible cysteine protease; late embryogenesis abundant protein;
 KW LEA; dehydrin; DHN; abscisic acid-induced protein kinase; gene therapy;
 KW CYS; seed development; plant tolerance; germination; plant protectant;
 KW ryegrass; primer; ss.

XX Lolium perenne.
 XX WO200290547-A1.

XX 14-NOV-2002.

XX 07-MAY-2002; 2002WO-AU000564.

XX 07-MAY-2001; 2001AU-00004821.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.

XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2003-129183/12.

XX New isolated nucleic acid encoding ASR, A22, CYS, LEA, DHN or PKABA
 XX proteins, useful as molecular genetic markers, and in modifying plant
 XX and/or seed development and responses to stresses and adverse
 XX environmental stimuli.

XX Example 3; Page 29; 231pp; English.

XX The invention relates to nucleic acid encoding abscisic acid-inducible
 XX and stress responsive proteins (ASR and A22), stress-inducible cysteine
 XX proteases (CYS), late embryogenesis abundant proteins (LEA), dehydrins
 XX (DHN) and abscisic acid-induced protein kinases (PKABA). The invention
 XX also relates to a method for modification of plant and seed development
 XX and plant responses to stresses and stimuli. The invention is useful as
 XX molecular genetic markers. The method is useful for modifying plant
 XX response to an environmental stimulus, modifying plant tolerance to
 XX abiotic, osmotic and/or temperature stresses, modifying seed dormancy
 XX and/or germination, development, maturation, and modifying a plant
 XX developmental process. They are also useful for modifying plant tolerance
 XX and adaptation to stresses and adverse environmental stimuli. The
 XX invention is also used in gene therapy. The present sequence is a primer
 XX used for sequencing Lolium perenne lPLEAa cDNA

XX Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 68.9%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 37;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCATCCTT 18
 Db 3 GCGACTTGATCCTT 16

RESULT 7

AAF30498
 ID AAF30498 standard; DNA; 17 BP.

XX AAF30498;

XX 29-MAY-2001 (first entry)

XX Human PAK5 oligonucleotide.

XX PAK5; human; c-Jun N-terminal kinase kinase kinase; JNKKK;
 KW protein kinase; ultraviolet radiation; skin damage; inflammation;
 KW psoriasis; radioprotective; antiinflammatory; antipsoriatic; vulnery;

XX Homo sapiens.

XX EP1085093-A2.

XX 21-MAR-2001.

XX 12-SEP-2000; 2000EP-00307866.

```
XX 20-SEP-1999; 99US-0155029P.
PR (UNYV ) UNIV NEW YORK STATE.
PA Blumenberg M, Gazel AM;
XX WPI; 2001-236883/25.
XX New polynucleotides encoding c-Jun N-terminal kinase kinases i.e.
PT MLK4, PAK4, associated with skin damage for use in drug screening and
PT development.
XX Example 7; Page 20; 51pp; English.
XX This oligonucleotide was used to identify a genomic clone from a PI human
CC library that contained the PAK5 gene. An isolated clone was sequenced
CC (see AAF30490), showing it to be a partial PAK5 genomic clone. The full-
CC length gene (see AAF30492) was subsequently obtained. PAK5 is 1 of 4
CC novel c-Jun N-terminal kinase kinases (JNKKKs) of the invention.
CC MLK4, PAK4, PAK5 and YSK2 polynucleotides and their gene products can be
CC used to screen for compounds that affect the activity of a JNKKK or which
CC affect the expression of a gene encoding a JNKKK. Particularly useful are
CC drugs that reduce UV light-induced damage of the skin, inflammation and
CC psoriasis, and drugs that enhance wound healing
XX Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 65.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAGCGACTTCATCCT 17
DB 1 GAGTGACTCCATCCT 15

RESULT 8
ABQ84058
ID ABQ84058 standard; DNA; 15 BP.
XX AC ABQ84058;
XX 18-FEB-2003 (first entry)
DE Tubercle bacillus diagnosis probe M5.
XX Tubercle bacillus; diagnosis; probe; rpoB; DNA chip; drug tolerance;
KW deoxyribonucleic acid chip; ss.
XX Bacillus sp.
XX CN1351176-A.
XX 29-MAY-2002.
XX 31-OCT-2000; 2000CN-00133796.
XX 31-OCT-2000; 2000CN-00133796.
XX (MENG/) MENGSHU Y.
XX WPI; 2002-644410/70.
XX DNA chip for diagnosing tubercle bacillus and its drug tolerance.
XX Claim 1; Page 1 (Claims); 15pp; Chinese.
XX ABQ84043 to ABQ84083 represent specifically claimed DNA probes which can
CC be used in a deoxyribonucleic acid (DNA) chip (i) comprising 12-100 DNA
CC probes fixed to a glass plate, silicon chip, membrane or high-molecular
CC material. (i) is useful for diagnosing tubercle bacillus and its drug
CC tolerance. (i) has a high diagnosing efficiency and accuracy, low cost
```

```
CC and short detection time
XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGCGACTTCAT 14
DB 3 TGAGCGAATTCAT 15

RESULT 9
ADC33608
ID ADC33608 standard; DNA; 15 BP.
XX AC ADC33608;
XX 18-DEC-2003 (first entry)
DE M. tuberculosis oligonucleotide probe #16.
XX ss; probe; rifampin resistance; rpoB; tuberculosis.
KW Mycobacterium tuberculosis.
XX US2003104387-A1.
XX 05-JUN-2003.
XX 07-SEP-2001; 2001US-00949041.
XX 07-SEP-2001; 2001US-00949041.
XX (YANG/) YANG M.
XX (WOOH/) WOO H S.
XX Yang M, Woo HS;
XX WPI; 2003-787043/74.
XX Detecting tendency to rifampin resistance caused by mutation in RNA
PT polymerase beta-subunit gene of Mycobacterium tuberculosis.
XX Claim 20; SEQ ID NO 19; 27pp; English.
XX The invention relates to a method of detecting a tendency to rifampin
CC resistance caused by mutations in rpoB gene of Mycobacterium tuberculosis
CC comprising extracting DNA from M. tuberculosis cells, amplifying rpoB
CC gene to produce fluorescently labelled product, contacting the labelled
CC product with first and second array of oligonucleotide probes, detecting
CC fluorescent hybridisation signal and correlating with tendency to
CC rifampin resistance. The method is useful for detecting a tendency to
CC rifampin resistance caused by mutations in a rpoB gene of M.
CC tuberculosis. The method is easy to perform and is cost effective to be
CC performed on a large-scale basis. The results produced is reliable and
CC readily detectable. The method is easily adaptable to automation. The
CC present sequence represents a M. tuberculosis probe.
XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGCGACTTCAT 14
DB 3 TGAGCGAATTCAT 15

RESULT 10
AAF95009
```

```

ID AAF95009 standard; DNA; 17 BP.
XX AC AAF95009;
XX KW streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene;
XX DT 23-MAY-2001 (first entry)
XX DE Mutant capture oligonucleotide #2.
XX KW Tubercle bacillus; drug sensitivity; drug resistance; rifampicin;
XX KW streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs gene;
XX KW rpsL gene; inhA gene; katG gene; emmB gene; probe; PCR primer; ss.
XX OS Mycobacterium tuberculosis.
XX PN EP1076099-A2.
XX PD 14-FEB-2001.
XX PF 02-AUG-2000; 2000EP-00306563.
XX PR 03-AUG-1999; 99JP-00220357.
XX PA (NISN ) NISSHINO IND INC.
XX PA (SYST-) SYSTEM RES INC.
XX PI Suzuki Y, Nishida M, Takenishi S;
XX WI; 2001-246696/26.
XX DR New oligonucleotides, nucleic acid probes and primers are useful for
XX PT differentiating drug-resistance and determining infection with tubercle
XX PT bacilli.
XX PS Claim 8; Page 20; 114pp; English.
XX CC The present invention relates to oligonucleotides based on nucleotide
XX CC sequences obtained from both wild-type tubercle bacilli (wtTB) that are
XX CC susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are
XX CC resistant to a drug. The drugs used in the present invention are
XX CC rifampicin (RFP), streptomycin (SM), kanamycin (KM), isoniazid (INH) and
XX CC ethambutol (EB). The rpoB gene is responsible for resistance to RFP; the
XX CC rrs gene is responsible for resistance to SM and KM; the rpsL gene is
XX CC responsible for resistance to SM; the inhA gene is responsible for
XX CC resistance to INH; the katG gene is responsible for resistance to INH;
XX CC and the emmB gene is responsible for resistance to EB. The present
XX CC invention also relates to nucleic acid probes having part of a nucleotide
XX CC sequence of tubercle bacilli (TB) responsible for drug resistance and
XX CC primers used to generate the probes. The present sequence is an
XX CC oligonucleotide of the present invention. The oligonucleotides of the
XX CC present invention can be used to enable the differentiation of drug
XX CC resistance and the determination of infection with tubercle bacilli
XX CC simultaneously.
XX SQ Sequence 17 BP; 4 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 63.3%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 59;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCGAATTCAT 15

RESULT 11
ACC68036
ID ACC68036 standard; DNA; 17 BP.
XX AC ACC68036;
XX KW Murine oligonucleotide associated with tumour suppression, SEQ ID 5283.
XX DT 01-JUL-2003 (first entry)
XX DE

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WI; 2003-333167/31.
XX DR New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 648; 738pp; French.
XX CC The present invention relates to murine oligonucleotides (ACC62754-
XX CC ACC6806), which are associated with tumour suppression, tumour
XX CC reversion, apoptosis and virus resistance. The oligonucleotides are
XX CC useful as (1) as probes and primers for detecting, identifying,
XX CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
XX CC recombinant polypeptides. The oligonucleotides are useful for preparation
XX CC of pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia.
XX SQ Sequence 17 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCATCCTT 18
Db 1 GATCACTTCATCCTT 16

RESULT 12
ABF25604/c
ID ABF25604 standard; DNA; 13 BP.
XX AC ABF25604;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 125601 for detecting SNP TSC0031407.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.

```

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 125601; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 61.1%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX Db 12 ACTTCATCCTT 2
XX
XX RESULT 13
XX ABF25605
XX ID ABF25605 standard; DNA; 13 BP.
XX AC ABF25605;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 125602 for detecting SNP TSC0031407.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 125602; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
CC SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
CC
CC Query Match 61.1%; Score 11; DB 1; Length 13;
CC Best Local Similarity 100.0%; Pred. No. 60;
CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 8 ACTTCATCCTT 18
CC Db 2 ACTTCATCCTT 12
CC
CC RESULT 14
CC AAX31379/c
CC ID AAX31379 standard; DNA; 15 BP.
CC XX AAX31379;
CC AC AAX31379;
CC DT 21-MAY-1999 (first entry)
CC DE Tag sequence of a transcript decreased in colorectal cancer.
CC KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
CC KW diagnosis; prognosis; treatment; ss.
CC OS Homo sapiens.
CC PN WO9853319-A2.
CC XX 26-NOV-1998.
CC PF 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX Claim 1; Page 47; 120pp; English.
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer

SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGGCTTCAT 14
| | | | |
Db 15 GTGAGCGGCTTCAT 2

RESULT 15
ABK81202/c
ID ABK81202 standard; RNA; 15 BP.

AC ABK81202;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polyimmunoglobulin receptor (pIgR) associated RNA #2.
XX
KW Transcellular transport; transcytotic transport; paracellular transport;
KW respiratory system disorder; lung cancer; tumour; asthma;
KW pathogenic infection; allergy-related disorder;
KW gastrointestinal tract disorder; gastrointestinal hormone disorder;
KW Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR; ss.
XX
OS Unidentified.
XX
FN WO200228408-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030832.
XX
PR 02-OCT-2000; 2000US-0237929P.
PR 13-NOV-2000; 2000US-0248478P.
PR 14-NOV-2000; 2000US-0248819P.
PR 09-FEB-2001; 2001US-0267601P.
XX
PA (ARIZ-) ARIZEKE PHARM INC.
XX
PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
XX
XX WPI; 2002-416628/44.
XX

Complex useful for transporting active agent through epithelial barrier,
has biologically active portion and target element directed to ligand
that confers e.g. transcytotic properties to agent specific to ligand.

Disclosure; Page 90; 379pp; English.

The invention described a complex or compound (I) comprising a
biologically active portion and a target element (II) directed to a
ligand that confers transcellular, transcytotic or paracellular
transporting properties to an agent specifically bound to the ligand,
where (II) is not an antibody. Alternatively, (I) comprises two or more
(II) directed to one or more ligands. (I) is useful for delivering a
biologically active agent to an animal, for transporting an active agent
through an epithelial or mucosal barrier, and for treating or identifying
a disease in an animal e.g. diseases of the respiratory system including
lung cancer and tumours, asthma, pathogenic infections, allergy-related
disorders, gastrointestinal tract disorders, disorders relating to
gastrointestinal hormones, Chron's disease, eating disorders and any
disease or disorder involving polyimmunoglobulin receptor (pIgR)
displaying cells. This sequence represents an RNA associated with the
transport of biologically active agents across cellular barriers

SQ Sequence 15 BP; 3 A; 6 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGGCTTCAT 14
| | | | |
Db 14 GGGAGCGGCTTCAT 1

RESULT 16
ABK81201/c
ID ABK81201 standard; DNA; 15 BP.

AC ABK81201;
XX
DT 13-AUG-2002 (first entry)
XX
DE Polyimmunoglobulin receptor (pIgR) associated polynucleotide #3.
XX
KW Transcellular transport; transcytotic transport; paracellular transport;
KW respiratory system disorder; lung cancer; tumour; asthma;
KW pathogenic infection; allergy-related disorder;
KW gastrointestinal tract disorder; gastrointestinal hormone disorder;
KW Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR; ds.
XX
OS Unidentified.
XX
FN WO200228408-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030832.
XX
PR 02-OCT-2000; 2000US-0237929P.
PR 13-NOV-2000; 2000US-0248478P.
PR 14-NOV-2000; 2000US-0248819P.
PR 09-FEB-2001; 2001US-0267601P.
XX
PA (ARIZ-) ARIZEKE PHARM INC.
XX
PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
XX
XX WPI; 2002-416628/44.
XX
DR P-PSDB; ABG60649.
XX

Complex useful for transporting active agent through epithelial barrier,
has biologically active portion and target element directed to ligand
that confers e.g. transcytotic properties to agent specific to ligand.

Disclosure; Page 90; 379pp; English.

The invention described a complex or compound (I) comprising a
biologically active portion and a target element (II) directed to a
ligand that confers transcellular, transcytotic or paracellular
transporting properties to an agent specifically bound to the ligand,
where (II) is not an antibody. Alternatively, (I) comprises two or more
(II) directed to one or more ligands. (I) is useful for delivering a
biologically active agent to an animal, for transporting an active agent
through an epithelial or mucosal barrier, and for treating or identifying
a disease in an animal e.g. diseases of the respiratory system including
lung cancer and tumours, asthma, pathogenic infections, allergy-related
disorders, gastrointestinal tract disorders, disorders relating to
gastrointestinal hormones, Chron's disease, eating disorders and any
disease or disorder involving polyimmunoglobulin receptor (pIgR)
displaying cells. This sequence represents a polynucleotide associated
with the transport of biologically active agents across cellular barriers

SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGGCTTCAT 14
| | | | |
Db 14 GGGAGCGGCTTCAT 1

```
RESULT 17
ABK81200/c
ID ABK81200 standard; RNA; 15 BP.
XX
XX AC ABK81200;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE Polyimmunoglobulin receptor (pIgR) associated RNA #1.
XX
XX KW Transcellular transport; transcytotic transport; paracellular transport;
XX respiratory system disorder; lung cancer; tumour; asthma;
XX pathogenic infection; allergy-related disorder;
XX gastrointestinal tract disorder; gastrointestinal hormone disorder;
XX Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR; ss.
XX
XX OS Unidentified.
XX
XX PN W0200228408-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 02-OCT-2001; 2001WO-US030832.
XX
XX PR 02-OCT-2000; 2000US-0237929P.
XX
XX PR 13-NOV-2000; 2000US-0248478P.
XX
XX PR 14-NOV-2000; 2000US-0248819P.
XX
XX PR 09-FEB-2001; 2001US-0267601P.
XX
XX PA (ARIZ-) ARIZEKE PHARM INC.
XX
XX PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
XX
XX DR WPI; 2002-416628/44.
XX
XX PT Complex useful for transporting active agent through epithelial barrier,
XX has biologically active portion and target element directed to ligand
XX that confers e.g. transcytotic properties to agent specific to ligand.
XX
XX PS Disclosure; Page 89; 379pp; English.
XX
XX CC The invention described a complex or compound (I) comprising a
XX biologically active portion and a target element (II) directed to a
XX ligand that confers transcellular, transcytotic or paracellular
XX transporting properties to an agent specifically bound to the ligand,
XX where (II) is not an antibody. Alternatively, (I) comprises two or more
XX (II) directed to one or more ligands. (I) is useful for delivering a
XX biologically active agent to an animal, for transporting an active agent
XX through an epithelial or mucosal barrier, and for treating or identifying
XX a disease in an animal e.g. diseases of the respiratory system including
XX lung cancer and tumours, asthma, pathogenic infections, allergy-related
XX disorders, gastrointestinal tract disorders, disorders relating to
XX gastrointestinal hormones, Chron's disease, eating disorders and any
XX disease or disorder involving polyimmunoglobulin receptor (pIgR)
XX displaying cells. This sequence represents an RNA associated with the
XX transport of biologically active agents across cellular barriers
XX
XX SQ Sequence 15 BP; 3 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 60.0%; Score 10.8; DB 1; Length 15;
XX Best Local Similarity 85.7%; Pred. No. 73;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 GTGAGCGGCTTCAT 14
XX | | | | | | | |
XX 14 GGGAGCGGCTTCAT 1
XX
XX Db
XX
XX RESULT 18
XX ABK81199/c
XX ID ABK81199 standard; DNA; 15 BP.
XX
```

```
XX
XX AC ABK81199;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE Polyimmunoglobulin receptor (pIgR) associated polynucleotide #2.
XX
XX KW Transcellular transport; transcytotic transport; paracellular transport;
XX respiratory system disorder; lung cancer; tumour; asthma;
XX pathogenic infection; allergy-related disorder;
XX gastrointestinal tract disorder; gastrointestinal hormone disorder;
XX Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR; ds.
XX
XX OS Unidentified.
XX
XX PN W0200228408-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 02-OCT-2001; 2001WO-US030832.
XX
XX PR 02-OCT-2000; 2000US-0237929P.
XX
XX PR 13-NOV-2000; 2000US-0248478P.
XX
XX PR 14-NOV-2000; 2000US-0248819P.
XX
XX PR 09-FEB-2001; 2001US-0267601P.
XX
XX PA (ARIZ-) ARIZEKE PHARM INC.
XX
XX PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
XX
XX DR WPI; 2002-416628/44.
XX
XX DR P-PSDB; ABG60648.
XX
XX PT Complex useful for transporting active agent through epithelial barrier,
XX has biologically active portion and target element directed to ligand
XX that confers e.g. transcytotic properties to agent specific to ligand.
XX
XX PS Disclosure; Page 89; 379pp; English.
XX
XX CC The invention described a complex or compound (I) comprising a
XX biologically active portion and a target element (II) directed to a
XX ligand that confers transcellular, transcytotic or paracellular
XX transporting properties to an agent specifically bound to the ligand,
XX where (II) is not an antibody. Alternatively, (I) comprises two or more
XX (II) directed to one or more ligands. (I) is useful for delivering a
XX biologically active agent to an animal, for transporting an active agent
XX through an epithelial or mucosal barrier, and for treating or identifying
XX a disease in an animal e.g. diseases of the respiratory system including
XX lung cancer and tumours, asthma, pathogenic infections, allergy-related
XX disorders, gastrointestinal tract disorders, disorders relating to
XX gastrointestinal hormones, Chron's disease, eating disorders and any
XX disease or disorder involving polyimmunoglobulin receptor (pIgR)
XX displaying cells. This sequence represents a polynucleotide associated
XX with the transport of biologically active agents across cellular barriers
XX
XX SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 10.8; DB 1; Length 15;
XX Best Local Similarity 85.7%; Pred. No. 73;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 GTGAGCGGCTTCAT 14
XX | | | | | | | |
XX 14 GGGAGCGGCTTCAT 1
XX
XX Db
XX
XX RESULT 19
XX ABK32333/c
XX ID ABK32333 standard; DNA; 15 BP.
XX
XX XX ABK32333;
XX
XX AC ABK32333;
XX
XX DT 23-APR-2002 (first entry)
XX
```



```
XX DE Human colon cancer SAGE tag #434.
XX PF Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX KW cancer marker; ss.
XX OS Homo sapiens.
XX PN US6333152-B1.
XX PD 25-DEC-2001.
XX PF 20-MAY-1998; 98US-00081646.
XX PR 20-MAY-1998; 98US-00081646.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX DR WPI; 2002-153821/20.
XX PT New human nucleic acid containing specific SAGE tags, useful as
XX PT diagnostic markers for cancer, also derived probes.
XX PS Disclosure; Col 50; 161pp; English.
XX CC The invention relates to an isolated, purified human nucleic acid (I)
XX CC that has the same sequence as a mRNA found in humans and is a SAGE
XX CC (serial analysis of gene expression) tag comprising a single stranded
XX CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX CC diagnostic and prognostic markers of cancer, especially of the colon and
XX CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX CC SAGE tags of the invention
XX SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
    Query Match 60.0%; Score 10.8; DB 1; Length 15;
    Best Local Similarity 85.7%; Pred. No. 73;
    Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGGCTTCAT 14
Db 15 GTGAGCGGCTTCAT 2
RESULT 20
ABQ83715/c
ID ABQ83715 standard; DNA; 15 BP.
XX AC ABQ83715;
XX DT 28-JAN-2003 (first entry)
XX DE Exemplary DNA oligonucleotide sequence.
XX KW Trans epithelial transport; membrane bound vesicle; virion; liposome;
XX KW envelope; capsid; transmembrane domain; gene therapy; immunostimulant;
XX KW cytosolic; haemostatic; neuroprotective; antirheumatic; antiarthritic;
XX KW anticancer; antibacterial; anti-HIV; hepatotropic; virucide; exocytosis;
XX KW antiinflammatory; apical endocytosis; basolateral endocytosis; ADA-SCID;
XX KW transcytosis; monogenic disease; ADA deficiency; cystic fibrosis; ALS;
XX KW X-linked severe combined immunodeficiency; Haemophilia B; cancer; HIV;
XX KW chronic granulomatous disease; coronary artery disease; viral infection;
XX KW amyotrophic lateral sclerosis; rheumatoid arthritis; hepatitis; Herpes;
XX KW pathogenic disorder; human immunodeficiency virus; bacterial infection;
XX KW polyimmunoglobulin receptor; ss.
XX OS Synthetic.
XX PN WO200283840-A2.
```

```
XX PD 24-OCT-2002.
XX PF 03-APR-2002; 2002WO-US010647.
XX PR 03-APR-2001; 2001US-0281275P.
XX PA (ARIZ-) ARIZEKE PHARM INC.
XX PI Sheridan PL, Houston LL;
XX DR WPI; 2003-046923/04.
XX PT Fusion protein which confers the ability to penetrate epithelial cell
XX PT layer and to undergo paracellular transport, has a trans epithelial
XX PT delivery element and a transmembrane domain from different proteins.
XX PS Disclosure; Page 39; 160pp; English.
XX CC The present invention describes a fusion protein (I) comprising a
XX CC trans epithelial delivery element (TDE) from a first protein and a
XX CC transmembrane domain from a second protein, or comprising TDE and a viral
XX CC sequence that confers the ability to be associated with or incorporated
XX CC into an envelope or capsid protein of a virus. (I) has immunostimulant,
XX CC cytosolic, haemostatic, neuroprotective, antirheumatic, antiarthritic,
XX CC anticancer, antibacterial, anti-HIV, hepatotropic, virucide and
XX CC antiinflammatory activities, and can be used in gene therapy. (I) confers
XX CC the ability to undergo apical endocytosis, basolateral endocytosis,
XX CC apical or basolateral exocytosis, apical to basolateral transcytosis and
XX CC basolateral to apical transcytosis. Diseases treatable by gene therapy
XX CC include monogenic diseases such as X-linked severe combined
XX CC immunodeficiency, ADA deficiency (ADA-SCID), cystic fibrosis, Haemophilia
XX CC B, chronic granulomatous disease, cancers such as ovarian cancer, other
XX CC diseases such as coronary artery disease, amyotrophic lateral sclerosis
XX CC (ALS), rheumatoid arthritis, pathogenic disorders, including human
XX CC immunodeficiency virus (HIV), viral infections, hepatitis, non-specific
XX CC bacterial infection, tuberculosis, Herpes, Chlamydia and
XX CC gastrointestinal ulcer. The present sequence represents an
XX CC oligonucleotide which is given in the exemplification of the present
XX CC invention
XX SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
    Query Match 60.0%; Score 10.8; DB 1; Length 15;
    Best Local Similarity 85.7%; Pred. No. 73;
    Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGGCTTCAT 14
Db 14 GGGAGCGGCTTCAT 1
RESULT 21
ABQ83716/c
ID ABQ83716 standard; RNA; 15 BP.
XX AC ABQ83716;
XX DT 28-JAN-2003 (first entry)
XX DE Exemplary RNA oligonucleotide sequence.
XX KW Trans epithelial transport; membrane bound vesicle; virion; liposome;
XX KW envelope; capsid; transmembrane domain; gene therapy; immunostimulant;
XX KW cytosolic; haemostatic; neuroprotective; antirheumatic; antiarthritic;
XX KW anticancer; antibacterial; anti-HIV; hepatotropic; virucide; exocytosis;
XX KW antiinflammatory; apical endocytosis; basolateral endocytosis; ADA-SCID;
XX KW transcytosis; monogenic disease; ADA deficiency; cystic fibrosis; ALS;
XX KW X-linked severe combined immunodeficiency; Haemophilia B; cancer; HIV;
XX KW chronic granulomatous disease; coronary artery disease; viral infection;
XX KW amyotrophic lateral sclerosis; rheumatoid arthritis; hepatitis; Herpes;
XX KW pathogenic disorder; human immunodeficiency virus; bacterial infection;
XX KW tuberculosis; Chlamydia; gastrointestinal ulcer; piGR;
```

KW polyimmunoglobulin receptor; ss.
 XX Synthetic.
 OS
 XX WO200283840-A2.
 FN
 XX 24-OCT-2002.
 PD
 XX
 XX 03-APR-2002; 2002WO-US010647.
 PF
 XX 03-APR-2001; 2001US-0281275P.
 PR
 XX (ARIZ-) ARIZEKE PHARM INC.
 PA
 XX Sheridan PL, Houston LL;
 PI
 XX WPI; 2003-046923/04.
 DR
 XX
 XX Fusion protein which confers the ability to penetrate epithelial cell
 PT layer and to undergo paracellular transport, has a transmembrane
 PT delivery element and a transmembrane domain from different proteins.
 XX
 XX Disclosure; Page 39; 160pp; English.
 PS
 XX The present invention describes a fusion protein (I) comprising a
 CC transmembrane delivery element (TDE) from a first protein and a
 CC transmembrane domain from a second protein, or comprising TDE and a
 CC sequence that confers the ability to be associated with or incorporated
 CC into an envelope or capsid protein of a virus. (I) has immunostimulant,
 CC cytosstatic, haemostatic, neuroprotective, antirheumatic, antiarthritic,
 CC anticancer, antibacterial, anti-HIV, hepatotropic, virucide and
 CC antiinflammatory activities, and can be used in gene therapy. (I) confers
 CC the ability to undergo apical endocytosis, basolateral endocytosis,
 CC apical or basolateral exocytosis, apical to basolateral transcytosis and
 CC basolateral to apical transcytosis. Diseases treatable by gene therapy
 CC include monogenic diseases such as X-linked severe combined
 CC immunodeficiency, ADA deficiency (ADA-SCID), cystic fibrosis, Haemophilia
 CC B, chronic granulomatous disease, cancers such as ovarian cancer, other
 CC diseases such as coronary artery disease, amyotrophic lateral sclerosis
 CC (ALS), rheumatoid arthritis, pathogenic disorders, including human
 CC immunodeficiency virus (HIV), viral infections, hepatitis, non-specific
 CC bacterial infection, tuberculosis, Herpes, Chlamydia, and
 CC gastrointestinal ulcer. The present sequence represents an
 CC oligonucleotide which is given in the exemplification of the present
 CC invention
 XX
 XX Sequence 15 BP; 3 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
 SQ

Query Match 60.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 73;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGAGCGGACTTCAT 14
 Db 14 GGGAGCGGCTTCAT 1

RESULT 22
 AAF52638/c
 ID AAF52638 standard; DNA; 15 BP.
 XX
 XX AAF52638;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #3598.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS

KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI
 XX WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 8; Page 84; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 XX Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 57.8%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 89;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCCTT 18
 Db 12 GACTCCATCCTT 1

RESULT 23
 AAF52635/c
 ID AAF52635 standard; DNA; 15 BP.
 XX
 XX AAF52635;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #3595.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS

```

XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX DR WPI; 2001-041421/05.
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 84; 201pp; English.
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 57.8%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GACTTCATCCTT 18
DB 15 GACTCCATCCTT 4

RESULT 24
AAF52636/c
ID AAF52636 standard; DNA; 15 BP.
XX AC AAF52636;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #3596.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX OS
XX PN WO200078341-A1.
XX PD 28-DEC-2000.

```

```

XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX DR WPI; 2001-041421/05.
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 84; 201pp; English.
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 57.8%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GACTTCATCCTT 18
DB 14 GACTCCATCCTT 3

RESULT 25
AAF52637/c
ID AAF52637 standard; DNA; 15 BP.
XX AC AAF52637;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #3597.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX OS
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.

```

XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 84; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrheoa, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 SQ Query Match 57.8%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. NO. 89;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 7 GACTTCATCCCTT 18
 DB 13 GACTCCATCCCTT 2
 RESULT 26
 AAC85659
 ID AAC85659 standard; cDNA; 15 BP.
 XX AAC85659;
 AC 29-JUN-2001 (first entry)
 DT HTR1D allele specific primer #2.
 XX 5-hydroxytryptamine receptor 1D; HTR1D; serotonin; polymorphism;
 KW migraine; depression; primer; allele; PCR; polymerase chain reaction;
 KW primer; amplify; ss.
 OS Synthetic.
 XX WO200127311-A2.
 FN 19-APR-2001.
 XX 12-OCT-2000; 2000WO-US028115.
 XX 13-OCT-1999; 99US-0159257P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Choi JY, Denton RR, Nandabalan K, Stephens JC;
 PI WPI; 2001-282045/29.
 XX New variants of the receptor 5-hydroxytryptamine (serotonin) receptor 1D
 PT gene, useful to identify new drugs for migraine and depression have

PT single nucleotide variations at polymorphic sites.
 XX Claim 15; Page 20; 47pp; English.
 XX The sequences given in AAC85658-69 are allele-specific primers which were
 CC used to identify different gene polymorphisms in the human 5-
 CC hydroxytryptamine (serotonin) receptor 1D (HTR1D) gene. The HTR1D gene
 CC has been discovered to contain 2 new polymorphic sites, 186(A/G) and
 CC 1367(C/G), along with the already known 1350(T/C). The reference sequence
 CC may be used for studying the biological function of HTR1D, and to
 CC identify drugs that target HTR1D for the treatment of disorders related
 CC to it's abnormal expression or function. Such drugs may be used to treat
 CC migraine and other neurological disorders, and depression
 XX SQ Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 56.7%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 98;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 4 AGCGACTTCATCCCTT 18
 DB 1 AGCAAAGTCATCCCTT 15
 RESULT 27
 AAZ78865/C
 ID AAZ78865 standard; DNA; 10 BP.
 XX AAZ78865;
 AC 10-APR-2000 (first entry)
 DT Human dendritic cell SAGE tag, SEQ ID NO:1293.
 XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 DE APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX Homo sapiens.
 OS WO9965924-A2.
 FN 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013800.
 XX 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089911P.
 PR 19-JUN-1998; 98US-0089922P.
 PR 19-JUN-1998; 98US-0089933P.
 PR 19-JUN-1998; 98US-0089944P.
 PR 19-JUN-1998; 98US-0089972P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.

PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE//) ROBERTS B L.
 PA (SHAN//) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 DR
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 102; 130pp; English.
 PS
 XX Sequences AA27573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 55.6%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGAGCGACTT 11
 |||||
 DB 10 TGAGCGACTT 1
 RESULT 28
 ABI77129
 ID ABI77129 standard; DNA; 12 BP.
 XX
 AC ABI77129;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 377102 for detecting SNP TSC0007081.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Claim 1; SEQ ID NO 377102; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 55.6%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACTTCATCCT 17
 |||||
 DB 3 ACTTCATCCT 12
 RESULT 29
 ABI09824/c
 ID ABI09824 standard; DNA; 12 BP.
 XX
 AC ABI09824;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 309797 for detecting SNP TSC0023682.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX

```

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 309797; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCT 17
Db 11 ACTTCATCCT 2
|||||
|
RESULT 30
ABI79247/c
ID ABI79247 standard; DNA; 12 BP.
XX
XX AC ABI79247;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 379220 for detecting SNP TSC0063134.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide primer SEQ ID NO 379220 for detecting SNP TSC0063134.
XX
XX PA SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX PI (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX FN Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 379220; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCT 17
Db 11 ACTTCATCCT 2
|||||
|
RESULT 31
ABI11698/c
ID ABI11698 standard; DNA; 12 BP.
XX
XX AC ABI11698;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 311671 for detecting SNP TSC0024607.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide primer SEQ ID NO 311671 for detecting SNP TSC0024607.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX FN Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 311671; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCT 17
Db 12 ACTTCATCCT 3
|||||
|
RESULT 31
ABI11698/c
ID ABI11698 standard; DNA; 12 BP.
XX
XX AC ABI11698;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 311671 for detecting SNP TSC0024607.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide primer SEQ ID NO 311671 for detecting SNP TSC0024607.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX FN Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 311671; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCT 17
Db 12 ACTTCATCCT 3
|||||
|

```

```
Query Match      55.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACTTCATCCT 17
DB      11 ACTTCATCCT 2
      |||||
RESULT 32
ABH44338/c
ID ABH44338 standard; DNA; 13 BP.
AC ABH44338;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 244315 for detecting SNP TSC0059630.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 244315; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match      55.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACTTCATCCT 17
DB      11 ACTTCATCCT 2
      |||||
RESULT 33
ABH44339
ID ABH44339 standard; DNA; 13 BP.
AC ABH44339;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 205723 for detecting SNP TSC0050425.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 244315; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
```

```

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 205723; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 98;
XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 7 GACTTCATCCTT 18
Db :|||||||
13 RACTTCATCATT 2

RESULT 35
ABH05747
ID ABH05747 standard; DNA; 13 BP.
XX
XX ABH05747;
AC
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 205724 for detecting SNP TSC0050425.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 205723; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 55.6%; Score 10; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 98;
XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 7 GACTTCATCCTT 18
Db :|||||||
13 RACTTCATCATT 2

RESULT 36
AAQ51865/C
ID AAQ51865 standard; RNA; 14 BP.
XX
XX AAQ51865;
AC
XX 25-MAR-2003 (revised)
DT
XX 26-MAY-1994 (first entry)
DT
XX
XX PML mRNA ribozyme cleavable nucleotide 1069.
DE
XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CMU; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9323057-A1.
XX
XX 25-NOV-1993.
XX
XX 13-MAY-1993; 93WO-US004573.
XX
XX 14-MAY-1992; 92US-00882822.
XX
XX 14-MAY-1992; 92US-00882885.
XX
XX 26-AUG-1992; 92US-00936110.
XX
XX 26-AUG-1992; 92US-00936421.
XX
XX 26-AUG-1992; 92US-00936422.
XX
XX 26-AUG-1992; 92US-00936531.
XX
XX 26-AUG-1992; 92US-00936532.
XX
XX 07-DEC-1992; 92US-00987131.
XX
XX 19-JAN-1993; 93US-00006122.
XX
XX 19-JAN-1993; 93US-00008910.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Draper KG;
PI

```


XX WPI; 1993-386203/48.
 XX
 XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
 PT with tumours or mRNA expressed from gene encoding multiple drug
 PT resistance.
 XX
 XX Claim 3; Fig 4; 69pp; English.
 PS
 XX The sequences given in AAQ51825-2266 represent areas of mRNAs associated
 CC with development or maintenance of chronic myelogenous leukemia (CML),
 CC promyelocytic leukemia, Burkitt's lymphoma, or acute lymphocytic
 CC leukemia, follicular lymphoma, B-cell acute lymphocytic leukemia, breast
 CC cancer, colon carcinoma, neuroblastoma and lung cancer. The full length
 CC mRNAs containing these target sequences, encode aberrant cellular proteins
 CC which are able to control cellular proliferation and are directly linked
 CC to a leukemic phenotype. These target sequences are identified by the
 CC ribozyme of the invention. The ribozymes are formed in a hammerhead motif,
 CC but may also be formed in the motif of a hairpin, hepatitis delta virus,
 CC group I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and other
 CC animals by modulating expression of the corresponding gene. Cleavage of
 CC target mRNAs expressed in pre-neoplastic and transformed cells elicits
 CC inhibition of the transformed state. Multiple drug resistance (mdr-1)
 CC mRNA specific ribozymes remove the mechanism of drug resistance used by
 CC transformed cells and thus enhances drug therapies for tumours. The
 CC ribozymes may also be used to study genetic drift and mutations within
 CC cells. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 14 BP; 5 A; 1 C; 5 G; 0 T; 3 U; 0 Other;
 SQ

Query Match 55.6%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 ACTTCATCCT 17
 |||||
 Db 10 ACTTCATCCT 1

RESULT 37
 AAZ62824/C
 ID AAZ62824 standard; RNA; 15 BP.
 XX
 XX AAZ62824;
 AC
 XX
 DT 28-MAR-2000 (first entry)
 XX
 DE Substrate for HH ribozyme HCV-8366 which cleaves HCV RNA at nt. 8366.
 XX
 XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 FN WO9955847-A2.
 XX
 XX 04-NOV-1999.
 XX
 XX 26-APR-1999; 99WO-US009027.
 XX
 XX 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 98US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 PI
 XX WPI; 2000-062023/05.
 XX
 XX

PT Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX
 XX Claim 1; Page 64; 123pp; English.
 PS
 XX The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 XX Sequence 15 BP; 3 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
 SQ

Query Match 55.6%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGAGCGGACT 10
 |||||
 Db 10 GTGAGCGGACT 1

RESULT 38
 ABX00675/C
 ID ABX00675 standard; RNA; 15 BP.
 XX
 XX ABX00675;
 AC
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #457 for HCV hammerhead ribozyme #457.
 XX
 XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virocid;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 FN US2002082225-A1.
 XX
 XX 27-JUN-2002.
 PD
 XX 23-MAR-1999; 99US-00274553.
 XX
 XX 23-MAR-1999; 99US-00274553.
 PR
 XX (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
 PI
 XX WPI; 2002-617759/66.
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 PT replication and are useful to treat hepatitis C virus infections and
 PT cirrhosis, liver failure or hepatocellular carcinoma.
 XX

PS Claim 1; Page 34; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html

XX Sequence 15 BP; 3 A; 5 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACT 10

Db 10 GTGAGCGGACT 1

RESULT 39

ABCO1449

ID ABCO1449 standard; DNA; 13 BP.

AC ABCO1449;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 1440 for detecting SNP TSC0000506.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 1440; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCCTT 18

Db 1 CCACTACATCCTT 13

RESULT 40

ABH13586/C

ID ABH13586 standard; DNA; 13 BP.

XX ABH13586;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 213563 for detecting SNP TSC0052006.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 213563; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCCTT 18

```

Db      || ||||| |||
      13 CGCCTTCATCCTT 1

RESULT 41
ABH13587
ID ABH13587 standard; DNA; 13 BP.
XX AC
XX ABH13587;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 213564 for detecting SNP TSC0052006.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotide SEQ ID NO 213564 for detecting SNP TSC0052006.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 213564; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 1.1e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATCCTT 18
XX Db ||||| |||
XX 1 CGCCTTCATCCTT 13

RESULT 42
ABC01448/c
ID ABC01448 standard; DNA; 13 BP.
XX AC
XX ABC01448;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 1439 for detecting SNP TSC0000506.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 213564; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 9.8; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 1.1e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATCCTT 18
XX Db ||||| |||
XX 1 CGCCTTCATCCTT 13

RESULT 43
AAQ83299/c
ID AAQ83299 standard; DNA; 14 BP.
XX AC
XX AAQ83299;
XX
XX 25-MAR-2003 (revised)
XX 20-SEP-1995 (first entry)
XX
XX c-jun antisense oligonucleotide.
XX
XX c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
XX phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO9502051-A2.
XX
XX 19-JAN-1995.
XX
XX 06-JUL-1994; 94WO-EP002218.
XX
XX

```

```

PR 10-JUL-1993; 93EP-00111059.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
XX WPI; 1995-066896/09.
XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT treating neuronal injury, degeneration, cell death and/or neoplasms.
XX Claim 2; Page 30; 86pp; English.
XX Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC causal role in neuronal injury, degeneration, cell death and/or
CC neoplasms, can be used to prevent and treat such conditions. c-jun
CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC Preferably the antisense sequences are phosphorothioate oligonucleotides
CC since these are not destroyed as fast by endogenous factors as naturally
CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 14 BP; 2 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATCC 16
Db 13 AGCACTTCAACC 1

RESULT 44
AAAX31544/c
ID AAAX31544 standard; DNA; 15 BP.
XX
AC AAAX31544;
XX
XX 21-MAY-1999 (first entry)
XX
XX Tag sequence of a transcript increased in pancreatic cancer.
XX
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX
XX Homo sapiens.
XX
XX WO9853319-A2.
XX
XX 26-NOV-1998.
XX
XX 20-MAY-1998; 98WO-US010277.
XX
XX 21-MAY-1997; 97US-0047352P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW;
XX
XX WPI; 1999-070161/06.
XX
XX Use of isolated gene transcripts - useful for developing products for the
PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX
XX Claim 13; Page 60; 120pp; English.
XX
XX AAAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic cancer, or
CC in both. The tag sequences can be used to identify genes by matching the

tag to a gen data base member, or by using the tag sequences as probes to
CC isolate unidentified genes from cDNA libraries. The tag sequences can
CC also be used in a method for diagnosing colon or pancreatic cancer in a
CC sample suspected of being neoplastic. The method comprises comparing the
CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.
CC The transcript is identified by a tag selected from AAAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer
XX
SQ Sequence 15 BP; 4 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGACGCGACTTCAT 14
Db 14 TGAGAGACTGCAT 2

RESULT 45
AAAZ62650
ID AAZ62650 standard; RNA; 15 BP.
XX
AC AAZ62650;
XX
XX 28-MAR-2000 (first entry)
XX
XX Substrate for HH ribozyme HCV-4697 which cleaves HCV RNA at nt. 4697.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX
XX 18-SEP-1998; 98US-0100842P.
XX
XX 25-FEB-1999; 99US-00257608.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 58; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with

```

CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer

SQ Sequence 15 BP; 3 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|:|:|:|:|:|:|:
Db 3 GUGAUCGACUGCA 15

RESULT 46
ABK32498/c
ID ABK32498 standard; DNA; 15 BP.

XX AC ABK32498;

XX DT 23-APR-2002 (first entry)

XX DE Human pancreatic cancer SAGE tag #50.

XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX KW cancer marker; ss.

XX OS Homo sapiens.

XX PN USG333152-B1.

XX PD 25-DEC-2001.

XX PF 20-MAY-1998; 98US-00081646.

XX PR 20-MAY-1998; 98US-00081646.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;

XX DR WPI; 2002-153821/20.

XX PT New human nucleic acid containing specific SAGE tags, useful as
XX PT diagnostic markers for cancer, also derived probes.

XX PS Disclosure; Col 69; 161pp; English.

XX CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention

SQ Sequence 15 BP; 4 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
|:|:|:|:|:|:|:
Db 14 TGAGAGACTGCAT 2

RESULT 47
ABX00501
ID ABX00501 standard; RNA; 15 BP.

XX AC ABX00501;

XX DT 23-DEC-2002 (first entry)

XX DE Hepatitis C virus substrate #283 for HCV hammerhead ribozyme #283.

XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX KW type I interferon; interferon alpha; interferon beta; cytosolic;
XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.

XX PN US2002082225-A1.

XX PD 27-JUN-2002.

XX PF 23-MAR-1999; 99US-00274553.

XX PR 23-MAR-1999; 99US-00274553.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PA (ROBE/) ROBERTS B.

XX PA (PAVC/) PAVCO P A.

XX PA (MACE/) MACEJACK D.

XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;

XX DR WPI; 2002-617759/66.

XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX PT replication and are useful to treat hepatitis C virus infections and
XX PT cirrhosis, liver failure or hepatocellular carcinoma.

XX PS Claim 1; Page 29; 80pp; English.

XX CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipdbIDentry.html

XX SQ Sequence 15 BP; 3 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
|:|:|:|:|:|:|:
Db 3 GUGAUCGACUGCA 15

RESULT 48
ABQ84087.
ID ABQ84087 standard; DNA; 15 BP.

XX AC ABQ84087;

XX DT 18-FEB-2003 (first entry)

XX RpoB probe M6.
XX
XX
XX Tubercle bacillus; diagnosis; probe; rpoB; DNA chip; drug tolerance;
KW deoxyribonucleic acid chip; ss.
XX
XX Bacillus sp.
XX
XX CN1351176-A.
XX
XX 29-MAY-2002.
XX
XX 31-OCT-2000; 2000CN-00133796.
XX
XX 31-OCT-2000; 2000CN-00133796.
XX
XX (MENG/) MENG SU Y.
XX
XX WPI; 2002-644410/70.
XX
XX DNA chip for diagnosing tubercle bacillus and its drug tolerance.
XX
XX
XX Disclosure; Fig 2; 15pp; Chinese.
XX
XX ABQ84043 to ABQ84083 represent specifically claimed DNA probes which can
CC be used in a deoxyribonucleic acid (DNA) chip (I) comprising 12-100 DNA
CC probes fixed to a glass plate, silicon chip, membrane or high-molecular
CC material. (I) is useful for diagnosing tubercle bacillus and its drug
CC tolerance. (I) has a high diagnosing efficiency and accuracy, low cost
CC and short detection time. The present sequence represents an rpoB probe
CC which is used in the exemplification of the present invention
XX
XX Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
SQ

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCAATTCAT 15

RESULT 49
ABQ84046
ID ABQ84046 standard; DNA; 15 BP.
XX
XX AC ABQ84046;
XX
XX 18-FEB-2003 (first entry)
XX
XX Tubercle bacillus diagnosis probe W4.
XX
XX Tubercle bacillus; diagnosis; probe; rpoB; DNA chip; drug tolerance;
KW deoxyribonucleic acid chip; ss.
XX
XX Bacillus sp.
XX
XX CN1351176-A.
XX
XX 29-MAY-2002.
XX
XX 31-OCT-2000; 2000CN-00133796.
XX
XX 31-OCT-2000; 2000CN-00133796.
XX
XX (MENG/) MENG SU Y.
XX
XX WPI; 2002-644410/70.
XX
XX DNA chip for diagnosing tubercle bacillus and its drug tolerance.
XX
XX Claim 1; Page 1 (Claims); 15pp; Chinese.

XX
CC ABQ84043 to ABQ84083 represent specifically claimed DNA probes which can
CC be used in a deoxyribonucleic acid (DNA) chip (I) comprising 12-100 DNA
CC probes fixed to a glass plate, silicon chip, membrane or high-molecular
CC material. (I) is useful for diagnosing tubercle bacillus and its drug
CC tolerance. (I) has a high diagnosing efficiency and accuracy, low cost
CC and short detection time
XX
XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCAATTCAT 15

RESULT 50
ACC73410
ID ACC73410 standard; DNA; 15 BP.
XX
XX AC ACC73410;
XX
XX 15-JUL-2003 (first entry)
XX
XX Mycobacterium antibiotic resistance differentiating probe rpo 513-WQ.
DE
XX Mycobacterium probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
KW
XX Mycobacterium sp.
XX
XX WO2003031654-A1.
XX
XX 17-APR-2003.
XX
XX 09-OCT-2002; 2002WO-KR001885.
XX
XX 09-OCT-2001; 2001KR-00062125.
XX
XX (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C.
PA (PARK/) PARK H.
XX
XX Kim C, Park H, Jang H, Song E;
XX
XX WPI; 2003-403109/38.
XX
XX Microarray for simultaneously genotyping Mycobacteria species,
PT differentiating Mycobacterium tuberculosis strains and detecting
PT antibiotic-resistant strains, comprises specific probes on a support.
XX
XX Claim 14; Page 68; 76pp; English.
XX
XX The invention relates to a microarray comprising a support, a first probe
CC for genotyping Mycobacterium species, second probe for differentiating
CC Mycobacterium tuberculosis strains, and a third probe for detecting
CC antibiotic-resistant strains, where the probes are immobilized on the
CC support. This sequence represents an example of the third probe used for
CC detecting antibiotic resistance in Mycobacterium strains. The array is
CC useful for simultaneously genotyping Mycobacterium species,
CC differentiating M. tuberculosis strains and detecting antibiotic-
CC resistant strains
XX
XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCAATTCAT 15

Df 2 TGAGCCATTCAT 14

RESULT 51
ADC33596
ID ADC33596 standard; DNA; 15 BP.
XX
AC ADC33596;
XX
XX 18-DEC-2003 (first entry)
XX
XX M. tuberculosis oligonucleotide probe #4.
DE
XX ss; probe; rifampin resistance; rpoB; tuberculosis.
KW
XX Mycobacterium tuberculosis.
OS
XX US2003104387-A1.
PN
XX 05-JUN-2003.
PD
XX 07-SEP-2001; 2001US-00949041.
PF
XX 07-SEP-2001; 2001US-00949041.
PR
XX (YANG/) YANG M.
PA (WOOH/) WOO H S.
PA Yang M, Woo HS;
PI
XX WPI; 2003-787043/74.
DR
XX Detecting tendency to rifampin resistance caused by mutation in RNA polymerase beta-subunit gene of Mycobacterium tuberculosis.
PT
XX Claim 19; SEQ ID NO 7; 27pp; English.
PS
XX The invention relates to a method of detecting a tendency to rifampin resistance caused by mutations in rpoB gene of Mycobacterium tuberculosis comprising extracting DNA from M. tuberculosis cells, amplifying rpoB gene to produce fluorescently labelled product, contacting the labelled product with first and second array of oligonucleotide probes, detecting fluorescent hybridisation signal and correlating with tendency to rifampin resistance. The method is useful for detecting a tendency to rifampin resistance caused by mutations in a rpoB gene of M. tuberculosis. The method is easy to perform and is cost effective to be performed on a large-scale basis. The results produced are reliable and readily detectable. The method is easily adaptable to automation. The present sequence represents a M. tuberculosis probe.

XX
SQ Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.8%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGCGACTTTCAT 14
Db 3 TGAGCCATTCAT 15
|||||
|||

RESULT 52
ABC71483
ID ABC71483 standard; DNA; 13 BP.
XX
AC ABC71483;
XX
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 71500 for detecting SNP TSC0018510.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW (EPIG-) EPIGENOMICS AG.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic
XX Homo sapiens.
OS WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
PT
XX Claim 1; SEQ ID NO 71500; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI99989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
Query Match 53.3%; Score 9.6; DB 1; Length 13;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Oy 7 GACTTCATCC 16
Db 1 RACTTCATCC 10
|||||
|||

RESULT 53
ABC71482/c
ID ABC71482 standard; DNA; 13 BP.
XX
AC ABC71482;
XX
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 71499 for detecting SNP TSC0018510.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 71499; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 53.3%; Score 9.6; DB 1; Length 13;
XX Best Local Similarity 90.0%; Pred. No. 1.2e+02;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 7 GACTTCATCC 16
XX Db 13 RACTTCATCC 4
XX
XX RESULT 54
XX ABF42964/c
XX ID ABF42964 standard; DNA; 13 BP.
XX AC ABF42964;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 142961 for detecting SNP TSC0035861.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 142961; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 1 Other;
XX
XX Query Match 53.3%; Score 9.6; DB 1; Length 13;
XX Best Local Similarity 90.0%; Pred. No. 1.2e+02;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCCT 17
XX Db 13 RCTTCATCCCT 4
XX
XX RESULT 55
XX ABF42965
XX ID ABF42965 standard; DNA; 13 BP.
XX AC ABF42965;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 142962 for detecting SNP TSC0035861.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 142962; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 1 Other;


```

Query Match      53.3%; Score 9.6; DB 1; Length 13;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACTTCATCCT 17
Db      1 RCTTCATCCT 10

RESULT 56
ABF42960/c
ID ABF42960 standard; DNA; 13 BP.
XX
AC ABF42960;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 142957 for detecting SNP TSC0035861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
FS Claim 1; SEQ ID NO 142957; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;

Query Match      53.3%; Score 9.6; DB 1; Length 13;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACTTCATCCT 17
Db      13 RCTTCATCCT 4

RESULT 57
ABF42961
ID ABF42961 standard; DNA; 13 BP.
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 304527 for detecting SNP TSC0020981.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

```

```

XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 304527; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX ||||| |||||
XX 1 ACTTCCTCCTT 11
XX
XX RESULT 59
XX ABH68283
XX ID ABH68283 standard; DNA; 12 BP.
XX
XX AC ABH68283;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 268260 for detecting SNP TSC0001019.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX DE Oligonucleotide primer SEQ ID NO 268260 for detecting SNP TSC0001019.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

```

```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 268260; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATCC 16
XX ||||| |||||
XX 2 CGATTTCATCC 12
XX
XX Db
XX
XX RESULT 60
XX ABI16330
XX ID ABI16330 standard; DNA; 12 BP.
XX
XX AC ABI16330;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 316303 for detecting SNP TSC0027389.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 316303; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 52.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 1 ACTTCATCCTT 11
 |||||
 1 ACTTCATCCTT 11
 RESULT 61
 ABI40174/c
 ID ABI40174 standard; DNA; 12 BP.
 XX
 AC ABI40174;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 340147 for detecting SNP TSC0041367.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 340147; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 52.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18

Db 11 ATTTCATCCTT 1
 |||||
 11 ATTTCATCCTT 1
 RESULT 62
 ABH90125
 ID ABH90125 standard; DNA; 12 BP.
 XX
 AC ABH90125;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 290118 for detecting SNP TSC0014221.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 290118; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 52.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 1 ACTTCATCCTT 11
 |||||
 1 ACTTCATCCTT 11
 RESULT 63
 ABI59049/c
 ID ABI59049 standard; DNA; 12 BP.
 XX
 AC ABI59049;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 359022 for detecting SNP TSC0051426.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 359022; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 11 ACTTCATCATT 1
RESULT 64
ABH68729
ID ABH68729 standard; DNA; 12 BP.
XX
XX ABH68729;
AC
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 268706 for detecting SNP TSC0001326.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX

PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 268706; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 2 ACTTCCTTCCTT 12
RESULT 65
ABI40489/C
ID ABI40489 standard; DNA; 12 BP.
XX
XX ABI40489;
AC
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 340462 for detecting SNP TSC0041544.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 340462; 29pp + Sequence Listing; German.
PS

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
|||||
Db 12 ACTTCCTCCTT 2

RESULT 66
ABI51369
ID ABI51369 standard; DNA; 12 BP.
XX AC ABI51369;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 351342 for detecting SNP TSC0047239.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX PS Claim 1; SEQ ID NO 351342; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
|||||
Db 12 ACTTCCTCCTT 2

RESULT 66
ABI51369
ID ABI51369 standard; DNA; 12 BP.
XX AC ABI51369;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 351342 for detecting SNP TSC0047239.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX PS Claim 1; SEQ ID NO 351342; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
|||||
Db 2 ACTTCCTCCTT 12

RESULT 67
ABI75389
ID ABI75389 standard; DNA; 12 BP.
XX AC ABI75389;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 375362 for detecting SNP TSC0061218.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX PS Claim 1; SEQ ID NO 375362; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
|||||
Db 2 ACATCATCCTT 12

RESULT 68

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 12 ACATCATCCTT 2
|||||

RESULT 71
ABH40385
ID ABH40385 standard; DNA; 13 BP.
XX
XX AC ABH40385;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 240362 for detecting SNP TSC0058636.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 240362; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 2 ACTTCATCCTT 12
|||||

RESULT 72
ABH56983
ID ABH56983 standard; DNA; 13 BP.
XX
XX AC ABH56983;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 256960 for detecting SNP TSC0008901.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 256960; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 3 AATTTCATCCTT 13
|||||

RESULT 73

```
ABC78469
ID ABC78469 standard; DNA; 13 BP.
AC ABC78469;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 78486 for detecting SNP TSC0019989.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 78486; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 CGACTTCATCC 16
XX
XX 3 CCATTCATCC 13
XX
XX RESULT 74
ABC63957
ID ABC63957 standard; DNA; 13 BP.
XX
XX ABC63957;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 63974 for detecting SNP TSC0016888.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 78486; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 CGACTTCATCC 16
XX
XX 3 CCATTCATCC 13
XX
XX RESULT 74
ABC63957
ID ABC63957 standard; DNA; 13 BP.
XX
XX ABC63957;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 63974 for detecting SNP TSC0016888.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 63974; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCTT 18
XX
XX 1 ACTTCATCAT 11
XX
XX RESULT 75
ABC67524/c
ID ABC67524 standard; DNA; 13 BP.
XX
XX ABC67524;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 67541 for detecting SNP TSC0017645.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
```


XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 67541; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGACTTCATCC 16
 DB 12 CGCTTCATCC 2
 RESULT 76
 ABF25609
 ID ABF25609 standard; DNA; 13 BP.
 XX AC ABF25609;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 125606 for detecting SNP TSC0031407.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 125606; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 1 A; 5 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 DB 2 ACTTCGCTT 12
 RESULT 77
 ABF73761
 ID ABF73761 standard; DNA; 13 BP.
 XX AC ABF73761;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 173758 for detecting SNP TSC0043268.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 173758; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;

XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 125605; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 12 ACTTCGTCCTT 2
 ||||| |||||
 RESULT 81
 ABH02049
 ID ABH02049 standard; DNA; 13 BP.
 AC ABH02049;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 202026 for detecting SNP TSC0049668.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
 XX Claim 1; SEQ ID NO 202026; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 52.2%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 3 ACTTCACCTT 13
 ||||| |||||
 RESULT 82
 ABC67525
 ID ABC67525 standard; DNA; 13 BP.
 AC ABC67525;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 67542 for detecting SNP TSC0017645.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 67542; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGCTTCATCC 16
|||
Db 2 CGCTTCATCC 12

RESULT 83
ABH56982/C
ID ABH56982 standard; DNA; 13 BP.

XX AC ABH56982;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 256959 for detecting SNP TSC0008901.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 256959; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18

|||
Db 11 AATTTCATCCTT 1

RESULT 84

ABF34091
ID ABF34091 standard; DNA; 13 BP.

XX AC ABF34091;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 134088 for detecting SNP TSC0033432.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 134088; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18

|||
Db 2 ACTTCATCCTT 12

RESULT 85

ABC67933
ID ABC67933 standard; DNA; 13 BP.

XX AC ABC67933;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 67950 for detecting SNP TSC0017746.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB0000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 67950; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 3 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 3 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 XX
 XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
 XX Best Local Similarity 90.9%; Pred. No. 1.3e+02; Mismatches 0; Gaps 0;
 XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 3 ACTTCATCCTT 13
 ||||| |||
 RESULT 86
 ABC83972/c
 ID ABC83972 standard; DNA; 13 BP.
 XX
 XX AC ABC83972;
 XX
 XX 21-FEB-2002 (first entry)
 DT
 XX
 XX Oligonucleotide SEQ ID NO 83989 for detecting SNP TSC0021128.
 DE
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX
 XX 18-OCT-2001.
 PD
 XX
 XX 06-APR-2001; 2001WO-IB0000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX

PA (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 83989; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
 XX Best Local Similarity 90.9%; Pred. No. 1.3e+02; Mismatches 1; Indels 0; Gaps 0;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCTT 18
 Db 13 ACTTCATCATT 3
 ||||| |||
 RESULT 87
 ABC72103
 ID ABC72103 standard; DNA; 13 BP.
 XX
 XX AC ABC72103;
 XX
 XX 21-FEB-2002 (first entry)
 DT
 XX
 XX Oligonucleotide SEQ ID NO 72120 for detecting SNP TSC0018635.
 DE
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX
 XX 18-OCT-2001.
 PD
 XX
 XX 06-APR-2001; 2001WO-IB0000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 72120; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
|||||
Db 1 CGACTTCATCC 11

RESULT 89
ABC99862/c
ID ABC99862 standard; DNA; 13 BP.

XX AC ABC99862;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 99879 for detecting SNP TSC0024822.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 99879; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX SQ Sequence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 13 ACTTCATCCTT 3

RESULT 89
ABH40384/c
ID ABH40384 standard; DNA; 13 BP.

XX AC ABH40384;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 240361 for detecting SNP TSC0058636.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 240361; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 12 ACTTCATCCTT 2

RESULT 90
ABC67932/c
ID ABC67932 standard; DNA; 13 BP.

```

XX AC ABC67932;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 67949 for detecting SNP TSC0017746.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 67949; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 7 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTCATCCTT 1

RESULT 91
ABC72102/c
ID ABC72102 standard; DNA; 13 BP.
XX AC ABC72102;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 72119 for detecting SNP TSC0018635.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX

```

```

PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 72119; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
Db 13 CGACTTCATCC 3

RESULT 92
ABC83973
ID ABC83973 standard; DNA; 13 BP.
XX AC ABC83973;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 83990 for detecting SNP TSC0021128.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX

```

```
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 83990; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 8 ACTTCATCCTT 18
XX | | | | | | | |
XX 1 ACTTCATCATTT 11
XX
XX RESULT 93
XX ABC44363
XX ID ABC44363 standard; DNA; 13 BP.
XX
XX AC ABC44363;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 44380 for detecting SNP TSC0013030.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 44380; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX
XX QY 6 CGACTTCATCC 16
XX | | | | | | | |
XX 1 CCATTTCATCC 11
XX
XX Db
XX
XX RESULT 94
XX ABC99863
XX ID ABC99863 standard; DNA; 13 BP.
XX
XX AC ABC99863;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 99880 for detecting SNP TSC0024822.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 99880; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 52.2%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 CGACTTCATCC 16
XX | | | | | | | |
XX 1 CCATTTCATCC 11
XX
XX Db
XX
XX RESULT 94
XX ABC99863
XX ID ABC99863 standard; DNA; 13 BP.
XX
XX AC ABC99863;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 99880 for detecting SNP TSC0024822.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 99880; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
```


XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ. ID NO 212548; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 2 ACTTCATCCTT 12
RESULT 99
ID ABF25606 standard; DNA; 13 BP.
XX AC ABF25606;
XX
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 125603 for detecting SNP TSC0031407.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

PS Claim 1; SEQ ID NO 125603; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 12 ACTTCATCCTT 2
RESULT 99
ID ABF34090 standard; DNA; 13 BP.
XX AC ABF34090;
XX
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 134087 for detecting SNP TSC0033432.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 134087; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

```

CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match      52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
Db 12 ACTTCATCCTT 2

RESULT 100
ABH02048/c
ID ABH02048 standard; DNA; 13 BP.
XX AC ABH02048;
XX
XX
XX 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 202025 for detecting SNP TSC0049668.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 202025; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match      52.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 18
Db 11 ACTTCACCTT 1

RESULT 101
AAF77604/c
ID AAF77604 standard; DNA; 14 BP.
XX AC AAF77604;
XX
XX 29-MAY-2001 (first entry)
DE Modified transcription initiation site Paramyxovirus related oligo #24.
KW Transcription initiation sequence; viral vector; vaccine; therapy; ds.
XX Unidentified.
XX
XX WO200118223-A1.
XX 15-MAR-2001.
XX
XX 06-SEP-2000; 2000WO-JP006051.
XX
XX 06-SEP-1999; 99JP-00252231.
XX (DNAV-) DNAMEC RES INC.
XX
XX Nagai Y, Kato A, Hasegawa M;
XX WPI; 2001-244576/25.
XX
XX Paramyxovirus vectors with modified transcription initiation sequences
XX for increased expression of foreign genes in production of drugs and
XX vaccines.
XX
XX Example 1; Fig 2; 65pp; Japanese.
XX
XX The present invention describes a paramyxovirus vector DNA in which the
XX transcription initiation sequence has been modified to modify the
XX expression of a gene located downstream of the transcription initiation
XX sequence. This is useful in the production of mutant paramyxovirus
XX vectors with elevated gene expression and a more rapid proliferation than
XX the wild-type vector, which can then be used for more efficient
XX production of drug substances and vaccines
XX
XX Sequence 14 BP; 5 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match      51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GCGACTTCATCCTT 18
Db 14 GGGACTTTATCCTT 1

RESULT 102
AAL42211
ID AAL42211 standard; RNA; 14 BP.
XX AC AAL42211;
XX
XX 29-AUG-2003 (revised)
DT 28-NOV-2002 (first entry)
XX
XX Hansenula wingei U3 small nucleolar RNA (snRNA) 3' hinge region.
XX
XX U3 snRNA 3' hinge region; ss; antibiotic agent screening; fungi;
XX U3 small nucleolar RNA domain 1 hinge region; snRNA; pre-rRNA;
XX 18S rRNA subunit; cell growth inhibition; fungal infection;
XX protozoa infection; Chagas disease; Trypanosoma cruzi infection;
XX Pneumocystis carinii infection; coccidiosis; Bimera infection.
XX
XX Pichia canadensis.
XX
XX WO200201953-A1.

```

XX 10-JAN-2002.
PD
XX
XX 28-JUN-2001; 2001WO-US020520.
PF
XX
XX 30-JUN-2000; 2000US-0215572P.
PR
XX
XX (UYBR-) UNIV BROWN RES FOUND.
PA
XX
XX Gerbi S, Borovjagin A, Lange TS;
FI
XX
XX WPI; 2002-154668/20.
DR
XX
XX Identification of antibiotic agents, useful to treat opportunist
PT infections in humans and domestic animals, comprises disrupting binding
PT of specific regions of U3 small nucleolar ribonucleic acid to
PT complementary sequences in pre-rRNA.
XX
XX Disclosure; Page 18; 74pp; English.
PS
XX
XX The invention comprises a method of screening for antibiotic agents. The
CC method involves disrupting binding of the 5' and 3' hinge regions of
CC domain I of U3 small nucleolar RNA (snRNA) to complementary sequences in
CC the ribosomal RNA precursor (pre-rRNA). Thereby preventing processing of
CC the pre-rRNA into a functional 18S rRNA subunit of the cellular
CC translation machinery. The method of the invention is useful in screening
CC for antibiotics which can be used to inhibit cell growth of infectious
CC organisms and/or treat opportunistic infections in eukaryotic hosts (i.e.
CC humans and domestic animals). The antibiotics identified by the method of
CC the invention may be used to treat opportunistic infections in humans
CC (e.g. fungi, protozoa and multicellular parasites, Chagas disease caused
CC by Trypanosoma cruzi, and pneumocystis carinii infections in
CC immunocompromised hosts). The antibodies identified by the method of the
CC invention may also be used to treat infections in domesticated animals
CC (e.g. coccidiosis in poultry caused by infection with Eimeria). The
CC present RNA sequence represents the Hansenula wingei U3 snRNA 3' hinge
CC region. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 14 BP; 4 A; 5 C; 3 G; 0 T; 2 U; 0 Other;
SQ

Query Match 51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GAGCGACTTCATCC 16
Db 1 GAGCCACUGAUC 14
||||| : : : :
||| : : : :
RESULT 103
AAT29317
ID AAT29317 standard; DNA; 10 BP.
XX
XX AAT29317;
AC
XX
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
DE
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
XX Synthetic.
OS
XX
XX WO9531574-A1.
PN
XX
XX 23-NOV-1995.
DT
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
DE
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
XX Synthetic.
OS
XX
XX WO9531574-A1.
PN
XX
XX 23-NOV-1995.
DT
XX
XX 12-MAY-1995; 95WO-US006032.
PF
XX
XX

PR 16-MAY-1994; 94US-00242887.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA
XX
XX Lopeznieta CE, Nigam SK;
FI
XX
XX WPI; 1996-010958/01.
DR
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
PS
XX
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
CC from them, which target mammalian G-protein coupled receptor coding
CC sequences, together comprise a PCR primer kit. The kit is used in a new
CC method for the characterisation of nucleic acid sequences obtd. from
CC mammalian biological samples, which comprises PCR amplification and
CC indexing of the prods. w.r.t the primer pair that hybridised to its
CC delineating subsequences. The method may be used in the identification,
CC cloning and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
SQ

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTTCATCCT 17
Db 1 CTTCATCCT 9
|||||
|||
RESULT 104
AAT29316
ID AAT29316 standard; DNA; 10 BP.
XX
XX AAT29316;
AC
XX
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
DE
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
XX Synthetic.
OS
XX
XX WO9531574-A1.
PN
XX
XX 23-NOV-1995.
DT
XX
XX 12-MAY-1995; 95WO-US006032.
PF
XX
XX 16-MAY-1994; 94US-00242887.
PR
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA
XX
XX Lopeznieta CE, Nigam SK;
FI
XX
XX WPI; 1996-010958/01.
DR
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
XX Claim 46; Page 55; 72pp; English.
PS
XX
XX

CC The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 CTTTCATCCT 17
 Db 1 CTTTCATCCT 9
 |||||

RESULT 105
 AAT29296
 ID AAT29296 standard; DNA; 10 BP.
 XX
 AC AAT29296;

DT 25-MAR-2003 (revised)
 DT 28-JUN-1996 (first entry)

XX 5'-primer for mammalian G-protein coupled receptor coding sequences.

DE 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 XX characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.

XX Synthetic.

XX WO9531574-A1.

XX 23-NOV-1995.

XX 12-MAY-1995; 95WO-US006032.

XX 16-MAY-1994; 94US-00242887.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Lopezniato CE, Nigam SK;

XX WPI; 1996-010958/01.

XX Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.

XX Claim 46; Page 55; 72pp; English.

XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 CTTTCATCCT 17
 Db 2 CTTTCATCCT 10
 |||||

RESULT 106
 AAZ83547
 ID AAZ83547 standard; DNA; 10 BP.
 XX
 AC AAZ83547;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #2781.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX Claim 1; Page 133; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.

XX Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 2 CTTTCATCCT 10

RESULT 107
AAF35047/c
ID AAF35047 standard; DNA; 10 BP.

XX AC AAF35047;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1786.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPT; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX PS Example; Page 63; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 9 CTTTCATCCT 1

RESULT 108
AAF41819/c

XX ID AAF41819 standard; DNA; 10 BP.

XX AC AAF41819;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8558.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPT; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX PS Example; Page 305; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGCGACTTC 12
|||||||
Db 9 AGCGACTTC 1

RESULT 109
AAF39735/c
ID AAF39735 standard; DNA; 10 BP.

XX AC AAF39735;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6474.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velulescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX PS Example; Page 231; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
|||||||
Db 9 CTTTCATCCT 1

RESULT 110
AAF34938/c
ID AAF34938 standard; DNA; 10 BP.

XX AC AAF34938;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1677.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velulescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX PS Example; Page 59; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially

CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTCAT 14
 Db 9 CGACTTCAT 1

RESULT 111
 AAF34381/c
 ID AAF34381 standard; DNA; 10 BP.

XX AC AAF34381;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1120.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

PS Example; Page 40; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
 Db 9 AGCGACTTC 1

RESULT 112

AAS95622

ID AAS95622 standard; DNA; 10 BP.

XX AC AAS95622;

XX DT 14-FEB-2002 (first entry)

XX DE Apolipoprotein C-IV allele-specific oligonucleotide #43.

XX KW Apolipoprotein C-IV; APOC4; human; antilipemic; haplotyping;
 KW hypertriglyceridaemia; allele-specific oligonucleotide; ASO; ss.

XX OS Homo sapiens.

XX PN WO200177127-A2.

XX PD 18-OCT-2001.

XX PF 10-APR-2001; 2001WO-US011715.

XX PR 11-APR-2000; 2000US-0195825P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PA (LEE H/) LEE H H.

XX PI Choi JY, Kliem SE, Koshy B;

XX DR WPI; 2002-041284/05.

XX New haplotypes of human apolipoprotein C-IV gene, useful to diagnose and
 PT treat diseases associated with its activity such as hypertriglyceridaemia.

PS Claim 18; Page 14; 64pp; English.

XX The invention relates to haplotyping the apolipoprotein C-IV (APOC4) gene
 CC of an individual, comprising determining if the individual has one of the
 CC APOC4 haplotypes or haplotype pairs fully defined in the specification.
 CC Haplotyping the APOC4 gene of an individual, comprises determining the
 CC identity of the nucleotide at two or more polymorphic sites in one copy
 CC of the gene. The method also comprises identifying an association between
 CC a trait and a haplotype or haplotype pair of the APOC4 gene, comprising
 CC comparing the frequency of the haplotype/pair in a population exhibiting
 CC the trait with that of a reference population. A higher frequency in the
 CC trait population indicates the trait is associated with the haplotype.
 CC The polymorphisms and screened compounds are useful for developing
 CC treatment for diseases associated with APOC4 activity such as
 CC hypertriglyceridaemia. AAS95580-AAS95634 represent human apolipoprotein C
 CC -IV allele-specific oligonucleotides of the invention


```
XX SQ Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
Db 1 CTTTCATCCT 9

RESULT 113
ABV64594
ID ABV64594 standard; cDNA; 11 BP.
XX AC ABV64594;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 2380.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
XX SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 114
ABV64594
ID ABV64594 standard; cDNA; 11 BP.
XX AC ABV64594;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 2380.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
XX SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 115
AAD34602/c
ID AAD34602 standard; DNA; 11 BP.
XX AC AAD34602;
XX DT 16-JUL-2002 (first entry)
XX DE Human CYP2C19 gene polymorphic site 1060 detecting antisense G variant.
XX KW Human; CYP2C19 gene; cytochrome P450 2C19; S-mephenytoin-4'-hydroxylase;
KW drug metabolism; diagnosis; detection; xenobiotic; variant; SNP;
KW single nucleotide polymorphism; ds.
XX
```

```
ABV72015
ID ABV72015 standard; cDNA; 11 BP.
XX AC ABV72015;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 9801.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX The invention relates to in vitro identification (M1) of genes expressed
in the skin of humans or animals by subjecting a mixture of genetically
encoded factors from skin, to serial analysis of gene expression (SAGE)
so as to identify skin-expressed genes and quantify their expression.
(M1) is useful for identifying genes involved in skin homeostasis; to
determine skin homeostasis and to test agent (A) that maintains or
promotes skin homeostasis or that can be used for treating skin
disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
XX SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 115
AAD34602/c
ID AAD34602 standard; DNA; 11 BP.
XX AC AAD34602;
XX DT 16-JUL-2002 (first entry)
XX DE Human CYP2C19 gene polymorphic site 1060 detecting antisense G variant.
XX KW Human; CYP2C19 gene; cytochrome P450 2C19; S-mephenytoin-4'-hydroxylase;
KW drug metabolism; diagnosis; detection; xenobiotic; variant; SNP;
KW single nucleotide polymorphism; ds.
XX
```


PT designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PS Claim 1; SEQ ID NO 304329; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TTCATCCTT 18
DB 12 TTCATCCTT 4
RESULT 118
ABI73201
ID ABI73201 standard; DNA; 12 BP.
XX
AC ABI73201;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 373174 for detecting SNP TSC0009601.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 373174; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TTCATCCTT 18
DB 1 TTCATCCTT 9
RESULT 119
ABI48663/c
ID ABI48663 standard; DNA; 12 BP.
XX
AC ABI48663;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 348636 for detecting SNP TSC0001012.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 348636; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TTCATCCTT 18

```

Db      10 TTCATCCTT 2
RESULT 120
ABI56153/c
ID      ABI56153 standard; DNA; 12 BP.
XX
XX
AC      ABI56153;
XX
XX      22-FEB-2002 (first entry)
DT
XX
XX      Oligonucleotide primer SEQ ID NO 356126 for detecting SNP TSC0049973.
DE
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX
XX      WO200177384-A2.
PN
XX
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
DT
XX
XX      07-APR-2000; 2000DE-01019173.
DE
XX
XX      (EPIG-) EPIGENOMICS AG.
KW
KW      Olek A, Piepenbrock C, Berlin K;
KW      WPI; 2001-657177/75.
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 372867; 29pp + Sequence Listing; German.
PS
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      50.0%; Score 9; DB 1; Length 12;
XX      Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX      Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      10 TTCATCCTT 18
XX      |||||
Db      11 TTCATCCTT 3
XX
XX
RESULT 121
ABI72894/c
ID      ABI72894 standard; DNA; 12 BP.
XX
XX
AC      ABI72894;
XX
XX      22-FEB-2002 (first entry)
DT
XX
XX      Oligonucleotide primer SEQ ID NO 372867 for detecting SNP TSC0059696.
DE
XX
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS
XX
XX      Homo sapiens.
OS
XX
XX      WO200177384-A2.
PN
XX
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX
XX      07-APR-2000; 2000DE-01019173.
PR
XX
XX      (EPIG-) EPIGENOMICS AG.
PA
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI
XX
XX      WPI; 2001-657177/75.
DR
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
XX      designed to detect single-nucleotide polymorphisms and cytosine
XX      methylation status.
XX
XX      Claim 1; SEQ ID NO 356126; 29pp + Sequence Listing; German.
PS
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      50.0%; Score 9; DB 1; Length 12;
XX      Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX      Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      10 TTCATCCTT 18
XX      |||||
Db      11 TTCATCCTT 3
XX
XX
RESULT 122
ABH74903/c
ID      ABH74903 standard; DNA; 12 BP.
XX
XX
AC      ABH74903;
XX
XX      22-FEB-2002 (first entry)
DT
XX
XX      Oligonucleotide primer SEQ ID NO 274890 for detecting SNP TSC0003716.
DE
XX
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS
XX
XX      Homo sapiens.
OS
XX
XX      WO200177384-A2.
PN
XX
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX
XX      07-APR-2000; 2000DE-01019173.
PR
XX

```

XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 274890; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 ACTTCATCC 16
 Db 9 ACTTCATCC 1
 RESULT 123
 ABH82223/C
 ID ABH82223 standard; DNA; 12 BP.
 XX ABH82223;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 282216 for detecting SNP TSC0010588.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 FN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 282216; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 9 CTTCATCCT 17
 Db 10 CTTCATCCT 2
 RESULT 124
 ABI22432
 ID ABI22432 standard; DNA; 12 BP.
 XX ABI22432;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 322405 for detecting SNP TSC0030847.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 FN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 322405; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB0000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 95713; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 11 CTTTCATCCT 3
 RESULT 128
 ABF60699
 ID ABF60699 standard; DNA; 13 BP.
 XX AC ABF60699;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 160696 for detecting SNP TSC0040466.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB0000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 160696; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 1 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 1.6e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 GACTTCATCCT 17
 Db 1 RACTTCATCCT 11
 RESULT 129
 ABF95511
 ID ABF95511 standard; DNA; 13 BP.
 XX AC ABF95511;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 195508 for detecting SNP TSC0048102.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB0000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 195508; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;
 SQ

Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 1.6e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
 Db :|||||||
 1 RCTTCATCCT 11

RESULT 130
 ABH33314/C
 ID ABH33314 standard; DNA; 13 BP.
 XX
 AC ABH33314;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 233291 for detecting SNP TSC0006073.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single-nucleotide polymorphisms and cytosine
 methylation status.
 XX
 Claim 1; SEQ ID NO 233291; 29pp + Sequence Listing; German.
 XX
 This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 XX
 Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 16
 Db :|||||||
 10 ACTTCATCCT 2

RESULT 131
 ABF6198/C
 ID ABF6198 standard; DNA; 13 BP.
 XX
 AC ABF6198;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 186195 for detecting SNP TSC0045867.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single-nucleotide polymorphisms and cytosine
 methylation status.
 XX
 Claim 1; SEQ ID NO 186195; 29pp + Sequence Listing; German.
 XX
 This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 XX
 Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db :|||||||
 9 CTTTCATCCT 1

RESULT 132
 ABF60696/C
 ID ABF60696 standard; DNA; 13 BP.
 XX
 AC ABF60696;
 XX
 DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 160693 for detecting SNP TSC0040466.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPiG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 160693; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 GACTTCCTCCT 17
Db :|||||
13 RACTTCCTCCT 3
RESULT 133
ABC57255
ID ABC57255 standard; DNA; 13 BP.
XX
XX ABC57255;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 57272 for detecting SNP TSC0015489.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 57272; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 ACTTCATCC 16
Db :|||||
5 ACTTCATCC 13
RESULT 134
ABC62600/C
ID ABC62600 standard; DNA; 13 BP.
XX
XX ABC62600;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 62617 for detecting SNP TSC0016596.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPiG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

XX PS Claim 1; SEQ ID NO 62617; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 12 TTCATCCTT 4
|||||

RESULT 135
ABH33315
ID ABH33315 standard; DNA; 13 BP.
XX AC ABH33315;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 233292 for detecting SNP TSC0006073.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 233292; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 4 ACTTCATCC 12
|||||

RESULT 136
ABF60697
ID ABF60697 standard; DNA; 13 BP.
XX AC ABF60697;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 160694 for detecting SNP TSC0040466.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 160694; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
Db 1 RACTTCCTCCT 11
:|||||

```

RESULT 137
ABC25977
ID ABC25977 standard; DNA; 13 BP.
XX
XX AC ABC25977;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 25994 for detecting SNP TSC0006701.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 25994; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 TTATCCTT 18
XX |||||
XX 2 TTATCCTT 10
XX
XX RESULT 138
ABF37452/C
ID ABF37452 standard; DNA; 13 BP.
XX
XX AC ABF37452;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 137449 for detecting SNP TSC0034348.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 25994; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 9 CTCATCCT 17
XX |||||
XX 12 CTCATCCT 4
XX
XX RESULT 139
ABF86199
ID ABF86199 standard; DNA; 13 BP.
XX
XX AC ABF86199;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 186196 for detecting SNP TSC0045867.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.

```

```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 137449; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 9 CTCATCCT 17
XX |||||
XX 12 CTCATCCT 4
XX
XX RESULT 139
ABF86199
ID ABF86199 standard; DNA; 13 BP.
XX
XX AC ABF86199;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 186196 for detecting SNP TSC0045867.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.

```

```
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 186196; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCCT 17
XX Db 5 CTTTCATCCT 13
XX
XX RESULT 140
XX ABH50895
XX ID ABH50895 standard; DNA; 13 BP.
XX AC ABH50895;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 250872 for detecting SNP TSC0061237.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX AC ABH50895;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 250872 for detecting SNP TSC0061237.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PP 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPTG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 250872; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCCT 17
XX Db 5 CTTTCATCCT 13
XX
XX RESULT 141
XX ABC94000
XX ID ABC94000 standard; DNA; 13 BP.
XX AC ABC94000;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 94017 for detecting SNP TSC0023488.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 94017; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 7 GACTTCATCCT 17
XX Db 1 RATTTCATCCT 11
XX
XX RESULT 141
XX ABC94000
XX ID ABC94000 standard; DNA; 13 BP.
XX AC ABC94000;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 94017 for detecting SNP TSC0023488.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 94017; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 1 Other;
```

```
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGACGCGACTT 11
Db 3 GTGACGCGATT 13

RESULT 142
ABF95510/c
ID ABF95510 standard; DNA; 13 BP.
XX
AC ABF95510;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 195507 for detecting SNP TSC0048102.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 195507; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 13 RCTTCATCCCT 3

RESULT 143
ABF24926/c
ID ABF24926 standard; DNA; 13 BP.
XX

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 13 TTCATCCTT 5

RESULT 144
ABF37666/c
ID ABF37666 standard; DNA; 13 BP.
XX
AC ABF37666;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 137663 for detecting SNP TSC0034410.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
```

```

XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 137663; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 1 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCC 16
XX Db 11 ACTTCATCC 3
XX
XX RESULT 145
XX ABF53607
XX ID ABF53607 standard; DNA; 13 BP.
XX
XX AC ABF53607;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 153604 for detecting SNP TSC0038834.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 137663; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 50.0%; Score 9; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCC 16
XX Db 11 ACTTCATCC 3
XX
XX RESULT 146
XX ABC25976/C
XX ID ABC25976 standard; DNA; 13 BP.
XX
XX AC ABC25976;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 25993 for detecting SNP TSC0006701.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 25993; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 12 TTCATCCTT 4
|||||
12 TTCATCCTT 4

RESULT 147
ABF53606/c
ID ABF53606 standard; DNA; 13 BP.
XX AC ABF53606;
XX
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 153603 for detecting SNP TSC0038834.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 153603; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 12 TTCATCCTT 18
|||||
12 TTCATCCTT 18

RESULT 148
ABH50894/c
ID ABH50894 standard; DNA; 13 BP.
XX AC ABH50894;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 250871 for detecting SNP TSC0061237.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 250871; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCCTT 17
Db 13 RATTTCATCCTT 3
|||||
13 RATTTCATCCTT 3

RESULT 149
ABH65795
ID ABH65795 standard; DNA; 13 BP.
XX AC ABH65795;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 265772 for detecting SNP TSC0064404.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 265772; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCATCC 16
Db 4 ACTTCATCC 12
RESULT 150
ABC95697
ID ABC95697 standard; DNA; 13 BP.
XX
XX ABC95697;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 95714 for detecting SNP TSC0023812.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 95714; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTTTCATCCT 17
Db 3 CTTTCATCCT 11
RESULT 151
ABF37667
ID ABF37667 standard; DNA; 13 BP.
XX
XX ABF37667;
AC
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 137664 for detecting SNP TSC0034410.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 137664; 29pp + Sequence Listing; German.
PS

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACTTCATCC 16
DB 3 ACTTCATCC 11
|||||

RESULT 152
ABH47184/c
ID ABH47184 standard; DNA; 13 BP.
XX AC ABH47184;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 247161 for detecting SNP TSC0060394.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPITG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 247161; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
DB 11 CTTTCATCCT 3
|||||

RESULT 153
ABH59422/c
ID ABH59422 standard; DNA; 13 BP.
XX AC ABH59422;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 259399 for detecting SNP TSC0062998.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPITG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 259399; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
DB 12 CTTTCATCCT 4
|||||

RESULT 154

```

ABC62601
ID ABC62601 standard; DNA; 13 BP.
AC ABC62601;
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 62618 for detecting SNP TSC0016596.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 62618; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TTATCCTT 18
Db 2 TTATCCTT 10

RESULT 155
ABF23816/c
ID ABF23816 standard; DNA; 13 BP.
XX
AC ABF23816;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 123813 for detecting SNP TSC0030953.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 62618; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TTATCCTT 18
Db 2 TTATCCTT 10

RESULT 155
ABF23816/c
ID ABF23816 standard; DNA; 13 BP.
XX
AC ABF23816;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 123813 for detecting SNP TSC0030953.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 123813; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 1 Other;
XX
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GACTTCATCCT 17
Db 13 RACTTACATCCT 3

RESULT 156
ABH47185
ID ABH47185 standard; DNA; 13 BP.
XX
AC ABH47185;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 247162 for detecting SNP TSC0060394.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

```

XX DR WPI; 2001-657177/75.
 XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 247162; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 3 CTTTCATCCT 11
 RESULT 157
 ABC96952/C
 ID ABC96952 standard; DNA; 13 BP.
 XX AC ABC96952;
 XX AC
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 96969 for detecting SNP TSC0024054.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 96969; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 GCGACTTCA 13
 Db 9 GCGACTTCA 1
 RESULT 158
 ABC86371
 ID ABC86371 standard; DNA; 13 BP.
 XX AC ABC86371;
 XX AC
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 86388 for detecting SNP TSC0021699.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB0000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 86388; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

```
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCATCC 16
   |||||
Db 2 ACTTCATCC 10
   |||||

RESULT 159
ABH65794/C
ID ABH65794 standard; DNA; 13 BP.
XX AC
XX ABH65794;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 265771 for detecting SNP TSC0064404.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 265771; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCATCC 16
   |||||
Db 10 ACTTCATCC 2
   |||||

RESULT 160
ABC96953
ID ABC96953 standard; DNA; 13 BP.
XX AC
XX ABC96953;
XX
```

```
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 96970 for detecting SNP TSC0024054.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 96970; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 GCGACTTCA 13
   |||||
Db 5 GCGACTTCA 13
   |||||

RESULT 161
ABC86370/C
ID ABC86370 standard; DNA; 13 BP.
XX AC
XX ABC86370;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 86387 for detecting SNP TSC0021699.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
```

XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 86387; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 ACTTCATCC 16
 Db 12 ACTTCATCC 4
 |||||
 RESULT 162
 ABF37453
 ID ABF37453 standard; DNA; 13 BP.
 AC ABF37453;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 137450 for detecting SNP TSC0034348.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
 XX Claim 1; SEQ ID NO 137450; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 CTTCATCCT 17
 Db 2 CTTCATCCT 10
 |||||
 RESULT 163
 ABF24927
 ID ABF24927 standard; DNA; 13 BP.
 AC ABF24927;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 124924 for detecting SNP TSC0031227.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 124924; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TTCACTCCTT 18
| | | | |
Db 1 TTCACTCCTT 9

RESULT 164
ABF60698/C
ID ABF60698 standard; DNA; 13 BP.

XX AC ABF60698;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 160695 for detecting SNP TSC0040466.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 160695; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 1 Other;
Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GACTTCATCCT 17
: | | | | |
Db 13 RACTTCTTCCT 3

RESULT 165
ABF63942/C

ID ABF63942 standard; DNA; 13 BP.

XX AC ABF63942;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 163939 for detecting SNP TSC0005894.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 163939; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 ACTTCATCC 16
| | | | |
Db 12 ACTTCATCC 4

RESULT 166
ABC57254/C

ID ABC57254 standard; DNA; 13 BP.

XX AC ABC57254;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 57271 for detecting SNP TSC0015489.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16

Db 2 ACTTCATCC 10

RESULT 169

ABH59423
 ID ABH59423 standard; DNA; 13 BP.

XX AC ABH59423;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 259400 for detecting SNP TSC0062998.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 259400; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17

Db 2 CTTTCATCCT 10

RESULT 170

AAA55920/c
 ID AAA55920 standard; DNA; 12 BP.

XX AC AAA55920;

XX DT 04-SEP-2000 (first entry)

XX DE Adapter linker nucleotide sequence SEQ ID NO:79.

XX KW Yeast; detection; protein-protein interaction; DNA-binding domain;
 KW characterisation; identification; protein pathway information;
 KW protein interaction domain; screening; PCR primer; adapter; linker;
 KW fusion protein; inhibitor; regulation; ss.

XX OS Synthetic.

XX FN US6057101-A.

XX PD 02-MAY-2000.

XX PF 13-JUN-1997; 97US-00874825.

XX PR 14-JUN-1996; 96US-00663824.

XX PA (CURA-) CURAGEN CORP.

XX PI Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;

XX DR WPI; 2000-349567/30.

XX Identifying, comparing and detecting inhibitors of protein-protein
 PT interactions within population of host cells, involves detecting
 PT regulation of transcription of nucleic acid sequence by fusion protein
 PT interaction.

XX Example; Col 131; 161pp; English.

XX The present invention describes a method for detecting (D) at least 1
 CC protein-protein interaction (PPI) by recombinantly expressing within a
 CC population of host cells, populations of first and second fusion proteins
 CC comprising DNA binding domain (DBD) and transcriptional regulatory domain
 CC (TRD) respectively and detecting the regulation of transcription of
 CC nucleotide sequence of host cells operably linked to a promoter driven by
 CC DBD. The detection method (D) is useful for identifying inhibitors of PPI
 CC for therapeutic use, and for detecting specific cell types, tissue types,
 CC stage of development and disease states. From the population of the
 CC proteins characteristic of the particular tissue or a cell-type, all
 CC possible detectable PPI that occur can be identified and genes encoding
 CC these proteins can be isolated. Thus, parallel analysis of two cell types
 CC enumerates PPI that are common to both and those that are specific to
 CC both. This analysis has significant value since PPI specific to a disease
 CC state can serve as therapeutic points of intervention. Inhibitors of PPI
 CC can also be isolated in rapid fashion. The number of false positives and
 CC low throughput are reduced. AAA55843 to AAA55963 and AA90961 are
 CC sequences used in the exemplification of the present invention

XX Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

QY      2 TCAGCGACTTCA 13
Db      12 TCAGCGACTGCA 1

RESULT 171
AAA73432/c
ID AAA73432 standard; DNA; 12 BP.
XX
AC AAA73432;
XX
DT 09-FEB-2001 (first entry)
XX
DE Linker RC15.
XX
KW Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW ss.
XX
OS Saccharomyces cerevisiae.
XX
PN US6083693-A.
XX
PD 04-JUL-2000.
XX
PF 14-JUN-1996; 96US-00663824.
XX
PR 14-JUN-1996; 96US-00663824.
PA (CURA-) CURAGEN CORP.
XX
PI Nandabalan K, Rothberg JM;
XX
DR WPI; 2000-464335/40.
XX
PT Detecting protein-protein interactions in protein populations useful for
PT identifying genes encoding the proteins, and inhibitors of the
PT interactions, by detecting transcriptional regulation leading to reporter
PT gene activation.
XX
PS Example; Col 103-104; 135pp; English.
XX
CC The present invention relates to methods for detecting and isolating
CC genes encoding proteins that interact with each other, via the
CC reconstitution of a transcription factor and hence reporter gene
CC activation. Proteins are fused to either the yeast DNA-binding domain of
CC a transcriptional activator or to the activation domain of a
CC transcriptional activator. The present sequence is a linker used in the
CC present invention as an adapter in the analysis of yeast fusion genes.
CC The present method may be used to identify protein-protein interactions
CC and genes encoding the interacting proteins relevant to a particular
CC tissue, stage or disease e.g. cancer
XX
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCAGCGACTTCA 13
Db      12 TCAGCGACTGCA 1

RESULT 172
ABH74215/c
ID ABH74215 standard; DNA; 12 BP.
XX
AC ABH74215;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 274200 for detecting SNP TSC0003474.
XX

```

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 274200; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal disorders, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGACTTCATCCT 17
Db 12 CTACTTCACCT 1

RESULT 173
ABI58053/c
ID ABI58053 standard; DNA; 12 BP.
XX
AC ABI58053;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358026 for detecting SNP TSC0050921.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.

```
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 358026; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GACTTCATCCTT 18
Db 12 GCCTCCATCCTT 1

RESULT 174
ABI65792/c
ID ABI65792 standard; DNA; 12 BP.
XX AC ABI65792;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 365765 for detecting SNP TSC0055318.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 365765 for detecting SNP TSC0055318.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 310210 for detecting SNP TSC0023863.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 310210 for detecting SNP TSC0023863.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 310210; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GACTTCATCCTT 18
Db 12 GACTTCATCCTT 1

RESULT 175
ABI10237/c
ID ABI10237 standard; DNA; 12 BP.
XX AC ABI10237;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 310210 for detecting SNP TSC0023863.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 310210; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
```

RESULT 177
ABI32036/C

```

XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 319268; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 7 GACTTCATCCTT 18
Db 12 GATTTCACCTT 1

RESULT 179
ABI08311/c
ID ABI08311 standard; DNA; 12 BP.
XX AC ABI08311;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 308284 for detecting SNP TSC0022939.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 319268; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 7 GACTTCATCCTT 18
Db 12 GATTTCACCTT 1

RESULT 180
ABI25036
ID ABI25036 standard; DNA; 12 BP.
XX AC ABI25036;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 325009 for detecting SNP TSC0032345.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 325009; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 4 AGCGACTTCATC 15
Db 12 AACGCCCTTCATC 1

```

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATC 15
Db 1 AAGCGCTTCATC 12
| | | | | | | | | | | | | |

RESULT 181

ABI11045
ID ABI11045 standard; DNA; 12 BP.

XX AC ABI11045;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 311018 for detecting SNP TSC0024273.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 311018; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCT 17
Db 1 CGAATTCATCT 12
| | | | | | | | | | | | | |

RESULT 182

ABI14744/c
ID ABI14744 standard; DNA; 12 BP.

XX AC ABI14744;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 314717 for detecting SNP TSC0026530.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 314717; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATC 15
Db 12 ACCGACTTCATC 1
| | | | | | | | | | | | | |

RESULT 183

ABI78596/c
ID ABI78596 standard; DNA; 12 BP.

XX AC ABI78596;

XX DT 22-FEB-2002 (first entry)

```
XX DE Oligonucleotide primer SEQ ID NO 378569 for detecting SNP TSC0062846.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 378569; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABP0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
    Query Match      48.9%; Score 8.8; DB 1; Length 12;
    Best Local Similarity 83.3%; Pred. No. 1.7e+02;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGCGACTTCATC 15
Db 12 ACCGACCTCATC 1
    |||||
RESULT 184
ABK13228
ID ABK13228 standard; DNA; 12 BP.
XX ABK13228;
AC ABK13228;
XX 23-APR-2002 (first entry)
XX Self-assembled monolayer sequence #1.
XX Self-assembled monolayer; SAM; ds; surface plasmon resonance chip;
XX biosensor; DNA hybridisation test; diagnostic mutation scanning;
XX forensic analysis; pharmacological study; cell sorting;
XX environmental monitoring; protein-protein interaction.
XX Unidentified.
XX OS US6322979-B1.
XX PN 27-NOV-2001.
XX PD
```

```
XX 21-APR-1999; 99US-00296078.
XX PF 26-SEP-1994; 94US-00312388.
XX PR 21-JAN-1997; 97US-00786187.
XX XX (HARD ) HARVARD COLLEGE.
XX PI Bamdad CC, Sigal GB, Strominger JL, Whitesides GM;
XX XX WPI; 2002-146684/19.
XX Capturing biological binding partner, useful e.g. for nucleic acid
XX hybridization tests, using surface that carries self-assembled monolayer
XX comprising specific capture agent.
XX Example 12; Fig 9; 28pp; English.
XX The invention relates to a new process of capturing a biological binding
XX partner (I) of a nucleic acid strand (II) comprising applying a test
XX sample to a surface that carries: (i) a binding species (III); and (ii) a
XX molecule (IV) that forms a mixed self-assembled monolayer (SAM) with
XX (III). (III) has formula X-R-NA (III) X = functional group that adheres
XX to the surface; R = spacer that promotes formation of SAM; and NA =
XX nucleic acid strand. The method is particularly used in surface plasmon
XX resonance chips (biosensors) for capturing DNA. Typical of many possible
XX applications are DNA hybridisation tests (e.g. diagnostic scanning for
XX mutations, forensic analysis, pharmacological studies, cell sorting,
XX environmental monitoring) in studies of protein-protein interactions
XX where DNA binding is important (e.g. transcriptional control of genes)
XX and in development of easy-analysis DNA computers. The use of a mixed SAM
XX improves sensitivity, with reduced non-specific binding, it ensures that
XX the binding region of (III) is directed away from the surface, making it
XX available for reaction. The present sequenc contains is used to
XX illustrate the method of the invention
XX SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
    Query Match      48.9%; Score 8.8; DB 1; Length 12;
    Best Local Similarity 83.3%; Pred. No. 1.7e+02;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTGAGCGGACTTC 12
Db 1 GTAAGCGGACTTC 12
    |||||
RESULT 185
AAD4523/c
ID AAD45523 standard; DNA; 12 BP.
XX AAD45523;
AC AAD45523;
XX 27-DEC-2002 (first entry)
XX RC15 linker DNA used to illustrate the method of the invention.
XX Protein-protein interaction; detection; cancer; linker; ss.
XX Unidentified.
XX OS US6410239-B1.
XX PN 25-JUN-2002.
XX PD 14-DEC-1999; 99US-00461125.
XX PF 14-JUN-1996; 96US-00663824.
XX PR 13-JUN-1997; 97US-00874825.
XX XX (CURA-) CURAGEN CORP.
XX Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;
```

```

XX DR WPI; 2002-654433/70.
XX
XX PT Detection of protein to protein interactions amongst two protein
XX PT populations useful e.g. to identify interactions specific for particular
XX PT tissues or diseases and to identify inhibitors of interactions uses a new
XX PT genetic method.
XX
XX PS Example; Col 197; 152pp; English.
XX
XX CC The present invention relates to novel methods for detecting protein to
XX CC protein interactions amongst two populations of proteins, each having a
XX CC complexity of at least 100. The method involves using new genetic methods
XX CC in which encoded proteins are fused to either the DNA-binding domain of a
XX CC transcriptional activator or the activation domain of a transcriptional
XX CC activator. The methods are useful to detect interacting proteins and to
XX CC identify protein-protein interactions specific for a particular species,
XX CC tissue, stage of development or disease state, e.g. by comparing protein-
XX CC protein interactions between populations from cDNA of cancerous or pre-
XX CC cancerous cells with those from non-cancerous cells. They are also useful
XX CC to identify inhibitors interfering with protein-protein interactions e.g.
XX CC potential drug candidates inhibiting interactions specific to cancerous
XX CC cells. The present sequence is a linker DNA used to illustrate the method
XX CC of the invention
XX
XX SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
      Query Match          48.9%; Score 8.8; DB 1; Length 12;
      Best Local Similarity 83.3%; Pred. No. 1.7e+02;
      Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGCGACTTCA 13
Db 12 TCAGCGACTGCA 1

RESULT 186
AAL42765
ID AAL42765 standard; DNA; 12 BP.
XX
XX AC AAL42765;
XX
XX DT 19-JUL-2002 (first entry)
XX
XX DE Self-assembled monolayer (SAM) DNA sequence 1.
XX
XX KW Self-assembled monolayer; SAM; ss; chelating agent; conjugate;
XX KW biological molecule capture; surface plasmon resonance sensor.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 1..12
XX FT /tag= a
XX FT /bound_moiety= "SAM DNA sequence 2"
XX FT /note= "Forms double stranded region with the nucleotide
XX FT shown in AAL42766"
XX
XX PN US2002042074-A1.
XX
XX PD 11-APR-2002.
XX
XX PF 25-JUL-2001; 2001US-00915187.
XX
XX PR 26-SEP-1994; 94US-00312388.
XX PR 21-JAN-1997; 97US-00786187.
XX PR 21-APR-1999; 99US-00296078.
XX
XX PA (HARD ) HARVARD COLLEGE.
XX
XX PI Bandad CC, Sigal GB, Strominger JL, Whitesides GM;
XX
XX DR WPI; 2002-371283/40.
XX
XX PT Conjugates forming self-assembled monolayers on gold surfaces, especially
XX PT in biosensors, comprise a chelating agent linked via a spacer to a
XX PT functional group.
XX
XX PS Example 12; Fig 9; 30pp; English.
XX
XX CC The invention comprises conjugates which contain a functional group that
XX CC adheres to a gold surface, a spacer that promotes the formation of a self-
XX CC assembled monolayer (SAM) of the conjugate, and a bi-, tri- or
XX CC quadridentate chelating agent that coordinates a metal ion. The
XX CC conjugates of the invention are useful for forming self-assembled
XX CC monolayers for capturing biological molecules on sensors, especially
XX CC surface plasmon resonance sensors. The present DNA sequence is shown in a
XX CC figure designed to illustrate the formation of a self-assembled monolayer
XX CC of a conjugate
XX
XX SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
      Query Match          48.9%; Score 8.8; DB 1; Length 12;
      Best Local Similarity 83.3%; Pred. No. 1.7e+02;
      Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGAGCGACTTC 12
Db 1 GTAAGCGAATTC 12

RESULT 187
AAL42766/C
ID AAL42766 standard; DNA; 12 BP.
XX
XX AC AAL42766;
XX
XX DT 19-JUL-2002 (first entry)
XX
XX DE Self-assembled monolayer (SAM) DNA sequence 2.
XX
XX KW Self-assembled monolayer; SAM; ss; chelating agent; conjugate;
XX KW biological molecule capture; surface plasmon resonance sensor.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 1..12
XX FT /tag= a
XX FT /bound_moiety= "SAM DNA sequence 1"
XX FT /note= "Forms double stranded region with the nucleotide
XX FT shown in AAL42765"
XX
XX PN US2002042074-A1.
XX
XX PD 11-APR-2002.
XX
XX PF 25-JUL-2001; 2001US-00915187.
XX
XX PR 26-SEP-1994; 94US-00312388.
XX PR 21-JAN-1997; 97US-00786187.
XX PR 21-APR-1999; 99US-00296078.
XX
XX PA (HARD ) HARVARD COLLEGE.
XX
XX PI Bandad CC, Sigal GB, Strominger JL, Whitesides GM;
XX
XX DR WPI; 2002-371283/40.
XX
XX PT Conjugates forming self-assembled monolayers on gold surfaces, especially
XX PT in biosensors, comprise a chelating agent linked via a spacer to a
XX PT functional group.
XX
XX PS Example 12; Fig 9; 30pp; English.
XX
XX CC The invention comprises conjugates which contain a functional group that

```

```

XX
XX PT Conjugates forming self-assembled monolayers on gold surfaces, especially
XX PT in biosensors, comprise a chelating agent linked via a spacer to a
XX PT functional group.
XX
XX PS Example 12; Fig 9; 30pp; English.
XX
XX CC The invention comprises conjugates which contain a functional group that
XX CC adheres to a gold surface, a spacer that promotes the formation of a self-
XX CC assembled monolayer (SAM) of the conjugate, and a bi-, tri- or
XX CC quadridentate chelating agent that coordinates a metal ion. The
XX CC conjugates of the invention are useful for forming self-assembled
XX CC monolayers for capturing biological molecules on sensors, especially
XX CC surface plasmon resonance sensors. The present DNA sequence is shown in a
XX CC figure designed to illustrate the formation of a self-assembled monolayer
XX CC of a conjugate
XX
XX SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
      Query Match          48.9%; Score 8.8; DB 1; Length 12;
      Best Local Similarity 83.3%; Pred. No. 1.7e+02;
      Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGAGCGACTTC 12
Db 1 GTAAGCGAATTC 12

RESULT 187
AAL42766/C
ID AAL42766 standard; DNA; 12 BP.
XX
XX AC AAL42766;
XX
XX DT 19-JUL-2002 (first entry)
XX
XX DE Self-assembled monolayer (SAM) DNA sequence 2.
XX
XX KW Self-assembled monolayer; SAM; ss; chelating agent; conjugate;
XX KW biological molecule capture; surface plasmon resonance sensor.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 1..12
XX FT /tag= a
XX FT /bound_moiety= "SAM DNA sequence 1"
XX FT /note= "Forms double stranded region with the nucleotide
XX FT shown in AAL42765"
XX
XX PN US2002042074-A1.
XX
XX PD 11-APR-2002.
XX
XX PF 25-JUL-2001; 2001US-00915187.
XX
XX PR 26-SEP-1994; 94US-00312388.
XX PR 21-JAN-1997; 97US-00786187.
XX PR 21-APR-1999; 99US-00296078.
XX
XX PA (HARD ) HARVARD COLLEGE.
XX
XX PI Bandad CC, Sigal GB, Strominger JL, Whitesides GM;
XX
XX DR WPI; 2002-371283/40.
XX
XX PT Conjugates forming self-assembled monolayers on gold surfaces, especially
XX PT in biosensors, comprise a chelating agent linked via a spacer to a
XX PT functional group.
XX
XX PS Example 12; Fig 9; 30pp; English.
XX
XX CC The invention comprises conjugates which contain a functional group that

```

CC figure designed to troubleshoot of a conjugate

ABC91635
ID ABC91635 standard; DNA; 13 BP.

AC ABC91635;

XX

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 91652 for detecting SNP TSC0022938.

XX

XX
XX

OS Homo sapiens.

XX

27 XX

XX
00-777-0000

FR 07-AR-R-2000; 2000EE-01019173;
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX
PI Olek A. Piepenbrock C. Berlin K;
XX

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 84

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

PT designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX
1770-1779

XX

CC This invention describes
CC acid (PNA) oligomers for

CC and cytosine methylation status in oligonucleotides are used for diagnosis

range of diseases in central nervous system

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC www.int/pub/epub/pct_sequences

ftp.wipo.int/pub/published pct sequences

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
SQ Sequence 13 BP; 4 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

ID ABF26209 standard; DNA; 13 BP.

AC ABF26209;

XX


```

DT 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 126206 for detecting SNP TSC0031578.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 126206; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATCCT 17
XX Db 1 CGCCTTCAACCT 12
XX
XX RESULT 191
XX ABF35407
XX ID ABF35407 standard; DNA; 13 BP.
XX
XX AC ABF35407;
XX
XX XX 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 135404 for detecting SNP TSC0033789.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX XX 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 135404 for detecting SNP TSC0033789.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX XX 18-OCT-2001.

```

```

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 135404; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATCCT 17
XX Db 1 CCACCTTCAACCT 12
XX
XX RESULT 192
XX ABF41254
XX ID ABF41254 standard; DNA; 13 BP.
XX
XX AC ABF41254;
XX
XX XX 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 141251 for detecting SNP TSC0035406.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

```

```
PT methylation status.
XX Claim 1; SEQ ID NO 141251; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 TGAGCGACTTCA 13
Db 2 TGAGCGATTTTA 13
|||||
|
RESULT 193
ABH43891
ID ABH43891 standard; DNA; 13 BP.
XX
XX AC ABH43891;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 243868 for detecting SNP TSC0059496.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 243868; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 6 CGACTTCATCCT 17
Db 2 CTACATCATCCT 13
|||||
|
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 5 GCGACTTCATCC 16
Db 2 GCGAATTCACCC 13
|||||
|
RESULT 194
ABH49687
ID ABH49687 standard; DNA; 13 BP.
XX
XX AC ABH49687;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 249664 for detecting SNP TSC0060992.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 249664; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 6 CGACTTCATCCT 17
Db 2 CTACATCATCCT 13
|||||
|
```

```

RESULT 195
ABC69498
ID ABC69498 standard; DNA; 13 BP.
XX
AC ABC69498;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 69515 for detecting SNP TSC0018092.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPITG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
PS Claim 1; SEQ ID NO 69515; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, cardiovascular and metabolic disorders. The
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGAGCGACTTCA 13
DB 2 TGAGCGAGTTAA 13
RESULT 196
ABC19584
ID ABC19584 standard; DNA; 13 BP.
XX
AC ABC19584;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 19601 for detecting SNP TSC0004067.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPITG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
PS Claim 1; SEQ ID NO 19601; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GAGCGACTTCA 14
DB 1 GAGCGAGCTTAT 12
RESULT 197
ABC57831/c
ID ABC57831 standard; DNA; 13 BP.
XX
AC ABC57831;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 57848 for detecting SNP TSC0015565.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

```

```

PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 57848; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 GTGAGCGACTTC 12
XX DB 13 GTGAGCGATTGC 2
XX
XX RESULT 198
XX ABF41255/C
XX ID ABF41255 standard; DNA; 13 BP.
XX
XX AC ABF41255;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 141252 for detecting SNP TSC0035406.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide SEQ ID NO 141252 for detecting SNP TSC0035406.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 141252; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TGAGCGACTTCA 13
XX DB 12 TGAGCGATTTTA 1
XX
XX RESULT 199
XX ABF26208/C
XX ID ABF26208 standard; DNA; 13 BP.
XX
XX AC ABF26208;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 126205 for detecting SNP TSC0031578.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 126205; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

```

```
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 CGACTTCATCCT 17
DB      13 CGCCTTCAACCT 2

RESULT 200
ABF64319
ID ABF64319 standard; DNA; 13 BP.
XX
AC ABF64319;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 164316 for detecting SNP TSC0041255.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 164316; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
XX
Query Match      48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 CGACTTCATCCT 17
DB      1 CGACCTCATACT 12

RESULT 201
ABH57611
ID ABH57611 standard; DNA; 13 BP.
XX
AC ABH57611;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 57847 for detecting SNP TSC0015565.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
```

PN WO200177384-A2.
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 57847; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 2 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTGAGCGACTTC 12
 Db 1 GTGAGCGATTGC 12
 |||||
 |||||
 RESULT 203
 ID ABH49686/c
 ABH49686 standard; DNA; 13 BP.
 XX
 AC ABH49686;
 XX
 DT 22-FEB-2002 (first entry)
 DE
 XX Oligonucleotide SEQ ID NO 249663 for detecting SNP TSC0060992.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 249663; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 48.9%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 CGACTTCATCCT 17
 Db 12 CTATCATCCT 1
 |||||
 |||||
 RESULT 204
 ABC69499/c
 ID ABC69499 standard; DNA; 13 BP.
 XX
 AC ABC69499;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 69516 for detecting SNP TSC0018092.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 69516; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 4 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAGCGACTTCA 13
DB 12 TGAGCGAGTTAA 1
|||||

RESULT 205

ABF95821
ID ABF95821 standard; DNA; 13 BP.

XX AC ABF95821;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 195818 for detecting SNP TSC0048172.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB0000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 195818; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGACTTCATCCT 17
DB 1 CTACTTCAACCT 12
|||||

RESULT 206

ABH43890/c
ID ABH43890 standard; DNA; 13 BP.

XX AC ABH43890;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 243867 for detecting SNP TSC0059496.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB0000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 243867; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 2 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CGGACTTCATCC 16
DB 12 CGGAATTCACCC 1
|||||

RESULT 207

ABC19585/c
ID ABC19585 standard; DNA; 13 BP.

XX AC ABC19585;

DT 20-FEB-2002 (first entry)

XX

```
DE Oligonucleotide SEQ ID NO 19602 for detecting SNP TSC0004067.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 19602; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Claim 1; SEQ ID NO 19602; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 3 GAGCGACTTCAT 14
Db 13 GAGCGACTTCAT 2
RESULT 208
ABF35406/C
ID ABF35406 standard; DNA; 13 BP.
XX
XX ABF35406;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 135403 for detecting SNP TSC0033789.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotide SEQ ID NO 19602 for detecting SNP TSC0004067.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotide SEQ ID NO 257589 for detecting SNP TSC0062671.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 135403; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 6 CGACTTCATCCT 17
Db 13 CCAGTTCACCT 2
RESULT 209
ABH57612/C
ID ABH57612 standard; DNA; 13 BP.
XX
XX ABH57612;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 257589 for detecting SNP TSC0062671.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 135403; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
SQ
```



```

RESULT 212
ABH57610/c
ID ABH57610 standard; DNA; 13 BP.
XX
XX
AC ABH57610;
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 257587 for detecting SNP TSC0062671.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 257587 for detecting SNP TSC0062671.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 257587; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Claim 1; SEQ ID NO 257587; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. NO. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCCT 17
Db 13 CGAATTTATCCT 2
XX
XX
RESULT 213
ABC91634/c
ID ABC91634 standard; DNA; 13 BP.
XX
XX
AC ABC91634;
XX
DT 21-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 91651 for detecting SNP TSC0022938.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 257587; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. NO. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGCACTTC 12
Db 12 GTAAACGACTTC 1
XX
XX
RESULT 214
ABC93880/c
ID ABC93880 standard; DNA; 13 BP.
XX
XX
AC ABC93880;
XX
DT 21-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 93897 for detecting SNP TSC0023460.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
DE 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX

```


CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;
Query Match 47.8%; Score 8.6; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
:|||||
Db 1 RACTTCATC 9

RESULT 222
ABC97420/C
ID ABC97420 standard; DNA; 13 BP.

XX AC ABC97420;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 97437 for detecting SNP TSC0024195.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 97437; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;

Query Match 47.8%; Score 8.6; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
:|||||

Db 13 RACTTCATC 5

RESULT 223

ABC99715
ID ABC99715 standard; DNA; 13 BP.

XX AC ABC99715;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 99732 for detecting SNP TSC0024786.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX PS Claim 1; SEQ ID NO 99732; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 1 Other;

Query Match 47.8%; Score 8.6; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
:|||||
Db 1 RACTTCATC 9

RESULT 224

AAT29329
ID AAT29329 standard; DNA; 10 BP.

XX AC AAT29329;

XX DT 25-MAR-2003 (revised)

XX DT 28-JUN-1996 (first entry)

XX DE 5'-primer for mammalian G-protein coupled receptor coding sequences.

XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.
 XX Synthetic.
 OS
 XX WO9531574-A1.
 XX
 XX 23-NOV-1995.
 PD
 XX 12-MAY-1995; 95WO-US006032.
 PF
 XX 16-MAY-1994; 94US-00242887.
 XX
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA
 XX Lopeznieta CE, Nigam SK;
 PI
 XX WPI; 1996-010958/01.
 DR
 XX Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.
 XX
 XX Claim 46; Page 55; 72pp; English.
 PS
 XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
 CC
 XX Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 46.7%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. NO. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 7 GACTTCATCC 16
 Db 1 GCCTTCATCC 10
 RESULT 225
 AAZ78312
 ID AAZ78312 standard; DNA; 10 BP.
 XX
 AC AAZ78312;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:740.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 XX
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013800.
 PF
 XX 19-JUN-1998; 98US-0089833P.
 PR

PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE)/ ROBERTS B L.
 PA (SHAN)/ SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 PT
 XX Claim 1; Page 86; 130pp; English.
 PS
 XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for

```
CC recruitment of immune effector cells
XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACTTCCTCCT 10

RESULT 226
AAZ82306/C
ID AAZ82306 standard; DNA; 10 BP.
XX
AC AAZ82306;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1540.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
PI WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 99; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
```

```
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 10 GACTTCGATCC 1

RESULT 227
AAZ83715
ID AAZ83715 standard; DNA; 10 BP.
XX
AC AAZ83715;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2949.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
PI WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 138; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
```


CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
| | | | | | | |
Db 1 ACTTCACCT 10

RESULT 228
AAZ82968/c
ID AAZ82968 standard; DNA; 10 BP.

XX AC AAZ82968;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #2202.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

XX PS Claim 1; Page 118; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCGACTTCA 13
| | | | | | | |
Db 10 AGTGACTTCA 1

RESULT 229
AAF35444/c
ID AAF35444 standard; DNA; 10 BP.

XX AC AAF35444;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2183.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UJVO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

XX PS Example; Page 78; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 CTTTCATCCTT 18
 Db 10 CTTTATCCTT 1
 RESULT 230
 AAF42018
 ID AAF42018 standard; DNA; 10 BP.
 XX
 AC AAF42018;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8757.
 XX
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 OS WO200077214-A2.
 PN
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 PA Velulescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 312; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GAGCGACTTC 12
 Db 1 GAGCGACTTC 10
 RESULT 231
 AAF37674/c
 ID AAF37674 standard; DNA; 10 BP.
 XX
 AC AAF37674;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4413.
 XX
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 OS WO200077214-A2.
 PN
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 PA Velulescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 157; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 CGACTTCATC 15
 |||||
 Db 10 CGTCTTCATC 1

RESULT 232
 AAL39530/C
 ID AAL39530 standard; DNA; 10 BP.
 XX
 AC AAL39530;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE CCBP2 detecting ASO primer SEQ ID No 57.

Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
 polymorphic gene variant; single nucleotide polymorphism; human; primer;
 PCR; ss.

XX Homo sapiens.
 XX WO200232926-A2.
 XX 25-APR-2002.
 XX 12-OCT-2001; 2001WO-US042685.
 XX 12-OCT-2000; 2000US-0239638P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Armstrong B, Kazemi A, Koshy B;
 FI WPI; 2002-435524/46.
 XX

New genetic variants having polymorphisms in the chemokine binding
 protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
 treating disorders affected by expression or function of the CCBP2
 isogene.
 XX
 PS Claim 15; Page 14; 84pp; English.

XX The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic
 CC variants of the CCBP2 gene are useful in studying the expression and
 CC function of CCBP2, and in expressing CCBP2 proteins for use in screening
 CC candidate drugs for treating diseases associated with CCBP2 activity.
 CC Polynucleotides comprising a polymorphic gene variant or fragment may be
 CC used for therapeutic purposes, where a patient could benefit from
 CC expression or increased expression of a particular CCBP2 protein isoform,

CC or an expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. The polynucleotides of the invention can be used to
 CC treat disorders related to the CCBP2 gene by gene therapy. This
 CC polynucleotide sequence represents a preferred ASO primer for detecting
 CC CCBP2 gene polymorphisms relating to the invention
 XX

SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCTT 18
 |||||
 Db 10 CTGCATCCTT 1

RESULT 233
 AAX59717
 ID AAX59717 standard; DNA; 11 BP.
 XX
 AC AAX59717;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Modified RNA oligonucleotide of the invention.
 XX
 KW Oligodeoxyribonucleotide; intersubunit linkage;
 KW phosphoramidate intersubunit; antisense activity; nuclease resistant;
 KW in-vitro cell growth inhibition assay; infection;
 KW smooth muscle cell proliferation disorder; inflammatory process;
 KW genetic disorder; cancer; ss.
 XX
 OS Synthetic.

XX WO9525814-A1.
 XX 28-SEP-1995.
 XX 20-MAR-1995; 95WO-US003575.
 XX 18-MAR-1994; 94US-00210505.
 XX 18-MAR-1994; 94US-00214599.
 XX (LYNX-) LYNX THERAPEUTICS INC.
 XX
 FI Gryaznov SM, Schultz RG, Chen J;
 XX WPI; 1995-344627/44.
 XX

Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance
 toward phosphodiesterase digestion, and form stable duplexes with DNA and
 RNA strands.

PS Disclosure; Page 53; 101pp; English.

XX The specification describes oligodeoxyribonucleotides having contiguous
 CC nucleoside subunits joined by intersubunit linkages, where at least 3
 CC contiguous subunits are joined by phosphoramidate intersubunits. The
 CC oligodeoxyribonucleotides has a sequence of nucleoside subunits effective
 CC to form a duplex with a target nucleic acid molecule. The
 CC oligodeoxyribonucleotides are more resistant to nuclease digestion and
 CC have improved RNA and dsDNA hybridisation characteristics, relative to
 CC oligonucleotides not containing N3'-P5' phosphoramidate linkages. They
 CC also have excellent antisense activity against complementary mRNA targets
 CC in in-vitro cell growth inhibition assays. They also exhibit low
 CC cytotoxicity. They may be used in diagnostic and therapeutic
 CC applications, e.g., in combatting infectious agents such as bacteria,
 CC viruses, etc. or in treatment of smooth muscle cell proliferation
 CC disorders, inflammatory processes, certain genetic disorders, cancers,

CC etc. . The present sequence represents an oligonucleotide of the invention
SQ Sequence 11 BP; 1 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTTCCTCTT 10

RESULT 234

AAX59718
ID AAX59718 standard; DNA; 11 BP.

AC AAX59718;

DT 22-JUL-1999 (first entry)

XX Modified oligonucleotide containing N3'-PS' phosphoramidates.

DE Oligodeoxyribonucleotide; intersubunit linkage;
KW phosphoramidate intersubunit; antisense activity; nuclease resistant;
KW in-vitro cell growth inhibition assay; infection;
KW smooth muscle cell proliferation disorder; inflammatory process;
KW genetic disorder; cancer; ss.

XX Synthetic.

OS Key Location/Qualifiers

XX modified_base 1..11

FT /*tag= a
FT /note= "each base is linked by N3'-PS' phosphoramidate
linkages"

PN WO9525814-A1.

XX 28-SEP-1995.

XX 20-MAR-1995; 95WO-US003575.

XX 18-MAR-1994; 94US-00210505.

XX 18-MAR-1994; 94US-00214599.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Gryaznov SM, Schultz RG, Chen J;

XX WPI; 1995-344627/44.

XX Oligo:nucleotide N3'-PS' phosphoramidate(s) - have improved resistance
toward phosphodiesterase digestion, and form stable duplexes with DNA and
RNA strands.

PS Disclosure; Page 53; 101pp; English.

XX The specification describes oligodeoxyribonucleotides having contiguous
nucleoside subunits joined by intersubunit linkages, where at least 3
contiguous subunits are joined by phosphoramidate intersubunits. The
oligodeoxyribonucleotides has a sequence of nucleoside subunits effective
to form a duplex with a target nucleic acid molecule. The
oligodeoxyribonucleotides are more resistant to nuclease digestion and
have improved RNA and deDNA hybridisation characteristics, relative to
oligonucleotides not containing N3'-PS' phosphoramidate linkages. They
also have excellent antisense activity against complementary mRNA targets
in in-vitro cell growth inhibition assays. They also exhibit low
cytotoxicity. They may be used in diagnostic and therapeutic
applications, e.g., in combatting infections agents such as bacteria,
viruses, etc. or in treatment of smooth muscle cell proliferation
disorders, inflammatory processes, certain genetic disorders, cancers,
etc. . The present sequence represents an oligonucleotide of the invention

XX SQ Sequence 11 BP; 1 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTTCCTCTT 10

RESULT 235

AAX59716
ID AAX59716 standard; DNA; 11 BP.

AC AAX59716;

DT 22-JUL-1999 (first entry)

XX Modified oligonucleotide of the invention.

DE Oligodeoxyribonucleotide; intersubunit linkage;
KW phosphoramidate intersubunit; antisense activity; nuclease resistant;
KW in-vitro cell growth inhibition assay; infection;
KW smooth muscle cell proliferation disorder; inflammatory process;
KW genetic disorder; cancer; ss.

XX Synthetic.

OS WO9525814-A1.

XX 28-SEP-1995.

XX 20-MAR-1995; 95WO-US003575.

XX 18-MAR-1994; 94US-00210505.

XX 18-MAR-1994; 94US-00214599.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Gryaznov SM, Schultz RG, Chen J;

XX WPI; 1995-344627/44.

XX Oligo:nucleotide N3'-PS' phosphoramidate(s) - have improved resistance
toward phosphodiesterase digestion, and form stable duplexes with DNA and
RNA strands.

PS Disclosure; Page 52; 101pp; English.

XX The specification describes oligodeoxyribonucleotides having contiguous
nucleoside subunits joined by intersubunit linkages, where at least 3
contiguous subunits are joined by phosphoramidate intersubunits. The
oligodeoxyribonucleotides has a sequence of nucleoside subunits effective
to form a duplex with a target nucleic acid molecule. The
oligodeoxyribonucleotides are more resistant to nuclease digestion and
have improved RNA and deDNA hybridisation characteristics, relative to
oligonucleotides not containing N3'-PS' phosphoramidate linkages. They
also have excellent antisense activity against complementary mRNA targets
in in-vitro cell growth inhibition assays. They also exhibit low
cytotoxicity. They may be used in diagnostic and therapeutic
applications, e.g., in combatting infections agents such as bacteria,
viruses, etc. or in treatment of smooth muscle cell proliferation
disorders, inflammatory processes, certain genetic disorders, cancers,
etc. . The present sequence represents an oligonucleotide of the invention

XX SQ Sequence 11 BP; 1 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

```
XX 13-APR-1999 (first entry)
DT
XX
XX N3-P5 phosphoramidate oligonucleotide #10.
DE
XX
XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT misc_difference 1..11
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT linkages; also optionally contains 2'-fluorine
FT nucleosides"
XX
XX US5859233-A.
PN
XX
XX 12-JAN-1999.
PD
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
PR
XX 14-JUN-1996; 96US-00663918.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
PA
XX Gryaznov SM, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;
PI Fearon KL;
XX
XX WPI; 1999-120007/10.
DR
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT the synthesis of oligo-nucleotide(s).
XX
XX Example 19; Col 45; 34bp; English.
PS
XX
XX This sequence represents an example of an oligonucleotide containing
CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC sequence is generated synthetically by using an amine-exchange reaction
CC of phosphoramidites in which a deprotected 3'-amino group of an
CC oligonucleotide chain is exchanged for the amino portion of a 5'-
CC phosphoramidite with a protected 3' amino group. The resulting
CC phosphoramidite internucleotide linkage is oxidised to form a stable
CC protected phosphoramidate linkage
XX
XX Sequence 11 BP; 1 A; 4 C; 0 G; 0 T; 6 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CUUCUCCUU 10
RESULT 239
AAX14902/c
ID AAX14902 standard; DNA; 11 BP.
XX
XX AAX14902;
AC
XX
XX 24-MAR-1999 (first entry)
DT
XX
XX Triple helix forming nucleotides 459-469 of 23S rRNA gene.
DE
XX
XX Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
XX Clostridium pasteurianum.
OS
XX
XX US5861244-A.
PN
```

```
XX 19-JAN-1999.
PD
XX
XX 22-DEC-1993; 93US-00173489.
PF
XX
XX 29-OCT-1992; 92US-00968436.
PR
XX
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
PA
XX
XX Hepburn AG, Wang C;
PI
XX
XX WPI; 1999-130384/11.
DR
XX
XX Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
XX Disclosure; Col 23-24; 168pp; English.
XX
XX The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
XX Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 11 CTTCTCCTCT 2
RESULT 240
ABQ87262/c
ID ABQ87262 standard; cDNA; 11 BP.
XX
XX ABQ87262;
AC
XX
XX 10-SEP-2002 (first entry)
DT
XX
XX Human skin stress/ageing related EST SEQ ID NO 1017.
DE
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200253773-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP015178.
PF
XX
XX 03-JAN-2001; 2001DE-01000121.
PR
XX (HENK ) HENKEL KGAA.
PA
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
PT
```

PT screening for cosmetic or therapeutic agents, based on differential gene expression.

PS Claim 8; Page 79; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention

CC Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
DB 11 ACTTCACCT 2

RESULT 241
ABV65942/c

ID ABV65942 standard; cDNA; 11 BP.

AC ABV65942;

XX 21-OCT-2002 (first entry)

DE Human skin EST 3728.

XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

PS Disclosure; Page 128; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GACTTCATCC 16
DB 10 GACTTCATCC 1

RESULT 242
ABV71195/c

ID ABV71195 standard; cDNA; 11 BP.

XX ABV71195;

XX 21-OCT-2002 (first entry)

DE Human skin EST 8981.

XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

PS Claim 24; Page 288; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
DB 11 ACTTCACCT 2

```
RESULT 243
ABV65721/c
ID ABV65721 standard; cDNA; 11 BP.
XX AC
XX AC ABV65721;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3507.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX KW In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 122; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX PS Sequence 11 BP; 2 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
XX CC Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX CC Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GACTTCATCC 16
DB 10 GACATCATCC 1
RESULT 244
ABV65991
ID ABV65991 standard; cDNA; 11 BP.
XX AC
XX AC ABV65991;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 3777.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX KW In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 122; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX PS Sequence 11 BP; 2 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
XX CC Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX CC Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GACTTCATCC 16
DB 10 GACATCATCC 1
RESULT 245
ABV63774/c
ID ABV63774 standard; cDNA; 11 BP.
XX AC
XX AC ABV63774;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 1560.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX KW In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 129; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX PS Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX CC Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX CC Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
DB 2 ACTTCATCCT 11
RESULT 246
ABV63774/c
ID ABV63774 standard; cDNA; 11 BP.
XX AC
XX AC ABV63774;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 1560.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX KW In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 129; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX PS Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX CC Query Match 46.7%; Score 8.4; DB 1; Length 11;
XX CC Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
DB 2 ACTTCATCCT 11
```


Qy 9 CTTCATCCTT 18

```
Db          3 CATCATCCTT 12

RESULT 248
AAT42900/c
ID AAT42900 standard; DNA; 12 BP.
XX
XX
AC AAT42900;
XX
DT 10-JUN-1997 (first entry)
XX
DE bcr2/abl2 breakpoint target sequence.
XX
KW single stranded; circular; target sequence; parallel; detection;
KW binding domain; anti-parallel; loop domain; complementarity; ss;
KW synthesis; regulation; drug delivery; biosynthesis; tumour cell.
XX
OS Synthetic.
XX
XX WO9630384-A1.
XX
PD 03-OCT-1996.
XX
PF 21-MAR-1996; 96WO-US003757.
XX
PR 30-MAR-1995; 95US-00413813.
XX
PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
XX Kool ET;
XX
XX WPI; 1996-455262/45.
XX
PT Single stranded circular oligo:nucleotide comprising parallel and or anti
PT -parallel binding domain - used to regulate biosynthesis of DNA, RNA or
PT protein in targetted mammalian tumour cell in vivo.
XX
PS Example 11; Page 135; 195pp; English.
XX
CC The sequences given in AAT42898-901 are single stranded (ss) circular
CC oligonucleotides and their targets, which are used in the inhibition of
CC the proliferation of myeloid leukaemia cells. These oligos are
CC specifically targetted to a region in the bcr3/abl2 gene 385 nucleotides
CC 5' to the bcr/abl junction, abd towards the bcr2/abl2 junction. These ss
CC circular oligonucleotides comprise a parallel binding (P) domain, and/or
CC an anti-parallel binding (AP) domain, and at least 1 loop domain. The P
CC and AP domains have sufficient complementarity to bind detectably to 1
CC strand of a defined nucleic acid target. The P domain is capable of
CC binding in a parallel manner to the target. The AP domain is capable of
CC binding in an anti-parallel manner to the target and the ends of the P
CC and AP domains are separated by the loop domains. The ss circular
CC oligonucleotides can be used to regulate the synthesis of DNA, RNA or
CC protein (pref. by DNA replication, DNA reverse transcription, RNA
CC splicing, RNA polyadenylation, RNA translocation or protein
CC translocation) by binding a target sequence in the template. They can
CC also be used to deliver a drug to a specific cell type by administering a
CC drug covalently bound to them (i.e. to regulate the biosynthesis of DNA,
CC RNA or protein in a targetted mammalian tumour cell in vivo, without
CC substantially altering the biosynthesis of the DNA). They can also be
CC used to detect a target nucleic acid by detecting an oligonucleotide-
CC target complex. The circular oligonucleotide can bind both single and
CC double stranded target nucleic acids, and has enhanced stability,
CC compared to linear forms
XX
SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCTT 18
Db 12 CTTTCATCCTT 3

RESULT 249
AAA55925
ID AAA55925 standard; DNA; 12 BP.
XX
XX
AC AAA55925;
XX
DT 04-SEP-2000 (first entry)
XX
DE Adapter linker nucleotide sequence SEQ ID NO:84.
XX
KW Yeast; detection; protein-protein interaction; DNA-binding domain;
KW characterisation; identification; protein pathway information;
KW protein interaction domain; screening; PCR primer; adapter; linker;
KW fusion protein; inhibitor; regulation; ss.
XX
OS Synthetic.
XX
XX US6057101-A.
XX
PD 02-MAY-2000.
XX
PF 13-JUN-1997; 97US-00874825.
XX
PR 14-JUN-1996; 96US-00663824.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;
XX WPI; 2000-349567/30.
XX
PT Identifying, comparing and detecting inhibitors of protein-protein
PT interactions within population of host cells, involves detecting
PT regulation of transcription of nucleic acid sequence by fusion protein
PT interaction.
XX
PS Example; Col 131; 161pp; English.
XX
CC The present invention describes a method for detecting (D) at least 1
CC protein-protein interaction (PPI) by recombinantly expressing within a
CC population of host cells, populations of first and second fusion proteins
CC comprising DNA binding domain (DBD) and transcriptional regulatory domain
CC (TRD) respectively and detecting the regulation of transcription of
CC nucleotide sequence of host cells operably linked to a promoter driven by
CC DBD. The detection method (D) is useful for identifying inhibitors of PPI
CC stage of development and disease states. From the population of the
CC for therapeutic use, and for detecting specific cell types, tissue types,
CC proteins characteristic of the particular tissue or a cell-type, all
CC possible detectable PPI that occur can be identified and genes encoding
CC these proteins can be isolated. Thus, parallel analysis of two cell types
CC enumerates PPI that are common to both and those that are specific to
CC both. This analysis has significant value since PPI specific to a disease
CC state can serve as therapeutic points of intervention. Inhibitors of PPI
CC can also be isolated in rapid fashion. The number of false positives and
CC low throughput are reduced. AAA55843 to AAA55963 and AAY90961 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 12 BP; 1 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GCGACTTCAT 14
Db 2 GCGACTTCAT 11

RESULT 250
AAA55940
ID AAA55940 standard; DNA; 12 BP.
```

```
XX AAA55940;
AC
XX
XX
DT 04-SEP-2000 (first entry)
XX
XX Adapter linker nucleotide sequence SEQ ID NO:99.
XX
XX Yeast; detection; protein-protein interaction; DNA-binding domain;
KW characterisation; identification; protein pathway information;
KW protein interaction domain; screening; PCR primer; adapter; linker;
KW fusion protein; inhibitor; regulation; ss.
XX
OS Synthetic.
XX
XX US6057101-A.
XX
XX 02-MAY-2000.
XX
XX 13-JUN-1997; 97US-00874825.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;
PI WPI; 2000-349567/30.
XX
XX Identifying, comparing and detecting inhibitors of protein-protein
PT interactions within population of host cells, involves detecting
PT regulation of transcription of nucleic acid sequence by fusion protein
PT interaction.
XX
XX Example; Col 131; 161pp; English.
XX
XX The present invention describes a method for detecting (D) at least 1
CC protein-protein interaction (PPI) by recombinantly expressing within a
CC population of host cells, populations of first and second fusion proteins
CC comprising DNA binding domain (DBD) and transcriptional regulatory domain
CC (TRD) respectively and detecting the regulation of transcription of
CC nucleotide sequence of host cells operably linked to a promoter driven by
CC DBD. The detection method (D) is useful for identifying inhibitors of PPI
CC for therapeutic use, and for detecting specific cell types, tissue types,
CC stage of development and disease states. From the population of the
CC proteins characteristic of the particular tissue or a cell-type, all
CC possible detectable PPI that occur can be identified and genes encoding
CC these proteins can be isolated. Thus, parallel analysis of two cell types
CC enumerates PPI that are common to both and those that are specific to
CC both. This analysis has significant value since PPI specific to a disease
CC state can serve as therapeutic points of intervention. Inhibitors of PPI
CC can also be isolated in rapid fashion. The number of false positives and
CC low throughput are reduced. AAA55943 to AAA55963 and AAY90961 are
CC sequences used in the exemplification of the present invention
XX
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 251
AAA73437
ID AAA73437 standard; DNA; 12 BP.
XX
XX AAA73437;
AC
XX
XX 09-FEB-2001 (first entry)
DT
XX
```

```
DE Linker JA7.
XX
XX Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW ss.
XX
XX Saccharomyces cerevisiae.
XX
XX US6083693-A.
XX
XX 04-JUL-2000.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Nandabalan K, Rothberg JM;
PI WPI; 2000-464335/40.
XX
XX Detecting protein-protein interactions in protein populations useful for
PT identifying genes encoding the proteins, and inhibitors of the
PT interactions, by detecting transcriptional regulation leading to reporter
PT gene activation.
XX
XX Example; Col 103-104; 135pp; English.
XX
XX The present invention relates to methods for detecting and isolating
CC genes encoding proteins that interact with each other, via the
CC reconstitution of a transcription factor and hence reporter gene
CC activation. Proteins are fused to either the yeast DNA-binding domain of
CC a transcriptional activator or to the activation domain of a
CC present invention as an adapter in the analysis of yeast fusion genes.
CC The present method may be used to identify protein-protein interactions
CC and genes encoding the interacting proteins relevant to a particular
CC tissue, stage or disease e.g. cancer
XX
XX Sequence 12 BP; 1 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 252
AAA73452
ID AAA73452 standard; DNA; 12 BP.
XX
XX AAA73452;
AC
XX
XX 09-FEB-2001 (first entry)
DT
XX
XX Linker JC7.
DE
XX
XX Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW ss.
XX
XX Saccharomyces cerevisiae.
XX
XX US6083693-A.
XX
XX 04-JUL-2000.
XX
XX 14-JUN-1996; 96US-00663824.
XX
XX 14-JUN-1996; 96US-00663824.
XX
```

PA (CURA-) CURAGEN CORP.
 XX
 PI Nandabalan K, Rothberg JM;
 XX
 DR WPI; 2000-464335/40.
 XX
 PT Detecting protein-protein interactions in protein populations useful for
 PT identifying genes encoding the proteins, and inhibitors of the
 PT interactions, by detecting transcriptional regulation leading to reporter
 PT gene activation.
 XX
 XX Example; Col 103-104; 135pp; English.
 PS
 CC The present invention relates to methods for detecting and isolating
 CC genes encoding proteins that interact with each other, via the
 CC reconstitution of a transcription factor and hence reporter gene
 CC activation. Proteins are fused to either the yeast DNA-binding domain of
 CC a transcriptional activator or to the activation domain of a
 CC transcriptional activator. The present sequence is a linker used in the
 CC present invention as an adapter in the analysis of yeast fusion genes.
 CC The present method may be used to identify protein-protein interactions
 CC and genes encoding the interacting proteins relevant to a particular
 CC tissue, stage or disease e.g. cancer
 XX
 SQ Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGACTTCAT 14
 DB 2 GCGCTTCAT 11
 RESULT 253
 AAH23505/c
 ID AAH23505 standard; DNA; 12 BP.
 XX AC AAH23505;
 XX
 DT 03-AUG-2001 (first entry)
 XX
 DE Antibacterial peptide nucleic acid oligonucleotide #18.
 XX
 KW Peptide nucleic acid; PNA; antimicrobial; antibiotic; cationic peptide;
 KW antisense; disinfectant; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "linked to AAB99988 by 8-amino-3,6-dioxaoctanoic
 FT acid"
 XX
 PN WO200127262-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-DK000581.
 XX
 PR 13-OCT-1999; 99DK-00001468.
 PR 15-OCT-1999; 99US-0159683P.
 XX
 PA (PANT-) PANTECO AS.
 XX
 PI Nielsen PE, Schou C, Wissenbach M;
 XX
 DR WPI; 2001-290722/30.
 XX
 XX Identifying target genes in a microorganism (e.g. Escherichia coli) as a

PT basis for anti-infective treatment comprises selecting potential targets
 PT known to be present and obtaining complementary (antisense) peptide
 PT nucleic acid sequences.
 XX
 PS Claim 31; Page 42; 57pp; English.
 XX
 CC The present invention describes a method of identifying target genes, for
 CC use in anti-infective treatments, in a microorganism, involving obtaining
 CC antisense peptide nucleic acid (PNA) sequences for potential target
 CC genes, mixing them with the organism in culture and comparing the growth
 CC in the presence and absence of the antisense PNA sequence, where a useful
 CC target gene is one which results in decreased growth when blocked by the
 CC antisense sequence. Antisense oligonucleotides are linked to cationic
 CC peptides via a linking group for use as antimicrobial compounds,
 CC particularly as antibiotics. The present sequence is an oligonucleotide
 CC useful as the antisense portion of a PNA in the present invention
 XX
 SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGAGCGACTT 11
 DB 11 TGAGCGACTT 2
 RESULT 254
 ABI38653
 ID ABI38653 standard; DNA; 12 BP.
 XX AC ABI38653;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 338626 for detecting SNP TSC0040587.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 338626; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
 |||||
 Db 2 ACTTCACCT 11

RESULT 255

ABH8708
 ID ABH8708 standard; DNA; 12 BP.

XX AC ABH8708;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 288701 for detecting SNP TSC0013636.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 288701; 29pp + Sequence Listing; German.

XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
 |||||
 Db 3 ACTTCATCCT 12

RESULT 256

ABI40787/c

ID ABI40787 standard; DNA; 12 BP.

XX AC ABI40787;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 340760 for detecting SNP TSC0010072.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 340760; 29pp + Sequence Listing; German.

XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
 |||||
 Db 12 ACTTCCTCT 3

RESULT 257

ABI71673/c

ID ABI71673 standard; DNA; 12 BP.

XX AC ABI71673;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 371646 for detecting SNP TSC0000146.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 371646; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. NO. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 9 CTTATCCTT 18
 DB 12 CTATCCTT 3
 RESULT 258
 ABI77738
 ID ABI77738 standard; DNA; 12 BP.
 XX AC
 XX ABI77738;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 377711 for detecting SNP TSC0062457.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 377711; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. NO. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 8 ACTTCATCCT 17
 DB 2 ACTTCACCT 11
 RESULT 259
 ABI66111/C
 ID ABI66111 standard; DNA; 12 BP.
 XX AC
 XX ABI66111;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 366084 for detecting SNP TSC0008114.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 366084; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
Db 11 AATTCATCCT 2
| | | | | | | |

RESULT 260
ABI02919/C
ID ABI02919 standard; DNA; 12 BP.

AC ABI02919;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 302892 for detecting SNP TSC0020209.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 302892; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
Db 12 ACTTCCTCCT 3
| | | | | | | |

RESULT 261
ABI15957
ID ABI15957 standard; DNA; 12 BP.

AC ABI15957;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 315930 for detecting SNP TSC0027171.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 315930; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCCT 17
Db 3 AATTCATCCT 12
| | | | | | | |

RESULT 262
ABI15994
ID ABI15994 standard; DNA; 12 BP.

```

XX AC AB115994;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 315967 for detecting SNP TSC0027203.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 315967; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 6 CGACTTCATC 15
XX | | | | |
XX 1 CCACCTTCATC 10
XX
XX RESULT 263
XX ABI72532
XX ID ABI72532 standard; DNA; 12 BP.
XX
XX AC ABI72532;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 372505 for detecting SNP TSC0059425.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX

```

```

PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 372505; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCT 17
XX | | | | |
XX 2 ACTCCATCCT 11
XX
XX Db
XX
XX RESULT 264
XX ABI63681
XX ID ABI63681 standard; DNA; 12 BP.
XX
XX AC ABI63681;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 363654 for detecting SNP TSC0053988.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX

```


XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 363654; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABCG9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
Db 3 ACTTCATCCT 12
|||||
RESULT 265
ABI21944
ID ABI21944 standard; DNA; 12 BP.
XX
AC ABI21944;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 321917 for detecting SNP TSC0030566.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 321917; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABCG9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 CTTTCATCCTT 18
Db 2 CTTTCATCCTT 11
|||||
RESULT 266
ABI10721/c
ID ABI10721 standard; DNA; 12 BP.
XX
AC ABI10721;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 310694 for detecting SNP TSC0024054.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 310694; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABCG9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      8 ACTTCATCCT 17
Db      12 ACTTCATCCT 3

RESULT 267
ABI12430
ID      ABI12430 standard; DNA; 12 BP.
XX
XX      AC      ABI12430;
XX
XX      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 312403 for detecting SNP TSC0025040.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
XX
XX      WO200177384-A2.
XX
XX      18-OCT-2001.
XX
XX      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 312403 for detecting SNP TSC0025040.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
XX
XX      WO200177384-A2.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-IB000713.
XX
XX      07-APR-2000; 2000DE-01019173.
XX
XX      (EPIG-) EPIGENOMICS AG.
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI      WPI; 2001-657177/75.
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 312403; 29pp + Sequence Listing; German.
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ      Query Match      46.7%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 2e+02;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACTTCATCCT 17
Db      1 ACTTCATCAT 10

RESULT 268
ABI42318
ID      ABI42318 standard; DNA; 12 BP.
XX
XX      AC      ABI42318;
XX
XX      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 345257 for detecting SNP TSC0043935.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
XX
XX      WO200177384-A2.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-IB000713.

```

```

DE      Oligonucleotide primer SEQ ID NO 342291 for detecting SNP TSC0042479.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
XX
XX      WO200177384-A2.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-IB000713.
XX
XX      07-APR-2000; 2000DE-01019173.
XX
XX      (EPIG-) EPIGENOMICS AG.
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI      WPI; 2001-657177/75.
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 342291; 29pp + Sequence Listing; German.
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
SQ      Query Match      46.7%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 2e+02;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACTTCATCCT 17
Db      3 ACTTAATCCT 12

RESULT 269
ABI45284/c
ID      ABI45284 standard; DNA; 12 BP.
XX
XX      AC      ABI45284;
XX
XX      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 345257 for detecting SNP TSC0043935.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
XX
XX      WO200177384-A2.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-IB000713.

```

XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 345257; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. NO. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 ACTTCATCCT 17
 |||||
 Db 11 ACATCATCCT 2
 RESULT 270
 ABI46259/c
 ID ABI46259 standard; DNA; 12 BP.
 AC AC
 XX ABI46259;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 346232 for detecting SNP TSC0044449.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 346232; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. NO. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CGACTTCATC 15
 |||||
 Db 12 CTACTTCATC 3
 RESULT 271
 ABI69695
 ID ABI69695 standard; DNA; 12 BP.
 XX AC ABI69695;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 369668 for detecting SNP TSC0057773.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 369668; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 3 CTTTCATCCT 12

RESULT 272
ABI80833
ID ABI80833 standard; DNA; 12 BP.
XX
AC ABI80833;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 380806 for detecting SNP TSC0005399.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 380806; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 3 ACTTCATCCT 12

RESULT 273
ABI37248
ID ABI37248 standard; DNA; 12 BP.
XX
XX ABI37248;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 337221 for detecting SNP TSC0039744.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 337221; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 3 CTTTCATCCTT 12

RESULT 274
ABI38368
ID ABI38368 standard; DNA; 12 BP.
XX
XX ABI38368;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 338341 for detecting SNP TSC0040412.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```

XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 338341; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 9 CTCATCCTT 18
XX DB 3 CTCCTCCTT 12
XX RESULT 275
XX ABI58052/c
XX ID ABI58052 standard; DNA; 12 BP.
XX AC ABI58052;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 358025 for detecting SNP TSC0050921.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.

```

```

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 358025; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 9 CTCATCCTT 18
XX DB 10 CTCCTCCTT 1
XX RESULT 276
XX ABI65300/c
XX ID ABI65300 standard; DNA; 12 BP.
XX AC ABI65300;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 365273 for detecting SNP TSC0055020.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 365273; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The

```



```

XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 340372 for detecting SNP TSC0041492.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPiG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 340372; 29pp + Sequence Listing; German.
XX PS This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
XX Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
Db 11 ACTTCACACT 2
||||| |||
RESULT 280
ABI49646/c
ID ABI49646 standard; DNA; 12 BP.
XX AC ABI49646;
XX XX 22-FEB-2002 (first entry)
XX DT Oligonucleotide primer SEQ ID NO 349619 for detecting SNP TSC0000115.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 340372; 29pp + Sequence Listing; German.
XX PS This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
XX Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
Db 11 ACTTCACACT 2
||||| |||
RESULT 280
ABI49646/c
ID ABI49646 standard; DNA; 12 BP.
XX AC ABI49646;
XX XX 22-FEB-2002 (first entry)
XX DT Oligonucleotide primer SEQ ID NO 349619 for detecting SNP TSC0050383.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 349619; 29pp + Sequence Listing; German.
XX PS This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
XX Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
Db 12 ACTTCACACT 3
||||| |||
RESULT 281
ABI56964
ID ABI56964 standard; DNA; 12 BP.
XX AC ABI56964;
XX XX 22-FEB-2002 (first entry)
XX DT Oligonucleotide primer SEQ ID NO 356937 for detecting SNP TSC0050383.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF Claim 1; SEQ ID NO 349619; 29pp + Sequence Listing; German.
XX PS This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
XX Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 8 ACTTCATCCT 17
Db 12 ACTTCACACT 3
||||| |||

```

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 356937; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18

Db 2 CTTTCATCCTT 11

RESULT 282

ABI61170/C

ID ABI61170 standard; DNA; 12 BP.

XX AC ABI61170;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 361143 for detecting SNP TSC0052469.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX Claim 1; SEQ ID NO 361143; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;

Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 17

Db 11 ACTTCATCCTT 2

RESULT 283

ABI64864/C

ID ABI64864 standard; DNA; 12 BP.

XX AC ABI64864;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 364837 for detecting SNP TSC0054755.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX Claim 1; SEQ ID NO 364837; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;

Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 17

Db 11 ACTTCATCCTT 2


```

Db      10 ATTTCATCCT 1
RESULT 284
ABI19099/c
ID      ABI19099 standard; DNA; 12 BP.
XX
XX
AC      ABI19099;
XX
XX      22-FEB-2002 (first entry)
DT
DE
DE      Oligonucleotide primer SEQ ID NO 319072 for detecting SNP TSC0029057.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX      WO200177384-A2.
PN
PD      18-OCT-2001.
XX
XX      22-FEB-2002 (first entry)
DT
DE
DE      Oligonucleotide primer SEQ ID NO 319072 for detecting SNP TSC0029057.
XX
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX      WO200177384-A2.
PN
PD      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX      07-APR-2000; 2000DE-01019173.
PR
XX      (EPIG-) EPIGENOMICS AG.
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI
XX      WPI; 2001-657177/75.
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 319072; 29pp + Sequence Listing; German.
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      46.7%; Score 8.4; DB 1; Length 12;
XX      Best Local Similarity 90.0%; Pred. No. 2e+02;
XX      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      9 CTTCATCCTT 18
XX      |||||
XX      10 CTTCATCCTT 1
XX
XX      RESULT 285
XX      ABI43005/c
XX      ID      ABI43005 standard; DNA; 12 BP.
XX
XX      AC      ABI43005;
XX
XX      22-FEB-2002 (first entry)
DT
DE
DE      Oligonucleotide primer SEQ ID NO 342978 for detecting SNP TSC0042816.
XX
XX
XX

```

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 357004; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 12 CTTTCATCATT 3
RESULT 287
ABI38765
ID ABI38765 standard; DNA; 12 BP.
XX AC ABI38765;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 338738 for detecting SNP TSC0040647.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 338738; 29pp + Sequence Listing; German.
PS
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCTT 10
RESULT 288
ABI22662
ID ABI22662 standard; DNA; 12 BP.
XX AC ABI22662;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 322635 for detecting SNP TSC0030983.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 322635; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

RESULT 290
ABI69275

```
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 281260; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCCTT 18
XX Db 10 CTTTATCCTT 1
XX
XX RESULT 292
XX ABI43520
XX ID ABI43520 standard; DNA; 12 BP.
XX AC ABI43520;
XX XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 343493 for detecting SNP TSC0006855.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 343493; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCCTT 18
XX Db 10 CTTTATCCTT 1
XX
XX RESULT 293
XX ABI52994/C
XX ID ABI52994 standard; DNA; 12 BP.
XX AC ABI52994;
XX XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 352967 for detecting SNP TSC0005329.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 352967; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
```

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

OY 9 CTTTCATCCTT 18
 Db 11 CATCATCCTT 2

RESULT 294
 ABI10951/c
 ID ABI10951 standard; DNA; 12 BP.

XX AC ABI10951;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 310924 for detecting SNP TSC0024213.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 310924; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GACTTCATCC 16
 Db 12 GACTTAATCC 3

RESULT 295
 ABI40854/c
 ID ABI40854 standard; DNA; 12 BP.

XX AC ABI40854;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 340827 for detecting SNP TSC0041695.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 340827; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 ACTTCATCCT 17
 Db 10 ACTTCCTCT 1

RESULT 296
 ABI22663
 ID ABI22663 standard; DNA; 12 BP.

XX AC ABI22663;

XX DT 22-FEB-2002 (first entry)

```
XX Oligonucleotide primer SEQ ID NO 322636 for detecting SNP TSC0030983.
DE
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 322636; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCT 17
XX 1 ATTTTCATCCT 10
XX
XX RESULT 297
XX ABI08313/c
XX ID ABI08313 standard; DNA; 12 BP.
XX
XX AC ABI08313;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 308286 for detecting SNP TSC0022939.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 322636; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCT 17
XX 1 ATTTTCATCCT 10
XX
XX RESULT 297
XX ABI08313/c
XX ID ABI08313 standard; DNA; 12 BP.
XX
XX AC ABI08313;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 308286 for detecting SNP TSC0022939.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 308286; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 46.7%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 CGACTTCATC 15
XX 10 CGCCTTCATC 1
XX
XX RESULT 298
XX ABI22803
XX ID ABI22803 standard; DNA; 12 BP.
XX
XX AC ABI22803;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 322776 for detecting SNP TSC0031055.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
```

XX Claim 1; SEQ ID NO 322776; 29pp + Sequence Listing; German.
PS
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTCAACCTT 10

RESULT 299
ABH76196/c
ID ABH76196 standard; DNA; 12 BP.
XX AC ABH76196;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 276189 for detecting SNP TSC0004112.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 276189; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 17
Db 10 ACTACATCCTT 1

RESULT 300
ABI50334/c
ID ABI50334 standard; DNA; 12 BP.
XX AC ABI50334;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 350307 for detecting SNP TSC0000731.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 350307; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 10 CTTCTCCTT 1


```

CC of the invention
XX Sequence 12 BP; 1 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
SQ

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGGCTTCAT 11

RESULT 306
AAV29361
ID AAT29361 standard; DNA; 10 BP.
XX AC AAT29361;
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
DE 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX Synthetic.
XX OS
XX PN WO9531574-A1.
XX 23-NOV-1995.
XX 12-MAY-1995; 95WO-US006032.
XX 16-MAY-1994; 94US-00242887.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX Lopeznielo CE, Nigam SK;
XX WPI; 1996-010958/01.
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX Claim 46; Page 55; 72pp; English.
XX
CC The 5'-primers AAT29262-382, and the complementary 3'-primers derived
CC from them, which target mammalian G-protein coupled receptor coding
CC sequences, together comprise a PCR primer kit. The kit is used in a new
CC method for the characterisation of nucleic acid sequences obtd. from
CC mammalian biological samples, which comprises PCR amplification and
CC indexing of the prods. w.r.t the primer pair that hybridised to its
CC delineating subsequences. The method may be used in the identification,
CC cloning and analysis of genes, e.g. in genome mapping, and disease
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
Db 3 CTTTCATCC 10

RESULT 307
AAV34979/c
ID AAV34979 standard; DNA; 10 BP.
XX AC AAV34979;
XX 13-OCT-1998 (first entry)
DE Synthetic Agaricus bisporus RAPD primer.
XX Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
XX Synthetic.
XX OS
XX PN WO9821975-A1.
XX 28-MAY-1998.
XX 19-NOV-1996; 96WO-US018686.
XX 19-NOV-1996; 96WO-US018686.
XX (AMYC-) AMYCEL INC.
XX Loftus MG, Lodder SC, Legg EJ;
PI WPI; 1998-312054/27.
XX New strains of Agaricus bisporus with improved cap whiteness - compared
PT with the U1 strain but retaining other desirable features of this strain.
XX Disclosure; Page 10; 26pp; English.
XX
CC The sequence is that of an RAPD (random amplified DNA) primer which was
CC used in the isolation of an Agaricus bisporus mushroom strain which has
CC whiter caps, less scaling than known strains, particularly for mushrooms
CC produced in the first break, so it is more valuable (suitable for
CC marketing fresh rather than canning). It also retains the desirable
CC characteristics (good cap shape and shelf life, thick stem and veil) of
CC the U1 strain
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGACTTC 12
Db 9 GCGACTTC 2

RESULT 308
AAV28665/c
ID AAV28665 standard; DNA; 10 BP.
XX AC AAV28665;
XX 07-APR-2000 (first entry)
DE Metastatic breast tumour cell upregulated transcript tag #1899.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX PN WO9965928-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX

```

```

PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 110; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTTTCATCC 16
Db 10 CTTTCATCC 3
RESULT 309
AAZ83780
ID AAZ83780 standard; DNA; 10 BP.
XX
AC AAZ83780;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #3014.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
FD 23-DEC-1999.
XX

PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 139; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 GAGCGACT 10
Db 3 GAGCGACT 10
RESULT 310
AAZ85774/C
ID AAZ85774 standard; DNA; 10 BP.
XX
AC AAZ85774;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5008.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
FD

```

```

PD 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 192; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
CC to AA286677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCC 16
XX |||||
XX 10 CTTTCATCC 3
XX
XX RESULT 311
XX AAF37636
XX ID AAF37636 standard; DNA; 10 BP.
XX
XX AC AAF37636;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4375.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.

```

```

XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 156; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 4 A; 2 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 7 GACTTCAT 14
XX |||||
XX 1 GACTTCAT 8
XX
XX Db
XX
XX RESULT 312
XX AAF34559/C
XX ID AAF34559 standard; DNA; 10 BP.
XX
XX AC AAF34559;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1298.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX serial analysis of gene expression; antifungal; tag; identification;
XX

```

KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 PD 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UWJO) UNIV JOHNS HOPKINS.
 PA Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 PS Example; Page 46; 419pp; English.
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33288 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GCGACTTC 12
 DB 8 GCGACTTC 1
 RESULT 313
 AAF35638/c
 ID AAF35638 standard; DNA; 10 BP.
 XX AAF35638;
 AC AAF35638;
 XX 23-MAR-2001 (first entry)
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2377.
 XX

KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 PD 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UWJO) UNIV JOHNS HOPKINS.
 PA Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 PS Example; Page 84; 419pp; English.
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33288 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACTTCATC 15
 DB 10 ACTTCATC 3
 RESULT 314
 ABK24272
 ID ABK24272 standard; DNA; 10 BP.
 XX ABK24272;
 AC ABK24272;
 XX 09-APR-2002 (first entry)
 DT

XX Retinaldehyde-binding protein 1 ASO primer extension primer #45.
DE Human; retinaldehyde-binding protein 1; ss; RLBp1; haplotype; primer;
KW genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
KW chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
XX Homo sapiens.
XX WO200192278-A2.
XX 06-DEC-2001.
XX 29-MAY-2001; 2001WO-US017252.
XX 26-MAY-2000; 2000US-0207618P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Choi JY, Kazemi A, Koshy B;
PI WPI; 2002-122053/16.
XX New genetic variants having polymorphisms in the retinaldehyde-binding
PT protein 1 gene, useful for studying the function of and for expressing
PT RLBp1 protein for use in screening drugs for treating diseases related to
PT RLBp1 activity.
XX Claim 18; Page 14; 107pp; English.
XX The invention relates to an isolated polynucleotide, which comprises
CC genes and haplotypes of the retinaldehyde-binding protein 1 (RLBp1) gene.
CC The polynucleotide comprises polymorphic sites in the RLBp1 gene, which
CC are referred to as PSL-24 to designate the order in which they are
CC genotyping the RLBp1 gene of an individual, a method for predicting a
CC haplotype pair for the RLBp1 gene of an individual, a method for
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of the RLBp1 gene, a composition comprising at least one
CC genotyping oligonucleotide for detecting a polymorphism in the RLBp1 gene
CC at a PS consisting of PSL-PS24, a kit for genotyping the RLBp1 gene of an
CC individual comprising a set of oligonucleotides designed to genotype each
CC of PSL-PS24 recombinant non-human organisms transformed or transfected
CC with the isolated polynucleotide, where the organism expresses a RLBp1
CC protein encoded by the first nucleotide sequence or expresses a RLBp1
CC protein encoded by the polymorphic variant sequence, an isolated
CC polypeptide comprising an amino acid sequence that is a polymorphic
CC variant of a reference sequence for the RLBp1 protein or its fragment, an
CC anti-RLBp1 antibody, a method for screening for drugs targeting the
CC isolated polypeptide, and a computer system for storing and analysing
CC polymorphism data for the RLBp1 oncogene gene. The polynucleotide
CC comprising polymorphisms in the RLBp1 gene is useful in studying the
CC expression and function of RLBp1, and in expressing RLBp1 protein for use
CC in screening candidate drugs to treat diseases related to RLBp1 activity
CC (e.g. autosomal recessive retinitis pigmentosa (arRP)). The methods and
CC haplotypes are useful in improving the efficiency and output of several
CC steps in the drug discovery and development process, including target
CC validation, identifying lead compounds, and early phase clinical trials.
CC These are also useful for designing clinical trials of candidate drugs
CC for treating a specific condition or disease, as well as for screening
CC compounds targeting RLBp1 to treat a specific condition or disease
CC predicted to be associated with RLBp1 activity. The kit and method are
CC useful for determining whether an individual has one of the haplotypes or
CC haplotype pairs cited above. The transgenic animals are useful for
CC studying expression of the RLBp1 isogenes in vivo, for in vivo screening
CC and testing of drugs targeted against RLBp1 protein, and for testing the
CC efficacy of therapeutic agents and compounds for retinal diseases in a
CC biological system. The gene for RLBp1 is located on chromosome 15q26. The
CC present sequence is an allele specific oligonucleotide (ASO) PCR primer
CC for amplifying a nucleic acid containing a polymorphic RLBp sequence,
XX using the primer extension method
XX Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
Oy 11 TCATCCTT 18
| | | | | | | |
Db 2 TCATCCTT 9
RESULT 315
AAD32203/C
ID AAD32203 standard; DNA; 10 BP.
XX AAD32203;
XX 18-JUN-2002 (first entry)
XX Human NFKBIB gene polymorphism detecting primer #2.
XX Human; drug screening; polymorphism; haplotype; immune system disorder;
KW nuclear factor of kappa light polypeptide gene enhancer; beta gene;
KW B-cell inhibitor; NFKBIB; gene therapy; chromosome 19q13.1; primer; ss.
XX Homo sapiens.
XX WO200212497-A2.
XX 14-FEB-2002.
XX 03-AUG-2001; 2001WO-US024303.
XX 03-AUG-2000; 2000US-0222552P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Choi JY, Kazemi A, Koshy B;
XX WPI; 2002-269091/31.
XX Novel human Nuclear Factor of Kappa Light Polypeptide Gene Enhancer in B-
PT Cells Inhibitor, Beta, (NFKBIB) gene polymorphic variants, useful for
PT screening drug candidates to treat disorders of the immune system.
XX Claim 18; Page 13; 71pp; English.
XX The invention relates to a polynucleotide sequence comprising a human
CC nuclear factor of kappa light polypeptide gene enhancer in B-cells
CC inhibitor, beta (NFKBIB) isogene. The NFKBIB is useful for screening
CC drugs and therapeutic purposes. The polymorphism and haplotype data is
CC useful for validating whether NFKBIB is a suitable target for drugs to
CC treat disorders of immune system, screening for such drugs and reducing
CC bias in clinical trials of such drugs. NFKBIB is useful in studying the
CC effect of variation on the biological activity of NFKBIB as well as on
CC the binding affinity of candidate drugs targeting disorders of immune
CC system. The isolated monoclonal antibody is useful for diagnostic and
CC prognostic formats and therapeutic methods. The genotyping method is
CC useful for determining whether an individual has one of haplotype or
CC haplotype pair. The haplotyping method is useful for improving efficiency
CC and outcome of several steps in discovery and development of drugs for
CC treating diseases associated with NFKBIB activity such as disorders of
CC immune system. The haplotyping method is also useful for validating
CC NFKBIB as a candidate target for treating a specific condition or disease
CC predicted to be associated with NFKBIB activity. The method is also
CC useful for screening compounds to treat a specific condition or disease
CC predicted to be associated with NFKBIB activity. NFKBIB gene is useful in
CC gene therapy and is located on chromosome 19q13.1. The present sequence
CC is human NFKBIB gene polymorphism detecting primer
XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8
 Db 8 GTGAGCGA 1

RESULT 316
 ID AAD31708/c
 AC AAD31708
 XX AAD31708
 DT 18-JUN-2002 (first entry)
 XX Human CD39L2 initiation start site #2.

XX Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
 KW dermatological; immunosuppressive; vulnary; neurotropic; anticonvulsant;
 KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH misc_signal 7..9
 FT /*tag= a
 FT /note= "Initiation codon"

XX US6350447-B1.
 XX 26-FEB-2002.
 XX 29-JAN-1999; 99US-00240639.
 XX 29-JAN-1999; 99US-00240639.
 XX (HYSE-) HYSEQ INC.
 XX Chadwick BP, Frischauf A;
 XX WPI; 2002-215262/27.

XX An isolated polypeptide with phosphohydrolase activity, designated
 CD39L2, useful to identify other proteins with which binding occurs or
 PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 PT sclerosis and osteoporosis.

XX Example; Col 56; 101pp; English.

XX The present invention relates to novel proteins with phosphohydrolase
 CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
 CC encoding such proteins. CD39L proteins are useful to treat infectious
 CC diseases caused by viral, bacterial, fungal or other infection that may
 CC be treatable with CD39L. They are useful in the treatment of various
 CC immune deficiencies and disorders, autoimmune disorders such as multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
 CC and conditions such as asthma and other respiratory problems, periodontal
 CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
 CC They may have utility in compositions used for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration as well as for wound
 CC healing and tissue repair and replacement and in the treatment of burns,
 CC incisions and ulcers. CD39L proteins may also be useful for proliferation
 CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
 CC the treatment of central nervous system diseases such as Alzheimer's

CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
 CC disease, peripheral nervous system diseases peripheral nerve injuries,
 CC peripheral neuropathy and localised neuropathies. They are also used to
 CC treat mechanical and traumatic disorders which involve degeneration,
 CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
 CC invention are also useful to promote better or faster closure of non-
 CC healing wounds, including pressure ulcers, ulcers associated with
 CC vascular insufficiency and surgical and traumatic wounds. They also
 CC exhibit anti-inflammatory activity and may be used to treat inflammatory
 CC conditions including chronic or acute conditions), including ischaemia-
 CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
 CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
 CC disease. The present sequence is human CD39L2 initiation start site

XX SQ Sequence 10 BP; 5 A; 1 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
 Db 10 TCATCCTT 3

RESULT 317
 AAD26873
 ID AAD26873 standard; DNA; 10 BP.
 XX AAD26873;
 AC AAD26873;
 XX 26-MAR-2002 (first entry)
 DT Human GPR4 gene polymorphism detecting primer #14.

XX Human; G-protein coupled receptor 4; GPR4; haplotyping; polymorphism;
 KW allele-specific oligonucleotide; ASO; primer; ss.
 XX Homo sapiens.
 XX WO200187904-A2.
 XX 22-NOV-2001.
 XX 09-MAY-2001; 2001WO-US015097.
 XX 17-MAY-2000; 2000US-0204928P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Duda AE, Kazemi A, Koshiy B;
 XX WPI; 2002-097579/13.

XX Haplotyping, (H1), the G-protein coupled receptor 4 (GPR4) gene of an
 PT individual, comprising determining which haplotype an individual.
 XX Claim 17; Page 13; 61pp; English.

XX The invention relates to G-protein coupled receptor 4 (GPR4) gene
 CC variants. The data about the GPR4 polynucleotides and polypeptides and
 CC the polymorphisms associated with them are useful for haplotyping at the
 CC GPR4 locus. Allele-specific oligonucleotide (ASO) is useful as probes and
 CC primers for assaying a polymorphism in GPR4 gene. The present sequence is
 CC a primer used to detect human GPR4 gene polymorphism

XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8

```

Db      3 GTGAGCGA 10
|||||
RESULT 318
AAF92032/c
ID AAF92032 standard; DNA; 12 BP.
XX
AC AAF92032;
XX
DT 14-MAY-2001 (first entry)
XX
DE Hairpin primer #2.
XX
KW Hairpin; detection; gene expression; ss.
XX
OS Synthetic.
XX
PN WO200112856-A2.
XX
PD 22-FEB-2001.
XX
PP 11-AUG-2000; 2000WO-US22246.
XX
PR 13-AUG-1999; 99US-0148870P.
XX
PR 06-APR-2000; 2000US-00544713.
XX
FA (UYUA ) UNIV YALE.
XX
PI Lizardi PM, Latimer DR;
XX
DR WPI; 2001-202879/20.
XX
XX Identifying nucleic acid fragments in samples, useful for analyzing
PT nucleic acid sequence tags, gene expression or gene-expression patterns,
PT involves amplifying nucleic acid fragments with a primer that can form a
PT hairpin structure.
XX
PS Disclosure; Fig 6; 105pp; English.
XX
CC The present invention relates to identifying nucleic acid fragments or
CC sequences in nucleic acid samples by amplifying nucleic acid fragments
CC using a primer that can form a hairpin structure. The amplified fragments
CC then undergo sequence-based coupling to detector probes and the coupled
CC fragments are detected. The invention is useful for the comprehensive
CC analysis of nucleic acid samples and for sequence-based detection of
CC nucleic acid fragments. In particular, the method is useful for analyzing
CC nucleic acid sequence tags, gene expression or gene-expression patterns.
CC The method may also be used for detecting amplified fragments having a
CC known sequence
XX
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACTT 11
Db 8 AGCGACTT 1
|||||
RESULT 319
ABH72504
ID ABH72504 standard; DNA; 12 BP.
XX
AC ABH72504;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 272489 for detecting SNP TSC0002833.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 272489; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCCTT 18
Db 5 TCATCCCTT 12
|||||
RESULT 320
ABH99093/c
ID ABH99093 standard; DNA; 12 BP.
XX
AC ABH99093;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299086 for detecting SNP TSC0018427.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```



```
Query Match      44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
Db 11 CTTTCATCC 4

RESULT 323
ABI57121/C
ID ABI57121 standard; DNA; 12 BP.
XX
XX
AC ABI57121;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 357094 for detecting SNP TSC0050474.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 357094; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match      44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 TTCATCCT 17
XX Db 12 TTCATCCT 5
XX
XX RESULT 324
XX ABI02510/C
XX ID ABI02510 standard; DNA; 12 BP.
XX
XX Query Match      44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 TTCATCCT 17
XX Db 12 TTCATCCT 5
XX
XX RESULT 324
XX ABI02510/C
XX ID ABI02510 standard; DNA; 12 BP.
XX
XX Query Match      44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 TTCATCCT 17
XX Db 12 TTCATCCT 5
XX
XX RESULT 325
XX ABI36184
XX ID ABI36184 standard; DNA; 12 BP.
XX
XX AC ABI36184;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 336157 for detecting SNP TSC0039220.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
```

```
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 336157; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 TCATCCTT 18
DB 2 TCATCCTT 9
RESULT 326
ABI72079/c
ID ABI72079 standard; DNA; 12 BP.
XX
AC ABI72079;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 372052 for detecting SNP TSC0059134.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 372052; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 TCATCCTT 18
DB 2 TCATCCTT 9
RESULT 327
ABI58718
ID ABI58718 standard; DNA; 12 BP.
XX
AC ABI58718;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358691 for detecting SNP TSC0051251.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 358691; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 9 CTTTCATCC 16
DB 11 CTTTCATCC 4
RESULT 327
ABI58718
ID ABI58718 standard; DNA; 12 BP.
XX
AC ABI58718;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358691 for detecting SNP TSC0051251.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB0000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 358691; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
```

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
Db 1 ACTTCATC 8
|||||
|
RESULT 328
ABI24046/C
ID ABI24046 standard; DNA; 12 BP.
XX AC
XX AC ABI24046;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 324019 for detecting SNP TSC0031735.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 324019; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
Db 1 ACTTCATC 8
|||||
|
RESULT 328
ABI24046/C
ID ABI24046 standard; DNA; 12 BP.
XX AC
XX AC ABI24046;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 324019 for detecting SNP TSC0031735.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 324019; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8
Db 10 GTGAGCGA 3
|||||
|
RESULT 329
ABI32606
ID ABI32606 standard; DNA; 12 BP.
XX AC
XX AC ABI32606;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 332579 for detecting SNP TSC0037006.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 332579; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
Db 5 TTCATCCT 12
|||||
|
RESULT 330
ABI58329/C
ID ABI58329 standard; DNA; 12 BP.
XX AC
XX AC ABI58329;
XX DT 22-FEB-2002 (first entry)
XX

DE Oligonucleotide primer SEQ ID NO 358302 for detecting SNP TSC0051045.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX PR 07-APR-2000; 2000DE-01019173.
 XX
 XX PA (EPIG-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX PS Claim 1; SEQ ID NO 358302; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 44.4%; Score 8; DB 1; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 8 ACTTCATC 15
 XX |||||
 XX 8 ACTTCATC 1
 XX
 XX RESULT 331
 XX ABH70603/C
 XX ID ABH70603 standard; DNA; 12 BP.
 XX
 XX AC ABH70603;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 270580 for detecting SNP TSC0002186.
 XX
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX PS Claim 1; SEQ ID NO 270580; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 44.4%; Score 8; DB 1; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 11 TCATCCTT 18
 XX |||||
 XX 9 TCATCCTT 2
 XX
 XX Db
 XX
 XX RESULT 332
 XX ABI38408/C
 XX ID ABI38408 standard; DNA; 12 BP.
 XX
 XX AC ABI38408;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 338381 for detecting SNP TSC0040438.
 XX
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX PR 07-APR-2000; 2000DE-01019173.
 XX
 XX PA (EPIG-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX

```
PS Claim 1; SEQ ID NO 338381; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCATCCTT 18
Db 12 TCATCCTT 5
RESULT 333
ABI74005
ID ABI74005 standard; DNA; 12 BP.
XX
AC ABI74005;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 373978 for detecting SNP TSC0060433.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 373978; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCATCCTT 18
Db 12 TCATCCTT 5
RESULT 334
ABH97016
ID ABH97016 standard; DNA; 12 BP.
XX
AC ABH97016;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297009 for detecting SNP TSC0017388.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 297009; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCATCCTT 18
Db 5 TCATCCTT 12
```

```

RESULT 335
ABI12331/c
ID ABI12331 standard; DNA; 12 BP.
XX AC
XX ABI12331;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 312304 for detecting SNP TSC0024988.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 312304; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 ACTTCATC 15
Db 8 ACTTCATC 1
|||||||
|||||||
RESULT 336
ABH67749/c
ID ABH67749 standard; DNA; 12 BP.
XX AC
XX ABH67749;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267726 for detecting SNP TSC0000491.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

```

```

XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 267726; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TTCATCCT 17
Db 9 TTCATCCT 2
|||||||
|||||||
RESULT 337
ABI06054/c
ID ABI06054 standard; DNA; 12 BP.
XX AC
XX ABI06054;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 306027 for detecting SNP TSC0021773.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.

```

```

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 306027; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 10 TTCATCCT 17
Db 9 TTCATCCT 2
|||||||
|||||||

RESULT 338
ABI08302
ID ABI08302 standard; DNA; 12 BP.
XX
XX AC ABI08302;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 308275 for detecting SNP TSC0022938.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 308275; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 10 TTCATCCT 17
Db 9 TTCATCCT 2
|||||||
|||||||

RESULT 338
ABI08302
ID ABI08302 standard; DNA; 12 BP.
XX
XX AC ABI08302;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 308275 for detecting SNP TSC0022938.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 308275; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 9 CTTTCATCC 16
Db 1 CTTTCATCC 8
|||||||
|||||||

RESULT 339
ABI59006
ID ABI59006 standard; DNA; 12 BP.
XX
XX AC ABI59006;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 358979 for detecting SNP TSC0051404.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 358979; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;

```


Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTTCATCCT 17
 |||||
 Db 5 TTTCATCCT 12
 |||||

RESULT 340
 ABH77981
 ID ABH77981 standard; DNA; 12 BP.
 XX
 AC ABH77981;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 364834 for detecting SNP TSC0054754.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 364834; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTTCATCCT 17
 |||||
 Db 1 TTTCATCCT 8
 |||||

RESULT 341
 ABH77981
 ID ABH77981 standard; DNA; 12 BP.
 XX
 AC ABH77981;

XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 277974 for detecting SNP TSC0005331.
 DE
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 277974; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACTTCATC 15
 |||||
 Db 5 ACTTCATC 12
 |||||

RESULT 342
 ABI29279/c
 ID ABI29279 standard; DNA; 12 BP.
 XX
 AC ABI29279;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 329252 for detecting SNP TSC0034844.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX

PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 329252; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ACTTCATC 15
 Db 12 ACTTCATC 5
 |||||
 RESULT 343
 ABI35506/C
 ID ABI35506 standard; DNA; 12 BP.
 XX
 AC ABI35506;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 335479 for detecting SNP TSC0038850.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 335479; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TCATCCTT 18
 Db 8 TCATCCTT 1
 |||||
 RESULT 344
 ABI13395/C
 ID ABI13395 standard; DNA; 12 BP.
 XX
 AC ABI13395;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 313368 for detecting SNP TSC0025704.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 313368; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCAT 14
|||||||
Db 12 GACTTCAT 5

RESULT 345
ABI14542
ID ABI14542 standard; DNA; 12 BP.
XX AC
XX ABI14542;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 314515 for detecting SNP TSC0026410.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
FF
XX
PR 07-APR-2000; 2000DE-01019173.
PR
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 314515; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABR00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||||||

Db 1 TCATCCTT 8

RESULT 346
ABI46271
ID ABI46271 standard; DNA; 12 BP.
XX AC
XX ABI46271;
XX
DT 22-FEB-2002 (first entry)
XX

DE Oligonucleotide primer SEQ ID NO 346244 for detecting SNP TSC0009635.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
PF 06-APR-2001; 2001WO-IB000713.
FF
XX
PR 07-APR-2000; 2000DE-01019173.
PR
XX
PA (EPIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

Claim 1; SEQ ID NO 346244; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABR00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
|||||||
Db 1 TTCATCCT 8

RESULT 347
ABI62400/c
ID ABI62400 standard; DNA; 12 BP.
XX AC
XX ABI62400;
XX
DT 22-FEB-2002 (first entry)
XX

DE Oligonucleotide primer SEQ ID NO 362373 for detecting SNP TSC0053188.
XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 362373; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 44.4%; Score 8; DB 1; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 TCATCCTT 18
 Db 12 TCATCCTT 5
 RESULT 348
 ABI10041/c
 ID ABI10041 standard; DNA; 12 BP.
 XX AC ABI10041;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 310014 for detecting SNP TSC0023776.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 310014; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
 XX
 XX Query Match 44.4%; Score 8; DB 1; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CGACTTCA 13
 Db 10 CGACTTCA 3
 RESULT 349
 ABI13456/c
 ID ABI13456 standard; DNA; 12 BP.
 XX AC ABI13456;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 313429 for detecting SNP TSC0025756.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 313429; 29pp + Sequence Listing; German.
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTATCCTT 17
Db 12 TTATCCTT 5
|||||

RESULT 350
ABI17083/C
ID AB117083 standard; DNA; 12 BP.

XX AC AB117083;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 317056 for detecting SNP TSC0027803.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 317056; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCATCCTT 18
Db 9 TCATCCTT 2
|||||

RESULT 351
ABI45520
ID AB145520 standard; DNA; 12 BP.

XX AC AB145520;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 345493 for detecting SNP TSC0006581.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 345493; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCATCCTT 18
Db 1 TCATCCTT 8
|||||

RESULT 352
ABI60787

DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 272954; 29pp + Sequence Listing; German.
PS
PS This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCATCCTT 18
Db 2 TCATCCTT 9
RESULT 355
ABH77014
ID ABH77014 standard; DNA; 12 BP.
XX
AC ABH77014;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 277007 for detecting SNP TSC0004358.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PP
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 277007; 29pp + Sequence Listing; German.
PS
PS This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCATCCTT 18
Db 3 TCATCCTT 10
RESULT 356
ABI49134/C
ID ABI49134 standard; DNA; 12 BP.
XX
AC ABI49134;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 349107 for detecting SNP TSC00045920.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PP
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 349107; 29pp + Sequence Listing; German.
PS
PS This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      8 ACTTCATC 15
Db      11 ACTTCATC 4
RESULT 357
ABI70363/c
ID      ABI70363 standard; DNA; 12 BP.
XX
AC      ABI70363;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 370336 for detecting SNP TSC0058125.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WI      WIPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 370336; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match      44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      11 TCATCCTT 18
Db      10 TCATCCTT 3
RESULT 358
ABI77059/c
ID      ABI77059 standard; DNA; 12 BP.
XX
AC      ABI77059;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 381150 for detecting SNP TSC0064202.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WI      WIPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 370332; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match      44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      9 CTTTCATCC 16
Db      9 CTTTCATCC 2
RESULT 359
ABI81177/c
ID      ABI81177 standard; DNA; 12 BP.
XX
AC      ABI81177;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 381150 for detecting SNP TSC0064202.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
```


PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 381150; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 11 TCATCCTT 18
 Db 12 TCATCCTT 5

 RESULT 360
 ABI03315
 ID ABI03315 standard; DNA; 12 BP.
 XX
 AC ABI03315;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 303288 for detecting SNP TSC0020422.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 303288; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 11 TCATCCTT 18
 Db 3 TCATCCTT 10

 RESULT 361
 ABI08303
 ID ABI08303 standard; DNA; 12 BP.
 XX
 AC ABI08303;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 308276 for detecting SNP TSC0022938.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 308276; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but

```

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
Db 1 CTTTCATCC 8

RESULT 362
ABI38045
ID ABI38045 standard; DNA; 12 BP.
XX
AC ABI38045;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 338018 for detecting SNP TSC0040212.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 338018; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
Db 1 TTCATCCT 8

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
Db 1 CTTTCATCC 8

RESULT 363
ABI46960/c
ID ABI46960 standard; DNA; 12 BP.
XX
AC ABI46960;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 346933 for detecting SNP TSC0044838.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 346933; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
Db 12 ACTTCATC 5

RESULT 364
ABI66089/c
ID ABI66089 standard; DNA; 12 BP.
XX
AC ABI66089;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 366062 for detecting SNP TSC0055517.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 366062; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 TCATCCTT 18
 Db 11 TCATCCTT 4
 RESULT 365
 ABI23145
 ID ABI23145 standard; DNA; 12 BP.
 XX AC ABI23145;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 323118 for detecting SNP TSC0031227.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 323118; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
 SQ Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 ACTTCATC 15
 Db 5 ACTTCATC 12
 RESULT 366
 ABI02982/C
 ID ABI02982 standard; DNA; 12 BP.
 XX AC ABI02982;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 302955 for detecting SNP TSC0020248.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 302955; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
 |||||
 Db 9 CTTTCATCC 2

RESULT 367
 ABI50485/C
 ID ABI50485 standard; DNA; 12 BP.
 XX
 AC ABI50485;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 350458 for detecting SNP TSC0046703.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 350458; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCC 16
 |||||
 Db 9 CTTTCATCC 2

RESULT 367
 ABI50485/C
 ID ABI50485 standard; DNA; 12 BP.
 XX
 AC ABI50485;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 350458 for detecting SNP TSC0046703.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 350458; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
 |||||
 Db 10 TCATCCTT 3

RESULT 368
 ABI73137/C
 ID ABI73137 standard; DNA; 12 BP.
 XX
 AC ABI73137;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 373110 for detecting SNP TSC0059849.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 373110; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
 |||||
 Db 11 TTCATCCT 4

RESULT 369
 ABI60786
 ID ABI60786 standard; DNA; 12 BP.
 XX
 AC ABI60786;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 373110 for detecting SNP TSC0059849.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 373110; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
 |||||
 Db 11 TTCATCCT 4

RESULT 369
 ABI60786
 ID ABI60786 standard; DNA; 12 BP.
 XX
 AC ABI60786;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 373110 for detecting SNP TSC0059849.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 373110; 29pp + Sequence Listing; German.

```

AC AB160786;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 360759 for detecting SNP TSC0052276.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 360759; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 TTCATCCT 17
XX |||||
XX 1 TTCATCCT 8
XX
XX RESULT 370
XX AB162796
XX ID AB162796 standard; DNA; 12 BP.
XX
XX AC AB162796;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 362769 for detecting SNP TSC0053437.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

```

```

XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 362769; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 44.4%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 ACTTCATC 15
XX |||||
XX 2 ACTTCATC 9
XX
XX Db
XX
XX RESULT 371
XX AB166538
XX ID AB166538 standard; DNA; 12 BP.
XX
XX AC AB166538;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 366511 for detecting SNP TSC0055803.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 36511; 29pp + Sequence Listing; German.

PS

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||||
4 TCATCCTT 11

Db

RESULT 372
ABI35956
ID ABI35956 standard; DNA; 12 BP.
XX
AC ABI35956;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 335929 for detecting SNP TSC0039115.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX

PS Claim 1; SEQ ID NO 335929; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8
|||||
4 GTGAGCGA 11

Db

RESULT 373
ABI32607
ID ABI32607 standard; DNA; 12 BP.
XX
AC ABI32607;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 332580 for detecting SNP TSC0037006.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX

PS Claim 1; SEQ ID NO 332580; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 323585; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 CTTTCATCC 16
Db 9 CTTTCATCC 2
RESULT 377
ABI09120
ID ABI09120 standard; DNA; 12 BP.
XX AC ABI09120;
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 309093 for detecting SNP TSC0023358.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ea;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 309093; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 44.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 TTCATCCT 17
Db 2 TTCATCCT 9
RESULT 378
ABI12330/C
ID ABI12330 standard; DNA; 12 BP.
XX AC ABI12330;
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 312303 for detecting SNP TSC0024988.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 312303; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

XX SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 44.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
 |||||
 Db 8 ACTTCATC 1

RESULT 379
 AAA60137
 ID AAA60137 standard; DNA; 11 BP.
 AC AAA60137;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Human APC gene scanning oligonucleotide # 3.
 XX
 KW Human; adenomatous polyposis carcinoma; APC; scanning oligonucleotide;
 KW colorectal cancer; genotype analysis;
 KW short oligonucleotide mass analysis; SOMA: ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FI misc_difference 1 /*tag= a
 FT /note= "5' pA"
 FT

XX WO2000031300-A2.
 XX
 PD 02-JUN-2000.
 XX
 XX 22-NOV-1999; 99WO-US027523.
 XX
 PR 24-NOV-1998; 98US-00198340.
 XX
 XX (UJVO) UNIV JOHNS HOPKINS.
 XX
 PI Laken SJ, Vogelstein B, Kinzler KW, Groopman JD, Jackson PE;
 PI Friesen MD;
 XX
 DR WPT; 2000-422808/36.
 XX
 PT Genotype analysis method, defined as SOMA (short oligonucleotide mass
 PT analysis), of short, defined amplification products using electro-spray
 PT ionization mass spectrometry, useful for analyzing the genotype of living
 PT organisms.
 XX
 PS Example 4; Page 16; 40pp; English.
 XX

The present invention relates to a method of genotype analysis in which
 short PCR products are analysed by electro-spray ionisation mass
 spectrometry (ESI-MS). This method has been named Short Oligonucleotide
 Mass Analysis (SOMA). Short oligonucleotides of the human adenomatous
 polyposis carcinoma (APC) gene variants 486, 545 and 1756 were produced
 by PCR. The APC gene variants 486, 545 and 1756 are not associated with
 colorectal cancer, but are common polymorphisms which can be used for
 linkage analysis in families with familial adenomatous polyposis. The
 present sequence is a sense scanning oligonucleotide used to detect the
 multiple variant oligonucleotides produced in the present invention

XX SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCATC 15

Db 1 GCGCTCTTCTC 11
 |||||
 RESULT 380
 AAS02889/C
 ID AAS02889 standard; DNA; 11 BP.
 AC AAS02889;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human pregnane X receptor (hPXR) gene, PCR primer #159.
 XX
 KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
 KW therapeutic; chemotherapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200120026-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-EP008827.
 XX
 PR 10-SEP-1999; 99EP-00118120.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Wojnowski L, Hustert E;
 XX
 DR WPT; 2001-273428/28.
 XX
 PT Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 XX
 PS Claim 37; Page 46; 108pp; English.
 XX
 CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
 CC sequences and PCR primers of the invention. The human pregnane X receptor
 CC sequences are used to make antibodies, or a substance capable of binding
 CC specifically to the gene product of hPXR gene, for diagnosing and
 CC treating various diseases, such as cancer, with drugs that are
 CC substrates, inhibitors or modulators of the hPXR gene product. The
 CC proteins can be used to identify and obtain products and drugs for
 CC treatment of diseases which are amenable to chemotherapy. The nucleic
 CC acids can be used in gene therapy for the treatment or prevention of
 CC disorders associated with hPXR expression
 XX
 SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
 |||||
 Db 11 TGAGCGGCTGC 1

RESULT 381
 AAS02888
 ID AAS02888 standard; DNA; 11 BP.
 AC AAS02888;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human pregnane X receptor (hPXR) gene, PCR primer #158.
 XX
 KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;

CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGAGCGACTTC 12
 DB 1 TGAGTGAATTC 11
 RESULT 384
 ABV69339
 ID ABV69339 standard; cDNA; 11 BP.
 XX
 AC ABV69339;
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 7125.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 PR (HENKEL) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 223; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGAGCGACTTC 12
 DB 1 TGAGTGAATTC 11
 RESULT 384
 ABV70617
 ID ABV70617 standard; cDNA; 11 BP.
 XX
 AC ABV70617;
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 6794.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 PR (HENKEL) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 214; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGAGCGACTTC 12
 DB 1 TGAGGAGCATC 11
 RESULT 386
 ABV70617
 ID ABV70617 standard; cDNA; 11 BP.
 XX
 AC ABV70617;
 DT 21-OCT-2002 (first entry)
 XX Human skin EST 6794.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 PR (HENKEL) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 214; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.6e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
DE Human skin EST 8403.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
XX PR
XX 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e-g. skin cancer.
XX Claim 24; Page 268; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGGGACTTTAT 11
||| ||| |||
RESULT 387
ABV70522/c
ID ABV70522 standard; cDNA; 11 BP.
XX AC
XX ABV70522;
XX 21-OCT-2002 (first entry)
XX DE
XX Human skin EST 8308.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
```

```
XX 03-JAN-2001; 2001DE-01000127.
XX PR (HENK ) HENKEL KGAA.
XX PA Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e-g. skin cancer.
XX Claim 24; Page 266; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX SQ Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GACTTCATCCT 17
Db 11 GAGTTTATCCT 1
||| ||| |||
RESULT 388
ABV62268
ID ABV62268 standard; cDNA; 11 BP.
XX AC
XX ABV62268;
XX 21-OCT-2002 (first entry)
XX DE
XX Human skin EST 54.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
XX 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e-g. skin cancer.
XX
```

```

PS Disclosure; Page 27; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
    Query Match      43.3%; Score 7.8; DB 1; Length 11;
    Best Local Similarity 81.8%; Pred. No. 2.6e+02;
    Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TGAGCGGCTTC 12
Db      1 TGTGCGGCTTC 11

RESULT 389
ABV63196
ID ABV63196 standard; cDNA; 11 BP.
XX
AC ABV63196;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 982.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENKEL ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 323; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
    Query Match      43.3%; Score 7.8; DB 1; Length 11;
    Best Local Similarity 81.8%; Pred. No. 2.6e+02;
    Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGCGACTTCAT 14
Db      11 AGCGACTTCCT 1

RESULT 390
ABV72111/c
ID ABV72111 standard; cDNA; 11 BP.
XX
AC ABV72111;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9897.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENKEL ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 323; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
    Query Match      43.3%; Score 7.8; DB 1; Length 11;
    Best Local Similarity 81.8%; Pred. No. 2.6e+02;
    Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGCGACTTCAT 14
Db      11 AGCGACTTCCT 1

```


PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 189; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db ||||| |||||
1 AGCGCCTTCCT 11
RESULT 394
ABV63101/c
ID ABV63101 standard; cDNA; 11 BP.
XX AC ABV63101;
XX 21-OCT-2002 (first entry)
XX Human skin EST 887.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENKEL) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 49; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db ||||| |||||
1 AGCGCCTTCCT 11
RESULT 395
ABV63610/c
ID ABV63610 standard; cDNA; 11 BP.
XX AC ABV63610;
XX 21-OCT-2002 (first entry)
XX Human skin EST 1396.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENKEL) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 63; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 2.6e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 GACTTCATCCT 17
Db ||||| |||||
11 GAGTTTATCCT 1

```
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTGCTCCTT 1

RESULT 396
ABV71031/c
ID ABV71031 standard; cDNA; 11 BP.
XX AC
XX ABV71031;
XX
DT 21-OCT-2002 (first entry)
XX DE
XX Human skin EST 8817.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 283; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTGCTCCTT 1

RESULT 397
ABV68543/c
ID ABV68543 standard; cDNA; 11 BP.
XX AC
XX ABV68543;
XX
DT 21-OCT-2002 (first entry)
XX DE
XX Human skin EST 7475.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX
PN WO200253774-A2.
XX
XX
```

```
XX 21-OCT-2002 (first entry)
DT XX
DE Human skin EST 6329.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 201; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACCGCATCCTT 1

RESULT 398
ABV69689
ID ABV69689 standard; cDNA; 11 BP.
XX
AC ABV69689;
XX
DT 21-OCT-2002 (first entry)
XX DE
XX Human skin EST 7475.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX
PN WO200253774-A2.
XX
XX
```



```

PD 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Claim 24; Page 235; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGGCTTC 12
Db 1 TGTGCGGCTTC 11

RESULT 399
ABK13229
ID ABK13229 standard; DNA; 11 BP.
XX
XX AC ABK13229;
XX
XX 23-APR-2002 (first entry)
XX
XX Self-assembled monolayer sequence containing a Lex B17 binding site.
XX
XX Self-assembled monolayer; SAM; ds; surface plasmon resonance chip;
XX biosensor; DNA hybridisation test; diagnostic mutation scanning;
XX forensic analysis; pharmacological study; cell sorting;
XX environmental monitoring; protein-protein interaction; lex B17.
XX
XX Unidentified.
XX
XX US6322979-B1.
XX
XX 27-NOV-2001.
XX
XX 21-APR-1999; 99US-00296078.
XX
XX 26-SEP-1994; 94US-00312388.
XX
XX 21-JAN-1997; 97US-00786187.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Bandad CC, Sigal GB, Strominger JL, Whitesides GM;
XX WPI; 2002-146684/19.
XX

XX Capturing biological binding partner, useful e.g. for nucleic acid
XX hybridization tests, using surface that carries self-assembled monolayer
XX comprising specific capture agent.
XX
XX Example 15; Fig 10; 28pp; English.
XX
XX The invention relates to a new process of capturing a biological binding
XX partner (I) of a nucleic acid strand (II) comprising applying a test
XX sample to a surface that carries: (i) a binding species (III); and (ii) a
XX molecule (IV) that forms a mixed self-assembled monolayer (SAM) with
XX (III). (III) has formula X-R-NA (III) X = functional group that adheres
XX to the surface; R = spacer that promotes formation of SAM; and NA =
XX nucleic acid strand. The method is particularly used in surface plasmon
XX resonance chips (biosensors) for capturing DNA. Typical of many possible
XX applications are DNA hybridisation tests (e.g. diagnostic scanning for
XX mutations, forensic analysis, pharmacological studies, cell sorting,
XX environmental monitoring) in studies of protein-protein interactions
XX where DNA binding is important (e.g. transcriptional control of genes)
XX and in development of easy-analysis DNA computers. The use of a mixed SAM
XX improves sensitivity, with reduced non-specific binding, it ensures that
XX the binding region of (III) is directed away from the surface, making it
XX available for reaction. The present sequence contains a lex B17 binding
XX site and is used to illustrate the method of the invention
XX
XX Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACTT 11
Db 1 GTAAGCGGAATT 11

RESULT 400
AAL42767
ID AAL42767 standard; DNA; 11 BP.
XX
XX AC AAL42767;
XX
XX 19-JUL-2002 (first entry)
XX
XX Self-assembled monolayer (SAM) DNA sequence 3.
XX
XX Self-assembled monolayer; SAM; ss; chelating agent; conjugate; triplex.
XX biological molecule capture; surface plasmon resonance sensor; triplex.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_binding 1..11
XX /*tag= a
XX /bound_moiety= "SAM DNA sequence 4"
XX /note= "Forms triple stranded region with the nucleotide
XX shown in AAL42768"
XX
XX US2002042074-A1.
XX
XX 11-APR-2002.
XX
XX 25-JUL-2001; 2001US-00915187.
XX
XX 26-SEP-1994; 94US-00312388.
XX
XX 21-JAN-1997; 97US-00786187.
XX
XX 21-APR-1999; 99US-00296078.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Bandad CC, Sigal GB, Strominger JL, Whitesides GM;
XX WPI; 2002-371283/40.
XX

```

XX Conjugates forming self-assembled monolayers on gold surfaces, especially
PT in biosensors, comprise a chelating agent linked via a spacer to a
PT functional group.

XX Example 12; Fig 10; 30pp; English.

XX The invention comprises conjugates which contain a functional group that
XX adheres to a gold surface, a spacer that promotes the formation of a self
XX -assembled monolayer (SAM) of the conjugate, and a bi-, tri- or
XX -adradentate chelating agent that coordinates a metal ion. The
XX conjugates of the invention are useful for forming self-assembled
XX monolayers for capturing biological molecules on sensors, especially
XX surface plasmon resonance sensors. The present DNA sequence is shown in a
XX figure designed to illustrate the formation of a self-assembled monolayer
XX of a conjugate

XX SQ Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
||| ||||| ||
Db 1 GTAAGCGAATT 11

RESULT 401
AAL42768/C
ID AAL42768 standard; DNA; 11 BP.
AC AAL42768;
XX
XX 19-JUL-2002 (first entry)
XX
XX Self-assembled monolayer (SAM) DNA sequence 4.

XX Self-assembled monolayer; SAM; ss; chelating agent; conjugate; triplex.
KW biological molecule capture; surface plasmon resonance sensor; triplex.
XX
XX Synthetic.

XX Key Location/Qualifiers
FT misc_binding 1..11
FT /*tag= a
FT /bound_moiety= "SAM DNA sequence 3"
FT /note= "Forms triple stranded region with the nucleotide
FT shown in AAL42767"

XX US2002042074-A1.

XX 11-APR-2002.

XX 25-JUL-2001; 2001US-00915187.

XX 26-SEP-1994; 94US-00312388.

XX 21-JAN-1997; 97US-00786187.

XX 21-APR-1999; 99US-00296078.

XX (HARD) HARVARD COLLEGE.

XX Bandad CC, Sigal GB, Strominger JL, Whitesides GM;

XX WPI; 2002-371283/40.

XX Conjugates forming self-assembled monolayers on gold surfaces, especially

XX in biosensors, comprise a chelating agent linked via a spacer to a
XX functional group.

XX Example 12; Fig 10; 30pp; English.

XX The invention comprises conjugates which contain a functional group that

CC adheres to a gold surface, a spacer that promotes the formation of a self
CC -assembled monolayer (SAM) of the conjugate, and a bi-, tri- or
CC -adradentate chelating agent that coordinates a metal ion. The
CC conjugates of the invention are useful for forming self-assembled
CC monolayers for capturing biological molecules on sensors, especially
CC surface plasmon resonance sensors. The present DNA sequence is shown in a
CC figure designed to illustrate the formation of a self-assembled monolayer
CC of a conjugate

XX SQ Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
||| ||||| ||
Db 11 GTAAGCGAATT 1

RESULT 402
AAQ52903
ID AAQ52903 standard; RNA; 12 BP.

XX AC AAQ52903;

XX 25-MAR-2003 (revised)

XX 26-MAY-1994 (first entry)

XX Influenza virus target sequence 13.

XX RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
XX picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
XX papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
XX T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus;
XX influenza virus; HSV; herpes simplex virus; vector; immune response;
XX antibody; ribozyme; viral RNA; treatment; ss.

XX Synthetic.

XX W09323569-A1.

XX 25-NOV-1993.

XX 29-APR-1993; 93WO-US004020.

XX 11-MAY-1992; 92US-00882689.

XX 14-MAY-1992; 92US-00882712.

XX 14-MAY-1992; 92US-00882713.

XX 14-MAY-1992; 92US-00882714.

XX 14-MAY-1992; 92US-00882823.

XX 14-MAY-1992; 92US-00882824.

XX 14-MAY-1992; 92US-00882886.

XX 14-MAY-1992; 92US-00882888.

XX 14-MAY-1992; 92US-00882889.

XX 14-MAY-1992; 92US-00882921.

XX 14-MAY-1992; 92US-00882922.

XX 14-MAY-1992; 92US-00883823.

XX 14-MAY-1992; 92US-00883849.

XX 14-MAY-1992; 92US-00884073.

XX 14-MAY-1992; 92US-00884074.

XX 14-MAY-1992; 92US-00884333.

XX 14-MAY-1992; 92US-00884422.

XX 14-MAY-1992; 92US-00884431.

XX 14-MAY-1992; 92US-00884436.

XX 14-MAY-1992; 92US-00884521.

XX 31-JUL-1992; 92US-00923738.

XX 26-AUG-1992; 92US-00935854.

XX 18-SEP-1992; 92US-00936086.

XX 15-OCT-1992; 92US-00948359.

XX 07-DEC-1992; 92US-00963322.

XX 07-DEC-1992; 92US-00987129.

XX 07-DEC-1992; 92US-00987130.


```
CC phosphoramidate AAV07769 displayed significant inhibitory activity
XX
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
| ||||| |||
Db 2 GGCTTCCTCCT 12

RESULT 405
AAZ41739/c
ID AAZ41739 standard; DNA; 12 BP.
XX
AC AAZ41739;
XX
DT 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX
DE Organic material detecting primer 100.
XX
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX
OS Synthetic.
XX
PN DE19914461-A1.
XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99DE-01014461.
XX
PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
PT Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
PS Example 1; Page 19; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-Z41855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
| ||||| |||
OS
```

```
Db 12 GACTTCGGCCT 2

RESULT 406
AAZ41523/c
ID AAZ41523 standard; DNA; 12 BP.
XX
AC AAZ41523;
XX
DT 19-JAN-2000 (first entry)
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #100.
DE
KW Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11276176-A.
XX
PD 12-OCT-1999.
XX
PF 31-MAR-1998; 98JP-00087652.
XX
PR 31-MAR-1998; 98JP-00087652.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 1999-626940/54.
XX
PT Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
XX
PS Claim 1; Page 9; 40pp; Japanese.
XX
CC A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC organic waste
XX
SQ Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
| ||||| |||
Db 12 GACTTCGGCCT 2

RESULT 407
AAZ55937
ID AAZ55937 standard; DNA; 12 BP.
XX
AC AAZ55937;
XX
DT 04-SEP-2000 (first entry)
XX
DE Adapter linker nucleotide sequence SEQ ID NO:96.
XX
KW Yeast; detection; protein-protein interaction; DNA-binding domain;
KW characterisation; identification; protein pathway information;
KW protein interaction domain; screening; PCR primer; adapter; linker;
KW fusion protein; inhibitor; regulation; ss.
XX
OS Synthetic.
```

```

XX US6057101-A.
PN
XX
XX 02-MAY-2000.
PD
XX
XX 13-JUN-1997; 97US-00874825.
PF
XX
XX 14-JUN-1996; 96US-00663824.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Knight JR, Kalbfleisch TS, Yang M, Nandabalan K, Rothberg JM;
PI
XX
XX WPI; 2000-349567/30.
DR
XX
XX Identifying, comparing and detecting inhibitors of protein-protein
PT
XX interactions within population of host cells, involves detecting
PT
XX regulation of transcription of nucleic acid sequence by fusion protein
PT
XX interaction.
XX
XX Example; Col 131; 161pp; English.
PS
XX
XX The present invention describes a method for detecting (D) at least 1
CC
XX protein-protein interaction (PPI) by recombinantly expressing within a
CC
XX population of host cells, populations of first and second fusion proteins
CC
XX comprising DNA binding domain (DBD) and transcriptional regulatory domain
CC
XX (TRD) respectively and detecting the regulation of transcription of
CC
XX nucleotide sequence of host cells operably linked to a promoter driven by
CC
XX DBD. The detection method (D) is useful for identifying inhibitors of PPI
CC
XX for therapeutic use, and for detecting specific cell types, tissue types,
CC
XX stage of development and disease states. From the population of the
CC
XX proteins characteristic of the particular tissue or a cell-type, all
CC
XX possible detectable PPI that occur can be identified and genes encoding
CC
XX these proteins can be isolated. Thus, parallel analysis of two cell types
CC
XX enumerates PPI that are common to both and those that are specific to
CC
XX both. This analysis has significant value since PPI specific to a disease
CC
XX state can serve as therapeutic points of intervention. Inhibitors of PPI
CC
XX can also be isolated in rapid fashion. The number of false positives and
CC
XX low throughput are reduced. AAA55943 to AAA55963 and AAY90961 are
CC
XX sequences used in the exemplification of the present invention
XX
XX Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGCTGCTTCAT 11
RESULT 408
AAA73449
ID AAA73449 standard; DNA; 12 BP.
AC
XX
XX AAA73449;
XX
XX 09-FEB-2001 (first entry)
DT
XX
XX Linker JCS.
DE
XX
XX Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
KW
XX
XX ss.
XX
XX Saccharomyces cerevisiae.
OS
XX
XX US6083693-A.
PN
XX
XX 04-JUL-2000.
PD
XX
XX 14-JUN-1996; 96US-00663824.
PF
XX
XX

```

```

PR 14-JUN-1996; 96US-00663824.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Nandabalan K, Rothberg JM;
PI
XX
XX WPI; 2000-464335/40.
DR
XX
XX Detecting protein-protein interactions in protein populations useful for
PT
XX identifying genes encoding the proteins, and inhibitors of the
PT
XX interactions, by detecting transcriptional regulation leading to reporter
PT
XX gene activation.
XX
XX Example; Col 103-104; 135pp; English.
PS
XX
XX The present invention relates to methods for detecting and isolating
CC
XX genes encoding proteins that interact with each other, via the
CC
XX reconstitution of a transcription factor and hence reporter gene
CC
XX activation. Proteins are fused to either the yeast DNA-binding domain of a
CC
XX transcriptional activator or to the activation domain of a
CC
XX transcriptional activator. The present sequence is a linker used in the
CC
XX present invention as an adapter in the analysis of yeast fusion genes.
CC
XX The present method may be used to identify protein-protein interactions
CC
XX and genes encoding the interacting proteins relevant to a particular
CC
XX tissue, stage or disease e.g. cancer
XX
XX Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGCTGCTTCAT 11
RESULT 409
AAC97874/c
ID AAC97874 standard; DNA; 12 BP.
AC
XX
XX AAC97874;
XX
XX 28-FEB-2001 (first entry)
DT
XX
XX Primer used to illustrate DNA amplification method SEQ ID 100.
DE
XX
XX Primer; amplification; selective; ss.
KW
XX
XX Synthetic.
OS
XX
XX JP2000270867-A.
PN
XX
XX 03-OCT-2000.
PD
XX
XX 19-MAR-1999; 99JP-00076844.
PF
XX
XX 19-MAR-1999; 99JP-00076844.
PR
XX
XX (SAOL) SANYO ELECTRIC CO LTD.
PA
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
XX WPI; 2001-011047/02.
DR
XX
XX Amplification of a DNA fragment and its apparatus.
PT
XX
XX Example 1; Page 9; 32pp; Japanese.
PS
XX
XX This invention relates to a method for amplifying a DNA fragment. The
CC
XX method comprises successive repetitions of heat-denaturing, annealing of
CC
XX a primer and an extending step using a DNA polymerase. The method makes
CC
XX use of a cDNA pool in which the primer is one primer or a pair of primer
CC
XX sets and has an amplification probability which allows it to amplify a

```

CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
 CC the limited number is in the range of 1 to 25). Also included in the
 CC invention are apparatus used for carrying out the method, a primer and a
 CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
 CC can be used to amplify a limited number of cDNAs from a pool in which a
 CC wide variety of cDNAs are present. Oligonucleotides AAC9775 - AAC97990
 CC represent primers used in an example illustrating the method of the
 CC invention

XX
 XX Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
 Db 12 GACTTCGGCCT 2
 ||||| |||

RESULT 410
 ABH97306
 ID ABH97306 standard; DNA; 12 BP.
 XX AC
 AC ABH97306;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide primer SEQ ID NO 297299 for detecting SNP TSC0017509.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 297299; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;

Qy 6 CGACTTCATCC 16
 Db 12 CAACCTCATCC 2
 ||||| |||

RESULT 412
 ABI04308/C
 ID ABI04308 standard; DNA; 12 BP.
 XX AC
 AC ABI04308;
 XX
 XX Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
 Db 12 CAACCTCATCC 2
 ||||| |||

RESULT 412
 ABI04308/C
 ID ABI04308 standard; DNA; 12 BP.
 XX AC
 AC ABI04308;
 XX

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
 Db 1 GTGGGCGAGTT 11
 ||| ||||| |||

RESULT 411
 ABI00329/C
 ID ABI00329 standard; DNA; 12 BP.
 XX AC
 AC ABI00329;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide primer SEQ ID NO 300302 for detecting SNP TSC0018963.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 300302; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
 Db 12 CAACCTCATCC 2
 ||||| |||

RESULT 412
 ABI04308/C
 ID ABI04308 standard; DNA; 12 BP.
 XX AC
 AC ABI04308;
 XX

```

DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 304281 for detecting SNP TSC0020848.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 304281; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 ACTTCATCCTT 18
Db 11 ATTTAATCCTT 1

RESULT 413
ABI35462
ID ABI35462 standard; DNA; 12 BP.
XX
AC ABI35462;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 335435 for detecting SNP TSC0038818.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 335435; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 ACTTCATCCTT 18
Db 11 ATTTAATCCTT 1

RESULT 414
ABI12630/C
ID ABI12630 standard; DNA; 12 BP.
XX
AC ABI12630;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 312603 for detecting SNP TSC0025165.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PP 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

```

```
PT methylation status.
XX Claim 1; SEQ ID NO 312603; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
Db 11 CCATTCCTCTCC 1

RESULT 415
ABI42674
ID ABI42674 standard; DNA; 12 BP.
XX AC ABI42674;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 342647 for detecting SNP TSC0042647.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; SB;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 342647; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
Db 11 CCATTCCTCTCC 1

RESULT 416
ABI54545/C
ID ABI54545 standard; DNA; 12 BP.
XX AC ABI54545;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 354518 for detecting SNP TSC0049117.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; SB;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 354518; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 12 ACTTAATCTT 2
```



```

RESULT 417
ABI64359
ID ABI64359 standard; DNA; 12 BP.
XX
XX
AC ABI64359;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 364332 for detecting SNP TSC0054402.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 364332; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCTT 18
XX 1 ACATCATCAT 11
XX
XX RESULT 418
ABI19294/c
ID ABI19294 standard; DNA; 12 BP.
XX
XX
XX ABI19294;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 319267 for detecting SNP TSC0029143.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 364332; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCTT 18
XX 1 ACATCATCAT 11
XX
XX RESULT 419
ABH72261/c
ID ABH72261 standard; DNA; 12 BP.
XX
XX
XX ABH72261;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 272240 for detecting SNP TSC0002748.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX

```

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 319267; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 8 ACTTCATCCTT 18
XX 11 ATTTCAACCTT 1
XX
XX RESULT 419
ABH72261/c
ID ABH72261 standard; DNA; 12 BP.
XX
XX
XX ABH72261;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 272240 for detecting SNP TSC0002748.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX

```

```

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 272240; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 11 ACATCAACCTT 1
RESULT 420
ABI23304/C
ID ABI23304 standard; DNA; 12 BP.
XX
XX AC ABI23304;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 323277 for detecting SNP TSC0031302.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 323277; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 11 ACATCAACCTT 1
RESULT 421
ABH76377/C
ID ABH76377 standard; DNA; 12 BP.
XX
XX AC ABH76377;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 276370 for detecting SNP TSC0004169.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 276370; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
SQ

```


CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
 SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
 Db 2 ACTTAATCTT 12

RESULT 427
 ABH88759/c
 ID ABH88759 standard; DNA; 12 BP.

XX AC ABH88759;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 288752 for detecting SNP TSC0013655.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX FA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 288752; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
 XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
 Db 11 CCACTCCATCC 1

RESULT 428

ABH68518
 ID ABH68518 standard; DNA; 12 BP.

XX AC ABH68518;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 268495 for detecting SNP TSC0001176.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX FA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 268495; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
 XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
 Db 1 CAAATTCATCC 11

RESULT 429

ABI04718
 ID ABI04718 standard; DNA; 12 BP.

XX AC ABI04718;

XX DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 304691 for detecting SNP TSC0021063.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 304691; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 1 CTACTTCATAC 11
RESULT 430
ABI33276/C
ID ABI33276 standard; DNA; 12 BP.
XX
XX AC ABI33276;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 333249 for detecting SNP TSC0037443.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 333249; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 12 ACTACATCCTT 2
RESULT 431
ABI14991/C
ID ABI14991 standard; DNA; 12 BP.
XX
XX AC ABI14991;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 314964 for detecting SNP TSC0026652.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

```
PS Claim 1; SEQ ID NO 314964; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX QY 1 GTGAGCGACTT 11
XX |||||||
XX Db 12 GTTAGCGATT 2
XX
XX
XX RESULT 432
XX ABI42352
XX ID ABI42352 standard; DNA; 12 BP.
XX AC
XX AC ABI42352;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 342325 for detecting SNP TSC0010808.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR Oligonucleotide primer SEQ ID NO 342325 for detecting SNP TSC0010808.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 342325; 29pp + Sequence Listing; German.
XX
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX QY 1 GTGAGCGACTT 11
XX |||||||
XX Db 12 GTTAGCGATT 2
XX
XX
XX RESULT 433
XX ABI65791/C
XX ID ABI65791 standard; DNA; 12 BP.
XX AC
XX AC ABI65791;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 365764 for detecting SNP TSC0055318.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 365764; 29pp + Sequence Listing; German.
XX
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX QY 8 ACTTCATCCTT 18
XX |||||||
XX Db 11 ACCTCAACCTT 1
```

```
RESULT 434
ABH71796
ID ABH71796 standard; DNA; 12 BP.
XX
XX
AC ABH71796;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 271773 for detecting SNP TSC0002613.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271773; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX ||||| |||
XX Db 2 ACTTCACACTTT 12
XX
XX RESULT 435
ABH97842/c
ID ABH97842 standard; DNA; 12 BP.
XX
XX ABH97842;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 297835 for detecting SNP TSC0017793.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271773; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX ||||| |||
XX Db 2 ACTTCACACTTT 12
XX
XX RESULT 436
ABH76914
ID ABH76914 standard; DNA; 12 BP.
XX
XX ABH76914;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 276907 for detecting SNP TSC0004330.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX
```



```
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 276907; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
SQ
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ACTTCATCCTT 18
DB 1 ACCTTCATCCTT 11
XX
XX RESULT 437
XX ABI37224
XX ID ABI37224 standard; DNA; 12 BP.
XX AC
XX ABI37224;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 337197 for detecting SNP TSC0039728.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 337197; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
SQ
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ACTTCATCCTT 18
DB 1 ACCTTCATCCTT 11
XX
XX RESULT 438
XX ABI12821/c
XX ID ABI12821 standard; DNA; 12 BP.
XX AC
XX ABI12821;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 312794 for detecting SNP TSC0025301.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 312794; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 CGACTTCATCC 16
DB 2 CGACTTCATCC 12
XX
XX RESULT 439
XX ABI12821/c
XX ID ABI12821 standard; DNA; 12 BP.
XX AC
XX ABI12821;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 312794 for detecting SNP TSC0025301.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 312794; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
```


PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 288070; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 ACTTCATCCTT 18
 DB 12 ACTTCATATTT 2
 RESULT 442
 ABI15737
 ID ABI15737 standard; DNA; 12 BP.
 XX
 AC ABI15737;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 315710 for detecting SNP TSC0027048.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 315710; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 ACTTCATCCTT 18
 DB 2 ACTTCATCATTT 12
 RESULT 443
 ABI44233/C
 ID ABI44233 standard; DNA; 12 BP.
 XX
 AC ABI44233;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 344206 for detecting SNP TSC0043439.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 344206; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 11 ACTTCATAATT 1

RESULT 444
ABI61270
ID ABI61270 standard; DNA; 12 BP.
XX AC ABI61270;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 361243 for detecting SNP TSC0052515.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 361243; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
|||||

Db 1 GTGAGGGAGTT 11

RESULT 445
ABI63212/C
ID ABI63212 standard; DNA; 12 BP.

XX AC ABI63212;
XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 363185 for detecting SNP TSC0053709.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 363185; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 11 ACTACAACCTT 1

RESULT 446
ABH72760
ID ABH72760 standard; DNA; 12 BP.

XX AC ABH72760;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 272745 for detecting SNP TSC0002926.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 272745; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 ACTTCATCCTT 18
 Db ||||| |||||
 2 ACTTCACCTTT 12
 RESULT 447
 ABI12247/c
 ID ABI12247 standard; DNA; 12 BP.
 XX AC ABI12247;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 312220 for detecting SNP TSC0024898.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 312220; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 8 ACTTCATCCTT 18
 Db ||||| |||||
 12 ACTTCACCTTT 2
 RESULT 448
 ABI37360
 ID ABI37360 standard; DNA; 12 BP.
 XX AC ABI37360;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 337333 for detecting SNP TSC0039823.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 337333; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
||||| ||| |||
Db 1 ACTTAATCTTT 11

RESULT 449
ABI13665/C
ID ABI13665 standard; DNA; 12 BP.
XX AC ABI13665;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 313638 for detecting SNP TSC0025880.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 313638; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
||||| ||| |||
Db 12 ACTACACCTT 2

RESULT 450
ABI76455
ID ABI76455 standard; DNA; 12 BP.
XX AC ABI76455;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 376428 for detecting SNP TSC0061813.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 376428; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
||||| ||| |||
Db 2 ACTACATCTT 12

RESULT 451
ABH72789/C

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 281739; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db |||||
2 AATTATCCTT 12
RESULT 454
ABH87544/C
ID ABH87544 standard; DNA; 12 BP.
XX AC ABH87544;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 287537 for detecting SNP TSC0013134.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; es;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
XX PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 287537; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db |||||
2 AATTATCCTT 12
RESULT 454
ABH87544/C
ID ABH87544 standard; DNA; 12 BP.
XX AC ABH87544;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 287537 for detecting SNP TSC0013134.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; es;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
XX PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 287537; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGACTT 11
Db |||||
11 GTGAGGGATT 1
RESULT 455
ABI15260
ID ABI15260 standard; DNA; 12 BP.
XX AC ABI15260;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 315233 for detecting SNP TSC0026790.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; es;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
XX PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 315233; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
SQ Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

QY      6 CGACTTCATCC 16
DB      2 CCACCTCATCC 12

RESULT 456
ABI46698/c
ID      ABI46698 standard; DNA; 12 BP.
XX
AC      ABI46698;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 346671 for detecting SNP TSC0044697.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 370631; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 ACTTCATCCTT 18
DB      11 ACTCTTCCTT 1

RESULT 457
ABI70658
ID      ABI70658 standard; DNA; 12 BP.
XX
AC      ABI70658;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 328317 for detecting SNP TSC0034234.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX

QY      1 GTGAGCGACTT 11
DB      2 GTGGGCGATT 12

RESULT 458
ABI28344/c
ID      ABI28344 standard; DNA; 12 BP.
XX
AC      ABI28344;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 370631 for detecting SNP TSC0034234.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX

```

```

PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 328317; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCTT 18
Db 12 ACATCATCCAT 2
XX
XX RESULT 459
XX ABI04684
XX ID ABI04684 standard; DNA; 12 BP.
XX
XX AC ABI04684;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 304657 for detecting SNP TSC0021039.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 328317; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCTT 18
Db 12 ACATCATCCAT 2
XX
XX RESULT 460
XX ABI32587/C
XX ID ABI32587 standard; DNA; 12 BP.
XX
XX AC ABI32587;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 332560 for detecting SNP TSC0036990.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 332560; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but

```

```
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
   ||| |||||
Db 11 ACTCTATCCTT 1

RESULT 461
ABI12589
ID ABI12589 standard; DNA; 12 BP.
XX
AC ABI12589;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 312562 for detecting SNP TSC0025147.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 312562; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
   ||| |||||
Db 2 CAACTTCATAC 12

RESULT 462
ABI173193
ID ABI173193 standard; DNA; 12 BP.
XX
AC ABI173193;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 373166 for detecting SNP TSC0059887.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 373166; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match      43.3%; Score 7.8; DB 1; Length 12;
  Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATCC 16
   ||| |||||
Db 1 CAACTTCATCC 11

RESULT 463
ABI1939
ID ABI1939 standard; DNA; 12 BP.
XX
AC ABI1939;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 381912 for detecting SNP TSC0064632.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```


CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 CGACTTCATCC 16
DB 11 CTACCTCATCC 1
RESULT 466
ABI18693/c
ID ABI18693 standard; DNA; 12 BP.
XX AC
XX ABI18693;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 318666 for detecting SNP TSC0028793.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 318666; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ACTTCATCCTT 18
DB 11 ACTATATCCTT 1
RESULT 467
ABH71715/c
ID ABH71715 standard; DNA; 12 BP.
XX AC
XX ABH71715;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 271692 for detecting SNP TSC0002593.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 271692; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ACTTCATCCTT 18
DB 12 ACTTCCTCAT 2
RESULT 468
ABI56467/c
ID ABI56467 standard; DNA; 12 BP.
XX

```
AC ABI56467;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 356440 for detecting SNP TSC0050111.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 356440; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX ||||| |||||
XX 12 ACTTATCTTT 2
XX
XX RESULT 469
XX ABI73121
XX ID ABI73121 standard; DNA; 12 BP.
XX
XX AC ABI73121;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 373094 for detecting SNP TSC0059838.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
```

```
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 373094; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCATCCTT 18
XX ||||| |||||
XX 1 ACTATATCCTT 11
XX
XX Db
XX
XX RESULT 470
XX ABI78897/C
XX ID ABI78897 standard; DNA; 12 BP.
XX
XX AC ABI78897;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 378870 for detecting SNP TSC0006391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX
```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 378870; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 11 ACCTACTTCAT 1
RESULT 471
ABI79114
ID ABI79114 standard; DNA; 12 BP.
XX
XX ABI79114;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 379087 for detecting SNP TSC0063074.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 379087; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTGAGCGACTT 11
Db 2 GTGAGGGGATTT 12
RESULT 472
ABI19115/C
ID ABI19115 standard; DNA; 12 BP.
XX
XX ABI19115;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 319088 for detecting SNP TSC0029063.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 319088; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 AGCGACTTCAT 14


```
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 314427; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 CGACTTCATCC 16
XX |||||
XX Db 12 CCGCTCATCC 2
XX
XX RESULT 476
XX ABI72561/c
XX ID ABI72561 standard; DNA; 12 BP.
XX AC ABI72561;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 372534 for detecting SNP TSC0059448.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal, respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR Oligonucleotide primer SEQ ID NO 372534 for detecting SNP TSC0059448.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal, respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 372534; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 CGACTTCATCC 16
XX |||||
XX Db 12 CCGCTCATCC 2
XX
XX RESULT 477
XX ABI78059/c
XX ID ABI78059 standard; DNA; 12 BP.
XX AC ABI78059;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 378032 for detecting SNP TSC0062593.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal, respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 378032; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 8 ACTTCATCCTT 18
XX |||||
XX Db 12 ATTTCATCTT 2
XX
XX RESULT 477
XX ABI78059/c
XX ID ABI78059 standard; DNA; 12 BP.
XX AC ABI78059;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 378032 for detecting SNP TSC0062593.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal, respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 378032; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
```

```
XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 12 ATTTCATCCCT 2

RESULT 478
ABI79441/C
ID ABI79441 standard; DNA; 12 BP.
XX AC ABI79441;
XX XX
DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 379414 for detecting SNP TSC0008590.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 379414; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ATTTCATTCCT 1

RESULT 479
ABI79441/C
ID ABI79441 standard; DNA; 12 BP.
XX AC ABI79441;
XX XX
DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 274643 for detecting SNP TSC0003624.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 274643; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 12 ACATCATCTT 2

RESULT 480
ABI74660/C
ID ABI74660 standard; DNA; 12 BP.
XX AC ABI74660;
XX XX
DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 274645 for detecting SNP TSC0003624.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
```


CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 5 A; 2 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
 Db 12 AGCGATTTAAT 2
 ||||| |||
 ||||| |||

RESULT 483
 ABI06143/C
 ID ABI06143 standard; DNA; 12 BP.
 XX
 AC ABI06143;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 306116 for detecting SNP TSC0021811.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 306116; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
 Db 12 AGCGATTTAAT 2
 ||||| |||
 ||||| |||

RESULT 483
 ABI06143/C
 ID ABI06143 standard; DNA; 12 BP.
 XX
 AC ABI06143;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 306116 for detecting SNP TSC0021811.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 306116; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 CGACTTCATCC 16
 Db 12 CTACTTCATAC 2
 ||||| |||
 ||||| |||

RESULT 484
 ABI09863/C
 ID ABI09863 standard; DNA; 12 BP.
 XX
 AC ABI09863;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 309836 for detecting SNP TSC0023694.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 309836; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
 Db 12 GACTTCCTACT 2
 ||||| |||
 ||||| |||

RESULT 485
 ABI39188/C
 ID ABI39188 standard; DNA; 12 BP.
 XX
 AC ABI39188;
 XX

```

DT 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 339161 for detecting SNP TSC0040871.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 339161; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 6 CGACTTCATCC 16
Db 12 CTACTTTATCC 2
XX
RESULT 486
ABI73827/c
ID ABI73827 standard; DNA; 12 BP.
XX
XX ABI73827;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 373800 for detecting SNP TSC0060326.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

```

```

XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 373800; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 8 ACTTCATCCTT 18
Db 11 ACTTCATTTT 1
XX
RESULT 487
ABH71716/c
ID ABH71716 standard; DNA; 12 BP.
XX
XX ABH71716;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 271693 for detecting SNP TSC0002593.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

```

PT methylation status.
XX Claim 1; SEQ ID NO 271693; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 12 ACTTCCTCGTT 2
|||||
RESULT 488
ABH97829
ID ABH97829 standard; DNA; 12 BP.
XX
XX AC ABH97829;
XX
XX DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297822 for detecting SNP TSC0017787.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 297822; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 2 CGAATTCCTCC 12
|||||
RESULT 489
ABI07180
ID ABI07180 standard; DNA; 12 BP.
XX
XX AC ABI07180;
XX
XX DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 307153 for detecting SNP TSC0022364.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 307153; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 2 ACTTCACCCCT 12
|||||

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; cancer; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 376101; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 ACTTCACCTT 18
Db 11 ACTTCACCTT 1

RESULT 492
ABI76128/c
ID ABI76128 standard; DNA; 12 BP.
XX AC ABI76128;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 376101 for detecting SNP TSC0061615.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 309081; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGAGCGACTT 11
Db 1 GTGAGCGCTTT 11

RESULT 491
ABI76128/c
ID ABI76128 standard; DNA; 12 BP.
XX AC ABI76128;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 376101 for detecting SNP TSC0061615.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```

```

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 377728; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 1 ACTTCACCTTT 11
RESULT 493
ABH68282
ID ABH68282 standard; DNA; 12 BP.
XX
XX ABH68282;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 268259 for detecting SNP TSC0001019.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 268259; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 1 ACTTCACCTTT 11
RESULT 494
ABH96294
ID ABH96294 standard; DNA; 12 BP.
XX
XX ABH96294;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 296287 for detecting SNP TSC0017004.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 296287; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 2 CAATTTCATCC 12
RESULT 494
ABH96294
ID ABH96294 standard; DNA; 12 BP.
XX
XX ABH96294;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 296287 for detecting SNP TSC0017004.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 296287; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
SQ

```



```
Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 2 ACTTAATCCAT 12

RESULT 495
ABH96483/C
ID ABH96483 standard; DNA; 12 BP.
XX AC
XX ABH96483;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 296476 for detecting SNP TSC0017098.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 296476; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match      43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACATCATCCTT 1

RESULT 496
ABI25488/C
ID ABI25488 standard; DNA; 12 BP.
XX AC
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 351220 for detecting SNP TSC0000813.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
```

PN WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 351220; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 8 ACTTCATCCTT 18
Db 2 ACATCATCCTT 12
||| ||||| |||
2 ACATCATCCTT 12
RESULT 498
ABI51908
ID ABI51908 standard; DNA; 12 BP.
XX AC ABI51908;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 351881 for detecting SNP TSC0047550.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX Oligonucleotide primer SEQ ID NO 351881 for detecting SNP TSC0047550.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 351220; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 8 ACTTCATCCTT 18
Db 2 ACATCATCCTT 12
||| ||||| |||
2 ACATCATCCTT 12
RESULT 498
ABI51908
ID ABI51908 standard; DNA; 12 BP.
XX AC ABI51908;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 351881 for detecting SNP TSC0047550.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 351881; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 8 ACTTCATCCTT 18
Db 2 ACTACATCCAT 12
||| ||||| |||
2 ACTACATCCAT 12
RESULT 499
ABI72639
ID ABI72639 standard; DNA; 12 BP.
XX AC ABI72639;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 372612 for detecting SNP TSC0059500.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 372612; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The


```
DE Oligonucleotide primer SEQ ID NO 299750 for detecting SNP TSC0018720.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 299750; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 12 ATTTCTCCTT 2
RESULT 503
ABI09761
ID ABI09761 standard; DNA; 12 BP.
XX AC ABI09761;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 309734 for detecting SNP TSC0023644.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
```

```
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 309734; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 1 CAATTTCATCC 11
RESULT 504
ABI10740
ID ABI10740 standard; DNA; 12 BP.
XX AC ABI10740;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 310713 for detecting SNP TSC0024065.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
```

```
PS Claim 1; SEQ ID NO 310713; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 1 ACTTCATCCTT 11

RESULT 505
ABI51909
ID ABI51909 standard; DNA; 12 BP.
XX
AC ABI51909;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 351882 for detecting SNP TSC0047550.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 351882; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 1 ACTTCATCCTT 11

RESULT 506
ABI70736/C
ID ABI70736 standard; DNA; 12 BP.
XX
AC ABI70736;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 370709 for detecting SNP TSC0006975.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 370709; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 12 AATACATCCTT 2
```

```
RESULT 507
ABI77347
ID ABI77347 standard; DNA; 12 BP.
AC ABI77347;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 377320 for detecting SNP TSC0007841.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WIPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 377320; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 2 CAACTTCATCC 12
RESULT 508
ABI63539
ID ABI63539 standard; DNA; 12 BP.
XX
AC ABI63539;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 363512 for detecting SNP TSC0053895.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WIPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 377320; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 ACTTCATCCTT 18
Db 1 ATTTCACCTT 11
RESULT 509
ABH76484
ID ABH76484 standard; DNA; 12 BP.
XX
AC ABH76484;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 276477 for detecting SNP TSC0004199.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
```

PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 276477; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTGACGACTT 11
 Db 1 GTGAGTGAAT 11
 RESULT 510
 ABI02467/C
 ID ABI02467 standard; DNA; 12 BP.
 XX
 XX AC ABI02467;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 302440 for detecting SNP TSC0019992.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX PR 07-APR-2000; 2000DE-01019173.
 XX
 XX PA (EPIG-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 302440; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 AGCGACTTCAT 14
 Db 12 ACCGACCTCAT 2
 RESULT 511
 ABI03957
 ID ABI03957 standard; DNA; 12 BP.
 XX
 XX AC ABI03957;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 303930 for detecting SNP TSC0020701.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX PR 07-APR-2000; 2000DE-01019173.
 XX
 XX PA (EPIG-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 303930; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 43.3%; Score 7.8; DB 1; Length 12;


```
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 364428; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CGACTTCATCC 16
Db 12 CTACTTCATTC 2
RESULT 515
ABL59978
ID ABL59978 standard; DNA; 12 BP.
XX
XX ABL59978;
AC
XX
XX 24-JUL-2002 (first entry)
DT
XX
XX Adapter oligonucleotide SEQ ID NO:13.
DE
XX
XX Exogenous regulatory molecule; DNA-binding domain; identification;
KW regulatory sequence element; characterisation; cellular domain;
KW isolation; adapter; ds.
XX
XX Synthetic.
OS
XX
XX WO200183819-A2.
FN
XX
XX 08-NOV-2001.
PD
XX
XX 27-APR-2001; 2001WO-US013562.
PF
XX
XX 28-APR-2000; 2000US-0200590P.
PR
XX 27-JUN-2000; 2000US-0214674P.
PR
XX 28-AUG-2000; 2000US-0228605P.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
PA
XX
XX Wolffe A, Urnov F, Guschin D, Collingwood T, Li X, Johnstone B;
PI
XX
XX WPI; 2002-179352/23.
DR
```

```
XX Designing exogenous regulatory molecules for regulating a gene of
XX interest comprises preparation based on identified regulatory sequence
XX elements from accessible regions of chromatin.
XX
XX Example 16; Page 108; 153pp; English.
XX
XX The present invention describes a method for designing exogenous
XX regulatory molecules (ERM) for regulating a gene of interest (I). The
XX method comprises: (a) providing polynucleotide sequences (II)
XX corresponding to accessible regions related to (I); (b) identifying
XX potential regulatory sequence elements (RSE) from (II); and (c) preparing
XX ERM, comprising selecting a DNA binding domain that activates or
XX represses (I), where the preparing comprises selecting the DNA binding
XX domain, the functional domain (or both) based upon the identified RSE.
XX The method can be used for designing one or more ERMs for regulating a
XX gene of interest. The present sequence represents an adapter
XX oligonucleotide, which is used in an example from the present invention
XX
XX Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GAGCGACTTCA 13
Db 1 GATCGAATTCA 11
RESULT 516
AAD45540
ID AAD45540 standard; DNA; 12 BP.
XX
XX AAD45540;
AC
XX
XX 27-DEC-2002 (first entry)
DT
XX
XX JC3 linker DNA used to illustrate the method of the invention.
DE
XX
XX Protein-protein interaction; detection; cancer; linker; ss.
KW
XX
XX Unidentified.
OS
XX
XX US6410239-B1.
FN
XX
XX 25-JUN-2002.
PD
XX
XX 14-DEC-1999; 99US-00461125.
PF
XX
XX 14-JUN-1996; 96US-00663824.
PR
XX 13-JUN-1997; 97US-00874825.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Nandabalan K, Rothberg JM, Yang M, Knight JR, Kalbfleisch TS;
XX
XX WPI; 2002-654433/70.
DR
XX
XX Detection of protein to protein interactions amongst two protein
XX populations useful e.g. to identify interactions specific for particular
XX tissues or diseases and to identify inhibitors of interactions uses a new
XX genetic method.
XX
XX Example; Col 203; 152pp; English.
XX
XX The present invention relates to novel methods for detecting protein to
XX protein interactions amongst two populations of proteins, each having a
XX complexity of at least 100. The method involves using new genetic methods
XX in which encoded proteins are fused to either the DNA-binding domain of a
XX transcriptional activator or the activation domain of a transcriptional
XX activator. The methods are useful to detect interacting proteins and to
XX identify protein-protein interactions specific for a particular species,
```

CC tissue, stage of development or disease state, e.g. by comparing protein-
CC protein interactions between populations from cDNA of cancerous or pre-
CC cancerous cells with those from non-cancerous cells. They are also useful
CC to identify inhibitors interfering with protein-protein interactions e.g.
CC potential drug candidates inhibiting interactions specific to cancerous
CC cells. The present sequence is a linker DNA used to illustrate the method
CC of the invention

XX
SQ Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| |||||
Db 1 AGCTGCTTCAT 11

RESULT 517
AAL42640
ID AAL70640 standard; DNA; 12 BP.

XX
AC AAL70640;

XX
DT 04-FEB-2002 (first entry)

XX
DE Adaptor-specific primer.

XX
KW Adaptor; regulatory sequence; mapping; database; library; chromatin;
XX
KW DNase I; ds.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT misc_feature 1..4

FT /*tag= C

FT /note= "5', single-stranded overhang"

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "5', phosphorylated"

XX
PN W0200183732-A2.

XX
PD 08-NOV-2001.

XX
PF 27-APR-2001; 2001WO-US040617.

XX
PR 28-APR-2000; 2000US-0200590P.

XX
PR 27-JUN-2000; 2000US-0214674P.

XX
PR 28-AUG-2000; 2000US-0228556P.

XX
PA (SANG-) SANGAMO BIOSCIENCES INC.

XX
PI Wolffe A, Urnov F, Guschin D, Collingwood T, Li X, Johnstone B;

XX
DR WPI; 2002-034512/04.

XX
PT Isolating a collection of polynucleotides corresponding to accessible
XX regions of cellular chromatin, for generating a polynucleotide library
XX and database, comprises using a probe or enzyme.

XX
PS Example 16; Page 116; i62pp; English.

XX
CC The present sequence is that of a double-stranded adaptor oligonucleotide
XX used in a method of the invention for construction of libraries enriched
XX in DNase I-accessible sequences. The invention provides methods for the
XX identification, isolation and characterization of regulatory sequences in
XX a cell of interest. The regulatory sequences are identified based upon
XX their differential accessibility in cellular chromatin compared to other
XX sequences. A rapid method for mapping DNase hypersensitive sites (which
XX can correspond to boundaries of accessible regions) with respect to a

CC particular gene involves ligation of an adaptor to the DNA ends generated
CC by DNase action, followed by amplification using an adaptor-specific
CC primer and a gene-specific primer. The invention also provides libraries
CC of regulatory sequences, databases comprising collections of regulatory
CC sequences for a cell of interest, computer programs for using the
CC databases to conduct genetic analyses, and use of the accessible
CC regulatory sequences in the design of vectors bearing transgenes

XX
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| |||||
Db 1 GATCGAATTCA 11

RESULT 518
AAL42640
ID AAL42640 standard; DNA; 12 BP.

XX
AC AAL42640;

XX
DT 08-AUG-2002 (first entry)

XX
DE Rice seed bZIP transcription factor PCR primer (GluA-3).

XX
KW Rice seed b-zipper 1; RISB21; ss; rice; b-ZIP transcription factor;

XX
KW novel plant; transgenic plant; seed production; higher nutrition;

XX
KW denser protein storage; PCR; primer.

XX
OS Oryza sativa.

XX
PN W0200231154-A1.

XX
PD 18-APR-2002.

XX
PF 11-OCT-2001; 2001WO-JP008936.

XX
PR 11-OCT-2000; 2000JP-00311295.

XX
PA (NORQ) NAT INST AGROBIOLOGICAL SCI.

XX
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

XX
PI Takaiwa F, Onodera Y;

XX
DR WPI; 2002-372276/40.

XX
PT Rice seed-originated bZIP type transcription factors regulating
XX expression of rice storage protein with binding activity to GCNA motif,
XX useful in constructing new breeds of plants to produce seeds with higher
XX nutrition.

XX
PS Claim 20; Fig 14; 124pp; Japanese.

XX
CC The invention comprises the amino acid and coding sequences of rice seed
XX b-ZIP type transcription factors (RISB21, RISB24 and RISB25). The DNA and
XX protein sequences of the rice seed b-ZIP transcription factors are useful
XX in constructing new breeds of plants (e.g. rice) - to produce seeds with
XX higher nutrition and denser protein storage. DNA sequences AAL42638 -
XX AAL42682 represent rice seed bZIP transcription factor PCR primers

XX
SQ Sequence 12 BP; 3 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACTT 11
||||| |||||
Db 2 GTGAGTCACTT 12

```

RESULT 519
AAI70659
ID AAI70659 standard; DNA; 12 BP.
XX
AC AAI70659;
XX
DT 04-FEB-2002 (first entry)
XX
DE Adaptor-specific oligonucleotide.
XX
KW Adaptor; regulatory sequence; mapping; database; library; chromatin;
KW DNase; mouse; signal transduction; cancer; osteoporosis;
KW cardiovascular disease; drug target; pharmacogenomics; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4
FT FT /*tag= C
FT FT /*note= "5' single-stranded overhang"
FT modified_base 1 /*tag= a
FT FT /*mod_base= OTHER
FT FT /*note= "5' phosphorylated"
XX
PN WO200184148-A2.
XX
FD 08-NOV-2001.
XX
XX
XX 27-APR-2001; 2001WO-US013827.
XX
XX 28-APR-2000; 2000US-0200590P.
XX 27-JUN-2000; 2000US-0214674P.
XX 28-AUG-2000; 2000US-0228608P.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Wolfe A, Urnov F, Guschin D, Collingwood T, Li X, Johnstone B;
XX WPI; 2002-034538/04.
XX
XX Identification of drugs for the treatment of cancer, cardiovascular
XX disease or osteoporosis comprises targeting gene regions of interest of
XX the transduction pathway.
XX
XX Example 16; Page 112; 152pp; English.
XX
XX The present sequence is that of a double-stranded adaptor oligonucleotide
XX used in a method of the invention for construction of libraries enriched
XX in DNase I-accessible sequences. This is an example of methods of the
XX invention designed to identify regulatory DNA regions according to their
XX differential accessibility in cellular chromatin compared to other
XX sequences. The method identifies DNase hypersensitive sites, which can
XX correspond to boundaries of accessible regions. The adaptor is ligated to
XX the DNA ends generated by DNase action. The invention provides methods
XX for: identifying a drug that affects accessible regions of cellular
XX chromatin; elucidating signal transduction pathways; facilitating
XX modulation of these pathways and/or of their associated genes; and
XX pharmacogenomically selecting an appropriate drug therapy. The methods
XX are useful for identifying drug targets which will be used to develop
XX treatments of cancer, cardiovascular disease and osteoporosis (claimed)
XX
XX Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;
XX Best Local Similarity 81.8%; Pred. No. 2.7e+02;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3 GAGCGACTTCA 13
XX |||||
XX 1 GATCGAATTCA 11

```

```

RESULT 520
ABZ72909/c
ID ABZ72909 standard; RNA; 12 BP.
XX
AC ABZ72909;
XX
DT 09-APR-2003 (first entry)
XX
DE Rod opsin hammerhead ribozyme oligonucleotide.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
XX 01-MAY-2002; 2002WO-US013679.
XX
XX 01-MAY-2001; 2001US-00847601.
XX
XX (UYFL) UNIV FLORIDA.
XX
XX Lewin AS, Shaw LC, Grant MB;
XX WPI; 2003-111880/10.
XX
XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.
XX
XX Example 5; Page 67; 115pp; English.
XX
XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide; or (e) a host cell
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration, (diabetic) retinopathy, or (age-related) macular
XX degeneration. (I) is also useful for manufacturing a medicament for
XX treating the diseases mentioned above, including autosome dominant
XX retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
XX for treating, decreasing the severity, or ameliorating the symptoms of a
XX pathological condition, e.g. atrophic or pigmented lesions of the eye,
XX blindness, a reduction in central or peripheral vision, or a reduction in
XX total vision. ABZ72763 to ABZ72953 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 12 BP; 4 A; 1 C; 4 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 43.3%; Score 7.8; DB 1; Length 12;

```

```
Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
Db 11 GAACTCATCCT 1

RESULT 521
ABV75305/C
ID AB223896 standard; DNA; 12 BP.
XX AC AB223896;
XX DT 18-MAR-2003 (first entry)
XX DE TERT minimal promoter 3'-end inserted nucleotide fragment.
XX KW TERT; telomerase reverse transcriptase; promoter; cytotstatic; anti-HIV;
XX KW osteopathic; dermatological; gene therapy; transcription factor; TF;
XX KW cardiant; human; ds.
XX OS Homo sapiens.
XX PN WO200290571-A2.
XX PD 14-NOV-2002.
XX PF 07-MAY-2002; 2002WO-US014740.
XX PR 08-MAY-2001; 2001US-0289641P.
XX PA (SIER-) SIERRA SCI INC.
XX PI Andrews WH;
XX DR WPI; 2003-120554/11.
XX CC New nucleic acid having a nucleotide sequence that is identical to a
XX CC telomerase reverse transcriptase (TERT) activator-binding site in the
XX CC minimal TERT promoter useful for treating cellular proliferative
XX CC diseases, e.g. cancer, AIDS.
XX PS Example; Page 45; 60pp; English.
XX CC The invention relates to a nucleic acid present in other than its natural
XX CC environment, having a nucleotide sequence that is the same or is
XX CC substantially identical to a telomerase reverse transcriptase (TERT)
XX CC activator binding site in the minimal TERT promoter. The nucleic acids,
XX CC agents and methods are useful for treating cellular proliferative
XX CC diseases, e.g. cancer, acquired immunodeficiency syndrome (AIDS),
XX CC cardiovascular diseases, or osteoporosis. They are also useful in immune
XX CC senescence and skin rejuvenation. The nucleic acids are also useful in
XX CC preparing constructs, e.g. vectors, expression systems, or probes. The
XX CC present sequence represents a DNA fragment inserted immediately upstream
XX CC of the translation initiation codon ATG at the 3'-end of the TERT minimal
XX CC promoter, to optimise translation
XX SQ Sequence 12 BP; 3 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACTT 11
Db 11 GTGGGCGCAATT 1

RESULT 522
ABV75305/C
ID ABV75305 standard; DNA; 12 BP.
XX
```

```
AC ABV75305;
XX DT 07-MAR-2003 (first entry)
XX DE Sequence inserted upstream of TERT start codon.
XX KW TERT; telomerase reverse transcriptase; TF-8; TF-13; repressor;
XX KW cardiovascular; osteopathic; virucide; transcription; ds.
XX OS Synthetic.
XX PN WO200290570-A2.
XX PD 14-NOV-2002.
XX PF 07-MAY-2002; 2002WO-US014720.
XX PR 08-MAY-2001; 2001US-0289717P.
XX PA (SIER-) SIERRA SCI INC.
XX PI Andrews WH;
XX DR WPI; 2003-103520/09.
XX CC New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor
XX CC binding site, useful in regulating TERT expression and for screening
XX CC agents that modulate TERT transcription repressing activity of the TF-8
XX CC and TF-13 sites.
XX PS Example; Page 28; 40pp; English.
XX CC The invention relates to a new telomerase reverse transcriptase (TERT) TF
XX CC -8 and/or TF-13 repressor binding site. The nucleic acid comprising the
XX CC binding site sequence is useful in preparing constructs, such as vectors
XX CC and expression systems, and probes for the TERT TF-8 and/or TF-13
XX CC repressor binding site in non-human animals. Modulating the transcription
XX CC repressing activity of TERT TF-8 and/or TF-13 repressor factors to
XX CC regulate telomerase expression, can be used in immortalization of cells,
XX CC production of reagents useful in life science research, and therapeutic
XX CC research. Inhibitors of TERT transcription repression by a TF-8 and/or TF
XX CC -13 repressor may be used for increasing the proliferative capacity of a
XX CC cell, and for treating progeria, Hutchinson-Gilford syndrome,
XX CC cardiovascular disease, osteoporosis, or AIDS. The present sequence
XX CC represents a sequence inserted upstream of an ATG codon, after the TERT
XX CC minimal promoter, to optimise translation
XX SQ Sequence 12 BP; 3 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGCACTT 11
Db 11 GTGGGCGCAATT 1

RESULT 523
AAN82164/C
ID AAN82164 standard; DNA; 10 BP.
XX AC AAN82164;
XX DT 25-MAR-2003 (revised)
XX DT 12-DEC-1990 (first entry)
XX DE Sequence #22 recognised by probe for 16S RNA gene of mycoplasma.
XX KW Mollicutes.
XX OS Mycoplasma.
XX
```

```

PN EP250662-A.
XX
XX
PD 07-JAN-1988.
XX
XX PF 25-JUN-1986; 86EP-00304919.
XX
XX PR 25-JUN-1986; 86EP-00304919.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Gobel U, Stanbridge EJ;
XX
XX DR WPI; 1988-000726/01.
XX
XX PT Detection of prokaryotic organisms - esp. mycoplasma by hybridisation
XX PT with an oligo:nucleotide probe complementary to nucleotide sequence in
XX PT the prokaryote.
XX
XX PS Claim 16; Page 6; 9pp; English.
XX
XX CC A probe which is complementary to this sequence can be used to detect
XX CC prokaryotes. See also AAN82143-71. (Updated on 25-MAR-2003 to correct PA
XX CC field.)
XX
XX SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
      Query Match 41.1%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 2.9e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCC 16
Db 10 ACGTCATCC 2

RESULT 524
AAQ45103/c
ID AAQ45103 standard; DNA; 10 BP.
XX
XX AC AAQ45103;
XX
XX DT 25-MAR-2003 (revised)
XX DT 02-NOV-1994 (first entry)
XX
XX 5'-primer #14 for investigating gene expression.
XX
XX PCR; polymerase chain reaction; amplification; primer; diagnosis;
XX KW gene expression; cancer; ss.
XX
XX OS Synthetic.
XX
XX PN DE4317414-C1.
XX
XX PD 21-APR-1994.
XX
XX PF 18-MAY-1993; 93DE-04317414.
XX
XX PR 18-MAY-1993; 93DE-04317414.
XX
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX PI Strauss M, Bauer D;
XX
XX DR WPI; 1994-110647/14.
XX
XX PT Diagnostic agent for investigating gene expression - comprises
XX PT oligonucleotide primer pairs formed from labelled 5'- and 3'-
XX PT oligonucleotide primers.
XX
XX PS Claim 7; Col 7; 6pp; German.
XX
XX CC AAQ45090-Q45115 are preferred 5'-primers for use with a pool of at least
XX CC 12 3'-primers coupled with a detectable label. The 5'-primers all contain

CC equal numbers of G+C and A+T nucleotides. The 288 (or more) combinations
CC of 5'- and 3'-primers are used in PCR amplifications as part of a method
CC for diagnosing gene expression. The amplified fragments are separated by
CC non-denaturing PAGE and the band pattern is compared to a standard.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
      Query Match 41.1%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 2.9e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GACTTCATC 15
Db 9 GACTTCATC 1

RESULT 525
AAQ96589/c
ID AAQ96589 standard; DNA; 10 BP.
XX
XX AC AAQ96589;
XX
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 184.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX OS Human immunodeficiency virus 1.
XX
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUFARLANE RED CROSS SOC.
XX
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX DR WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX
XX PS Claim 13; Page 190; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
      Query Match 41.1%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 2.9e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
Db 10 CTTTCATCCT 2

```

```

RESULT 526
AAQ96590/c
ID AAQ96590 standard; DNA; 10 BP.
XX
XX AC AAQ96590;
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 185.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
FN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
PR
XX (MACP-) MACFARLANE BURNET CENT MEDICAL.
FA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
FA
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
XX
XX WPI; 1995-293115/38.
DR
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 190; 301pp; English.
PS
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decaucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decaucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCT 17
Db 9 CTTTCCTCCT 1

RESULT 527
AAQ90123
ID AAQ90123 standard; cDNA; 10 BP.
XX
XX AAQ90123;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-NOV-1995 (first entry)
XX
XX PCR primer for the TCI gene.
DE
XX Tumour marker; invasive; metastatic; cancer; ss; palindromic PCR.
XX

```

```

OS Synthetic.
XX WO9511923-A1.
XX
XX 04-MAY-1995.
PD
XX
XX 31-OCT-1994; 94WO-US012502.
PF
XX
XX 29-OCT-1993; 93US-00146488.
PR
XX (DAND ) DANA FARBER CANCER INST INC.
FA
XX Chen LB, Bao S, Liu Y;
PI
XX WPI; 1995-178826/23.
DR
XX
XX New tumour marker TCI, corresp. DNA and monoclonal antibody - for
PT detecting, preventing and treating tumours, esp. in breast, colon and
PT gastrointestinal tract cancer.
PT
XX
XX Disclosure; Page 8; 84pp; English.
PS
XX
XX The sequence is that of a PCR primer used to isolate the TCI gene which
CC encodes the TCI tumour marker protein, by palindromic PCR. The gene and
CC its product may be used to detect tumours in blood, urine or sputum.
CC Inhibitors of TCI are used to treat late stage cancers and for preventing
CC tumour cell metastasis. See also AAQ90112-25. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TGAGCGACT 10
Db 1 TGAGCTACT 9

RESULT 528
AAT29328
ID AAT29328 standard; DNA; 10 BP.
XX
XX AC AAT29328;
XX
XX 25-MAR-2003 (revised)
DT 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
DE
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
XX Synthetic.
OS
XX
XX WO9531574-A1.
FN
XX
XX 23-NOV-1995.
PD
XX
XX 12-MAY-1995; 95WO-US006032.
PF
XX
XX 16-MAY-1994; 94US-00242887.
PR
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
PI
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
PT

```

PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.

PS Claim 46; Page 55; 72pp; English.

XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 PS from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
 Db 1 GCCTTCATC 9

RESULT 529.

AAT29318
 ID AAT29318 standard; DNA; 10 BP.

XX AC AAT29318;

XX 25-MAR-2003 (revised)
 DT 28-JUN-1996 (first entry)

XX 5'-primer for mammalian G-protein coupled receptor coding sequences.

DE 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.

XX Synthetic.

XX WO9531574-A1.

XX 23-NOV-1995.

XX 12-MAY-1995; 95WO-US006032.

XX 16-MAY-1994; 94US-00242887.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Lopeznieto CE, Nigam SK;

XX WPI; 1996-010958/01.

XX Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.

XX Claim 46; Page 55; 72pp; English.

XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 1 CTTTCATCCT 9

RESULT 530

AAT29339
 ID AAT29339 standard; DNA; 10 BP.

XX AC AAT29339;

XX 25-MAR-2003 (revised)
 DT 28-JUN-1996 (first entry)

XX 5'-primer for mammalian G-protein coupled receptor coding sequences.

DE 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.

XX Synthetic.

XX WO9531574-A1.

XX 23-NOV-1995.

XX 12-MAY-1995; 95WO-US006032.

XX 16-MAY-1994; 94US-00242887.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Lopeznieto CE, Nigam SK;

XX WPI; 1996-010958/01.

XX Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.

XX Claim 46; Page 55; 72pp; English.

XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
 Db 2 GCCTTCATC 10

RESULT 531

AAT29315

ID AAT29315 standard; DNA; 10 BP.
 XX AC AAT29315;
 XX DT 25-MAR-2003 (revised)
 XX DT 28-JUN-1996 (first entry)
 XX DE 5'-primer for mammalian G-protein coupled receptor coding sequences.
 XX KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
 KW characterisation; biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.
 XX OS Synthetic.
 XX FN WO9531574-A1.
 XX PD 23-NOV-1995.
 XX PF 12-MAY-1995; 95WO-US006032.
 XX PR 16-MAY-1994; 94US-00242887.
 XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX PI Lopeznieta CE, Nigam SK;
 XX DR WPI; 1996-010958/01.
 XX PT Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers used
 PT for genome mapping and disease diagnosis.
 XX PS Claim 46; Page 55; 72pp; English.
 CC The 5'-primers AAT29262-382, and the complementary 3'-primers derived
 CC from them, which target mammalian G-protein coupled receptor coding
 CC sequences, together comprise a PCR primer kit. The kit is used in a new
 CC method for the characterisation of nucleic acid sequences obtd. from
 CC mammalian biological samples, which comprises PCR amplification and
 CC indexing of the prods. w.r.t the primer pair that hybridised to its
 CC delineating subsequences. The method may be used in the identification,
 CC cloning and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 9 CTTTCATCCT 17
 Db 1 CTTTCATCAT 9

 RESULT 532
 AAT18634/c
 ID AAT18634 standard; DNA; 10 BP.
 XX AC AAT18634;
 XX DT 06-NOV-1996 (first entry)
 XX DE Arbitrary 5' oligodecamer DDRT-PCR primer U14.
 XX KW Differential display of mRNA; reverse transcription; DDRT-PCR; human;
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
 KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
 KW rheumatoid arthritis; polymerase chain reaction; ss.
 XX OS Synthetic.

XX EP705842-A2.
 XX PD 10-APR-1996.
 XX PF 02-OCT-1995; 95EP-00115510.
 XX PR 06-OCT-1994; 94EP-00115751.
 XX PA (FARH) HOECHST AG.
 XX PI Bartnik E, Margerie D;
 XX DR WPI; 1996-181045/19.
 XX PT Diagnosis and treatment of IL-1 mediated connective tissue diseases -
 PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
 PT antibodies to them.
 XX PS Example; Page 15; 31pp; English.
 CC The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which
 CC were used along with 4 degenerate 3' oligo dr primers for the
 CC differential display of human chondrocyte mRNA by reverse transcription
 CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA
 CC clones, which were then searched against DNA databases for homology to
 CC known human genes. The cDNA mols. can be used for the prodn. of gene
 CC specific primers and probes to isolate genes induced by treating (esp.
 CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the
 CC diagnosis of IL-1beta related connective tissue diseases, in partic.
 CC ossteoarthritis or rheumatoid arthritis
 XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 7 GACTTCATC 15
 Db 9 GACTTGTATC 1

 RESULT 533
 AAT69130/c
 ID AAT69130 standard; DNA; 10 BP.
 XX AC AAT69130;
 XX DT 26-FEB-1998 (first entry)
 XX DE Primer (12) for RT and DD-PCR of Murine metastatic mRNA.
 XX KW Mouse; murine; tumour; cancer; metastatic sequence; detection; diagnosis;
 KW treatment; metastasis; hyperplasia; dysplasia; hypertrophy; screening;
 KW reverse transcription; PCR; primer; differential display analysis; ss.
 XX OS Synthetic.
 OS Mus musculus.
 XX FN WO9718454-A2.
 XX PD 22-MAY-1997.
 XX PF 15-NOV-1996; 96WO-US018567.
 XX PR 16-NOV-1995; 95US-0006838P.
 XX PR 30-JAN-1996; 96US-00594031.
 XX PA (THOM/) THOMPSON T.
 XX PI Thompson T;
 XX

DR WPI; 1997-289397/26.
 XX Identifying tumour metastatic sequences - by introducing transfected
 PT cells into host mammal and analysing primary and metastatic sequences by
 PT differential display PCR.
 XX Example 3; Page 30; 102pp; English.
 PS Mouse Urogenital Sinus (UGS) tissue was isolated from 17 day old mouse
 CC embryos. The UGS cells were infected with retroviruses, cultured and
 CC implanted under the renal capsule of mice. Reconstitutions were harvested
 CC 5 weeks later, when they showed signs of distress from the tumour burden.
 CC Metastatised tumours were isolated from a site outside the renal capsule.
 CC RNA was isolated from primary tumours and metastases, reverse transcribed
 CC and subjected to differential display PCR, using the primers AAT69119-42.
 CC The sequences were analysed to obtain metastatic sequences. The method
 CC can be used to detect, diagnose and treat disorders related to
 CC metastasis, or treat malignant or non-malignant disorders, e.g.
 CC hyperplasia, dysplasia and hypertrophy. The metastatic sequence can be
 CC used to screen a biological sample for metastasis, and it or its
 CC expression product may also be used to treat a metastatic disorder
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 GACTTCATC 15
 Db 9 GACTTGATC 1
 RESULT 534
 AAX83302
 ID AAX83302 standard; DNA; 10 BP.
 XX
 AC AAX83302;
 XX
 DT 31-AUG-1999 (first entry)
 XX
 DE Breast cancer tumour specific cDNA isolation primer #17.
 XX
 KW Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
 KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9725426-A2.
 XX
 PD 17-JUL-1997.
 XX
 PF 10-JAN-1997; 97WO-US000485.
 XX
 PR 11-JAN-1996; 96US-00585392.
 PR 20-AUG-1996; 96US-00700014.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Frudakis TN, Smith JM, Reed SG;
 XX WPI; 1997-372865/34.
 XX
 XX Breast cancer-related DNA from retrovirus antigen (s) - useful for
 PT diagnosis and treatment of breast cancer.
 XX
 PS Example 1; Page 24; 221pp; English.
 XX
 CC Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
 CC specific clones (AAX83201-X83285 and AAX83331-X83415) which are expressed
 CC from a genomic region containing a human endogenous retrovirus
 CC (AAX83330). Detection of the clone sequences allows determination of the

CC presence of breast cancer in a mammal. Progression of breast cancer can
 CC be monitored by detecting the level of clone expression. Polypeptides
 CC encoded by the clones can be used in vaccines to inhibit or prevent
 CC breast cancer
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 1 CTTCAACT 9
 RESULT 535
 AAV69061
 ID AAV69061 standard; DNA; 10 BP.
 XX
 AC AAV69061;
 XX
 DT 22-JAN-1999 (first entry)
 XX
 DE Human breast tumour cDNA PCR primer #17.
 XX
 KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
 KW vaccine; epitope; endogenous; retroviral element; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845328-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US006939.
 XX
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Frudakis TN, Smith JM, Reed SG;
 XX WPI; 1998-557473/47.
 XX
 XX New DNA sequences isolated from endogenous human retroviral element - and
 PT related vectors, transformed cells, proteins and antibodies, useful for
 PT diagnosis, treatment and prevention of breast cancer.
 XX
 PS Example 1; Page 69; 173pp; English.
 XX
 CC The present sequence represents a PCR primer for human breast tumour cDNA
 CC nucleotide sequences. The present invention describes nucleotide
 CC sequences which encode human breast tumour specific polypeptides.
 CC Detection or measurement of human breast tumour specific polypeptides and
 CC nucleotide sequences, or the corresponding RNA in a sample, is used for
 CC diagnosis and monitoring of breast cancer. Human breast tumour specific
 CC polypeptides and nucleotide sequences, and the vectors containing the
 CC DNAs, are also useful in vaccines for inhibiting development (for
 CC prevention or therapy) of breast cancer. The polypeptides may also be
 CC used to raise monoclonal antibodies, used as immunoassay reagents
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 1 CTTCAACT 9

| | |
|------------|--|
| XX | AAX18617; |
| AC | |
| XX | |
| DT | 06-MAY-1999 (first entry) |
| XX | |
| XX | p53 serial analysis of gene expression tag #1. |
| DE | |
| XX | |
| KW | p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic; |
| XX | rat embryo fibroblast; REF; tumour suppressor; cell cycle control; |
| KW | tumorigenesis; diagnosis; ss. |
| OS | Synthetic. |
| OS | Rattus sp. |
| XX | |
| PN | WO9901581-A1. |
| XX | |
| PD | 14-JAN-1999. |
| XX | |
| PJ | 02-JUL-1998; 98WO-US013903. |
| XX | |
| XX | 02-JUL-1997; 97US-0051573P. |
| XX | (GENZ) GENZYME CORP. |
| PA | |
| XX | Madden SL, Galella EA, Bertelsen AH, Beaudry GA; |
| XX | WPI; 1999-106079/09. |
| DR | |
| XX | |
| PT | Diagnosis of cancer in potentially neoplastic samples - by comparing the |
| XX | level of transcription between RNA transcripts in two tissue samples, |
| PT | useful for providing an extensive profile of gene expression in rat |
| PT | embryo fibroblast (REF) cells. |
| PS | |
| XX | Example 2; Page 15; 32pp; English. |
| XX | |
| CC | A method has been developed for the diagnosis of cancer in potentially |
| CC | neoplastic samples. The method comprises comparing the level of |
| CC | transcription between RNA transcripts in two tissue samples (which are of |
| CC | the same type), where the first sample is potentially neoplastic, and the |
| CC | second sample is normal human tissue. The first sample is categorized as |
| CC | neoplastic if its level of transcription is lower than that of the second |
| CC | sample. The transcript is selected from Alb, RAS, U6 snRNA, 16S rRNA, BGR- |
| CC | 1, ribosomal protein S27, ETS-1, 28S rRNA, CGR11, and LIMK-2, and it is |
| CC | identified by a tag selected from ribosomal protein l13a, alpha-tubulin |
| CC | (T1) and (T2), thymosin beta-4, and gamma- actin. The present sequence |
| CC | represents a serial analysis of gene expression (SAGE) tag from the |
| CC | present invention. The use of SAGE tags provides an extensive profile of |
| CC | gene expression in rat embryo fibroblast (REF) cells containing the (non) |
| CC | -functional p53 tumour suppression gene. The discovery of new SAGE tags, |
| CC | which are regulated by p53, enables the diagnosis of genes that are |
| CC | related to cell cycle control and tumourigenesis |
| XX | |
| SQ | Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other; |
| | |
| | Query Match 41.1%; Score 7.4; DB 1; Length 10; |
| | Best Local Similarity 88.9%; Pred. No. 2.9e+02; |
| | Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
| OY | 1 GTGAGGCAC 9 |
| | |
| Db | 9 GTGAGGCAC 1 |
| | |
| RESULT 538 | |
| AAI14916/c | |
| ID | AAI14916 standard; DNA; 10 BP. |
| XX | |
| XX | AAI14916; |
| XX | |
| XX | |
| DT | 17-OCT-2003 (revised) |
| DT | 24-MAR-1999 (first entry) |
| XX | |
| DE | Triple helix forming nucleotides 1181-1190 of 23S rRNA gene |

XX Triple-helix forming region; Triplex formation; DNA detection;
 KW identification; bacteria; oncogene; virus; ds.
 XX
 OS Chlamydomophila caviae.
 XX
 PN US5861244-A.
 XX
 PD 19-JAN-1999.
 XX
 XX 22-DEC-1993; 93US-00173489.
 PF
 XX 29-OCT-1992; 92US-00968436.
 XX
 XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
 PA
 PI Hepburn AG, Wang C;
 XX
 XX WPI; 1999-130384/11.
 DR
 XX
 XX Assay of genetic sequences based on triplex formation from double
 PT stranded analyte - and hybrid of anchor and reporter sequences, with
 PT reporter released if triplex formation occurs, used e.g. to identify
 PT bacteria.
 XX
 XX Disclosure; Col 23-24; 168pp; English.
 PS
 XX The present sequence represents a potential triple-helix forming region.
 CC It can be used to demonstrate the assay of the invention. The assay
 CC comprises adding a sample containing double-stranded DNA test sequences,
 CC e.g. containing the present sequence, to an aqueous medium containing at
 CC least one complex of anchor DNA, attached to a solid support, and
 CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
 CC designed to form a triple-strand structure with part of the test
 CC sequence. Triplex formation results in displacement of the reporter DNA
 CC which is detected as an indication of the presence of the DNA test
 CC sequence. The method is used to detect DNA sequences, particularly for
 CC identification of bacteria (by detecting genes for ribosomal RNA) in
 CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 9 CTTTCCTCCT 1

RESULT 539
 AAZ08327
 ID AAZ08327 standard; DNA; 10 BP.
 XX
 XX
 AC AAZ08327;
 XX
 DT 13-OCT-1999 (first entry)
 XX
 DE Human lung tumour differential display PCR primer.
 XX
 XX Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
 KW immunotherapy; detection; inhibition; PCR primer; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX WO9938973-A2.
 PN
 XX
 XX 05-AUG-1999.
 PD
 XX 26-JAN-1999; 99WO-US001642.
 PF

XX 28-JAN-1998; 98US-00015022.
 PR 28-JAN-1998; 98US-00015029.
 PR 18-MAR-1998; 98US-00040828.
 PR 18-MAR-1998; 98US-00040831.
 PR 23-JUL-1998; 98US-00122191.
 PR 23-JUL-1998; 98US-00122192.
 PR 22-DEC-1998; 98US-00219245.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Reed SG, Lodes MJ, Frudakis TN, Mohamath R;
 PI WPI; 1999-479187/40.
 XX
 DR Lung tumor specific polynucleotides for inhibiting the development of
 PT lung cancer.
 PT
 XX Example 1; Page 83; 171pp; English.
 PS
 XX The present invention describes lung tumour specific polynucleotides and
 CC tumour antigens. AAZ07144 to AAZ07246 and AAZ08301 to AAZ08325 represent
 CC specifically claimed polynucleotides, and AAZ29486 to AAZ29571 represent
 CC amino acid sequences from the present invention. The lung tumour specific
 CC polynucleotides and polypeptides can be used in pharmaceutical
 CC compositions and vaccines to inhibit the development of lung cancer. They
 CC can also be used to detect lung cancer in a patient. Probes and
 CC antibodies derived from the lung tumour sequences are useful in detection
 CC of lung cancer. The present sequence represents a PCR primer used in an
 CC example from the present invention
 XX
 XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 1 CTTCAACCT 9

RESULT 540
 AAV45648/C
 ID AAV45648 standard; DNA; 10 BP.
 XX
 XX
 AC AAV45648;
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Probe for prokaryotic 16S RNA gene.
 XX
 XX Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;
 KW bacteraemia; septicaemia; ss.
 KW
 XX Synthetic.
 OS
 XX US5851767-A.
 PN
 XX 22-DEC-1998.
 PD
 XX 06-JUN-1995; 95US-00469600.
 PF
 XX 04-MAR-1985; 85US-00707725.
 PR 06-MAY-1988; 88US-00191852.
 PR 27-NOV-1991; 91US-00799856.
 PR 19-FEB-1993; 93US-00020874.
 PR 14-OCT-1993; 93US-00136723.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Stanbridge EJ, Gobel U;
 XX

```

DR WPI; 1999-094418/08.
XX
PT Detection of mycoplasma-specific or prokaryote-specific nucleic acids -
PS using mycoplasma-specific or prokaryote-specific probes.
XX
XX Claim 3; Col 8; 11pp; English.
XX
CC This sequence represents a probe based on prokaryotic 16S RNA genes that
CC can be used in the method of the invention. The method is for detecting
CC the presence of prokaryotic specific nucleic acids, and comprises: (a)
CC contacting a medium, which may contain a nucleic acid or nucleic acid
CC fragment from the prokaryote having a particular nucleotide sequence,
CC with an oligonucleotide comprising a nucleotide sequence complementary to
CC the particular nucleotide sequence, whereby the oligonucleotide
CC hybridises with any nucleic acid or nucleic acid fragment from the
CC prokaryote which may be present in the medium; and (b) detecting the
CC presence of any nucleic acid or nucleic acid fragment hybridised with the
CC oligonucleotide. The invention also relates to a method for determining
CC the presence of a mycoplasma. The detection process is useful for
CC contaminated cell cultures or other biological environments. The probes
CC can be used in the diagnosis of bacteraemia or septicaemia in mammals.
CC The process provides a rapid, simple, effective, sensitive and specific
CC mycoplasma detection system. The probes can be made specific for
CC individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and
CC eubacterial species
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACGTCATCC 2

RESULT 541
AAV62777/C
ID AAV62777 standard; RNA; 10 BP.
XX
XX AC AAV62777;
XX
XX DT 04-MAR-1999 (first entry)
XX
XX DE Probe for prokaryotic 16S RNA gene.
XX
XX KW Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;
XX KW bacteraemia; septicaemia; ss.
XX
XX OS Synthetic.
XX
XX US5851767-A.
XX
XX PD 22-DEC-1998.
XX
XX PF 06-JUN-1995; 95US-00469600.
XX
XX PR 04-MAR-1985; 85US-00707725.
XX PR 06-MAY-1988; 88US-00191852.
XX PR 27-NOV-1991; 91US-00799856.
XX PR 19-FEB-1993; 93US-00020874.
XX PR 14-OCT-1993; 93US-00136723.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX PI Stanbridge EJ, Gobel U;
XX
XX WPI; 1999-094418/08.
XX
XX Detection of mycoplasma-specific or prokaryote-specific nucleic acids -
XX PT using mycoplasma-specific or prokaryote-specific probes.
XX

```

```

PS Claim 19; Col 11; 11pp; English.
XX
XX This sequence represents a probe based on prokaryotic 16S RNA genes that
XX can be used in the method of the invention. The method is for detecting
XX the presence of prokaryotic specific nucleic acids, and comprises: (a)
XX contacting a medium, which may contain a nucleic acid or nucleic acid
XX fragment from the prokaryote having a particular nucleotide sequence,
XX with an oligonucleotide comprising a nucleotide sequence complementary to
XX the particular nucleotide sequence, whereby the oligonucleotide
XX hybridises with any nucleic acid or nucleic acid fragment from the
XX prokaryote which may be present in the medium; and (b) detecting the
XX presence of any nucleic acid or nucleic acid fragment hybridised with the
XX oligonucleotide. The invention also relates to a method for determining
XX the presence of a mycoplasma. The detection process is useful for
XX contaminated cell cultures or other biological environments. The probes
XX can be used in the diagnosis of bacteraemia or septicaemia in mammals.
XX The process provides a rapid, simple, effective, sensitive and specific
XX mycoplasma detection system. The probes can be made specific for
XX individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and
XX eubacterial species
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACGTCATCC 2

RESULT 542
AAV15563/C
ID AAV15563 standard; DNA; 10 BP.
XX
XX AC AAV15563;
XX
XX DT 06-MAY-1999 (first entry)
XX
XX DE Differential display RT-PCR primer used in analysis of murine TG.
XX
XX KW Origin binding protein Binding site III sequence; HSV-1; HSV-2;
XX KW viral infection; viral reactivation; interferon regulatory factor-1;
XX KW IRF-1; TIS7; interferon-alpha; IFN-alpha; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX WO9901464-A1.
XX
XX PD 14-JAN-1999.
XX
XX PF 01-JUL-1998; 98WO-US013733.
XX
XX PR 03-JUL-1997; 97US-0051633P.
XX PR 01-AUG-1997; 97US-0054515P.
XX PR 01-APR-1998; 98US-0080352P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (WIST-) WISTAR INST.
XX
XX Berger SL, Fraser NW, Leary JJ, Tal-Singer R;
XX
XX WPI; 1999-105992/09.
XX
XX Treating viral infection or reactivation, particularly Herpesvirus -
XX PT using compounds which modulate interferon pathways.
XX
XX Example 3; Page 39; 40pp; English.
XX
XX Differential display RT-PCR primers AAV15549-70 were used in the analysis
XX of murine trigeminal ganglia (TG) explants, to determine the level of
XX viral reactivation after treatment with the composition of the invention.
XX

```

CC The specification describes a for treating viral infection or
 CC reactivation. The method comprises contacting an individual with a
 CC compound which is an antagonist of the reaction between the origin
 CC binding protein Binding site III sequence from Herpes simplex virus (HSV)
 CC -1 and HSV-2 and interferon regulatory factor-1 (IRF-1). Alternatively,
 CC the compound lowers the level of IRF-1, IIS7, interferon (IFN)-alpha, or
 CC IFN-beta. The method can be used to treat viral reactivation in HSV
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
 |||||
 Db 9 GACTTCATC 1

RESULT 543
 AAZ79699
 ID AAZ79699 standard; DNA; 10 BP.

XX AC AAZ79699;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:2127.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX FN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090033P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX WPI; 2000-106077/09.

DR Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 125; 130pp; English.

XX Sequences AAZ77573-779709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells

XX SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCA 13

Db 2 GTGACTTCA 10

RESULT 544

AAZ77696/C

ID AAZ77696 standard; DNA; 10 BP.

XX AC AAZ77696;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:124.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PA (GENZ) GENZYME CORP.

PN WO9965924-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013800.
 PF 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 08-DEC-1998; 98US-0090080P.
 XX 98US-0111715P.
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 PS Claim 1; Page 67; 130pp; English.
 XX
 SS Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes

CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTTCATCCTT 18
 Db 10 TTTCATCCAT 2
 RESULT 545
 AAZ77629/C
 ID AAZ77629 standard; DNA; 10 BP.
 XX
 AC AAZ77629;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:57.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX

PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 65; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy for to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCTATCTCT 17
Db 10 CTTCTATCTCT 2

RESULT 546
AA278070
ID AA278070 standard; DNA; 10 BP.
XX
AC AA278070;
XX
XX 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag, SEQ ID NO:498.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.

XX WO9965924-A2.
XX 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013800.
XX 19-JUN-1998; 98US-00898833P.
XX 19-JUN-1998; 98US-00898844P.
XX 19-JUN-1998; 98US-00898853P.
XX 19-JUN-1998; 98US-00898878P.
XX 19-JUN-1998; 98US-00898911P.
XX 19-JUN-1998; 98US-00898922P.
XX 19-JUN-1998; 98US-00898933P.
XX 19-JUN-1998; 98US-00898983P.
XX 19-JUN-1998; 98US-00899977P.
XX 19-JUN-1998; 98US-00899999P.
XX 19-JUN-1998; 98US-00900000P.
XX 19-JUN-1998; 98US-00900035P.
XX 19-JUN-1998; 98US-00900036P.
XX 19-JUN-1998; 98US-00900039P.
XX 19-JUN-1998; 98US-00900040P.
XX 19-JUN-1998; 98US-00900041P.
XX 19-JUN-1998; 98US-00900042P.
XX 19-JUN-1998; 98US-00900043P.
XX 19-JUN-1998; 98US-00900044P.
XX 19-JUN-1998; 98US-00900045P.
XX 19-JUN-1998; 98US-00900047P.
XX 19-JUN-1998; 98US-00900048P.
XX 19-JUN-1998; 98US-00900072P.
XX 19-JUN-1998; 98US-00900076P.
XX 19-JUN-1998; 98US-00900077P.
XX 19-JUN-1998; 98US-00900078P.
XX 19-JUN-1998; 98US-00900079P.
XX 19-JUN-1998; 98US-00900080P.
XX 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 79; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy for to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
 |||||
 Db 2 GTGAGCCAC 10

RESULT 547

AAZ78751/c
 ID AAZ78751 standard; DNA; 10 BP.

AC AAZ78751;

DT 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:1179.

DE SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

PN W09965924-A2.

XX 23-DEC-1999.

PD 18-JUN-1999; 99WO-US013800.

PF 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.

PR 19-JUN-1998; 98US-0090079P.

PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 98; 130pp; English.

XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding or
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells

XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTGATCCT 17

Db 10 CGTCATCCT 2

RESULT 548

AAZ83025

ID AAZ83025 standard; DNA; 10 BP.

XX AAZ83025;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #2259.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.


```

XX PN WO9965928-A2.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 120; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 8 ACTTCATCC 16
Db 2 ACCTCATCC 10
RESULT 549
AAZ86370/c
ID AAZ86370 standard; DNA; 10 BP.
XX AC AAZ86370;
XX XX
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5604.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.

```

```

XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 206; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 9 CTTTCATCCT 17
Db 9 CCTTCATCCT 1
RESULT 550
AAZ86589
ID AAZ86589 standard; DNA; 10 BP.
XX AC AAZ86589;
XX XX
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5823.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

FN WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and

XX treatment of cancer.

XX Claim 1; Page 212; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCT 17

Db 2 CCTCATCCT 10

RESULT 551

AAZ82789/c

ID AAZ82789 standard; DNA; 10 BP.

AC AAZ82789; -

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #2023.

XX

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

FN WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 CC non-metastatic breast cancer cells, useful for diagnosis, prevention and
 CC treatment of cancer.

XX Claim 1; Page 113; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCT 17

Db 10 CTTTCCTCT 2

RESULT 552

AAZ80915

ID AAZ80915 standard; DNA; 10 BP.

XX AAZ80915;

XX 07-APR-2000 (first entry)

```

XX DE Metastatic breast tumour cell upregulated transcript tag #149.
XX DE
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX DE non-metastatic breast tumour tissue; gene therapy; anticancer;
XX DE antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 62; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCGACTTC 12
DB 1 AGCGCTTC 9
|||||
|||||

RESULT 553
AAZ83904
ID AAZ83904 standard; DNA; 10 BP.
XX AC AAZ83904;

```

```

XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #3138.
XX DE
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX DE non-metastatic breast tumour tissue; gene therapy; anticancer;
XX DE antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 142; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGACGCACT 10
DB 2 TGACCAACT 10
|||||
|||||

RESULT 554
AAZ84679/C
ID AAZ84679 standard; DNA; 10 BP.

```

```

XX AC AA284679;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #3913.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 163; 219pp; English.
XX CC AA280767 to AA283941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
XX CC to AA286677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 9 ACTTCCTCC 1

RESULT 555

```

```

AAZ81733
ID AA281733 standard; DNA; 10 BP.
XX AC AAZ81733;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #967.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 84; 219pp; English.
XX CC AA280767 to AA283941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
XX CC to AA286677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGACCGACT 10
Db 2 TGACGCGCT 10

```

```

RESULT 556
AAZ83460
ID AAZ83460 standard; DNA; 10 BP.
XX
XX
AC AAZ83460;
XX
XX
DT 07-APR-2000 (first entry)
XX
XX
DE Metastatic breast tumour cell upregulated transcript tag #2694.
XX
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX
OS Homo sapiens.
XX
XX
FN WO9965928-A2.
XX
XX
PD 23-DEC-1999.
XX
XX
PF 18-JUN-1999; 99WO-US013647.
XX
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX
PI Roberts BL, Shankara S;
XX
XX
DR WPI; 2000-106079/09.
XX
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX
PS Claim 1; Page 131; 21pp; English.
XX
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
XX
XX
SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCGACTTCA 13
|||||

```

```

Db 2 GCAACTTCA 10
RESULT 557
AAZ84920
ID AAZ84920 standard; DNA; 10 BP.
XX
XX
AC AAZ84920;
XX
XX
DT 07-APR-2000 (first entry)
XX
XX
DE Metastatic breast tumour cell downregulated transcript tag #4154.
XX
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX
OS Homo sapiens.
XX
XX
FN WO9965928-A2.
XX
XX
PD 23-DEC-1999.
XX
XX
PF 18-JUN-1999; 99WO-US013647.
XX
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX
PI Roberts BL, Shankara S;
XX
XX
DR WPI; 2000-106079/09.
XX
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX
PS Claim 1; Page 169; 21pp; English.
XX
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
XX
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Oy 9 CTTTCCTCT 17
    |||||
Db 2 CGTCATCCT 10

RESULT 558
AAZ86569/c
ID AAZ86569 standard; DNA; 10 BP.
XX
AC AAZ86569;
XX
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5803.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
XX
PR 19-JUN-1998; 98US-0089997P.
XX
PR 19-JUN-1998; 98US-0090039P.
XX
PR 19-JUN-1998; 98US-0090040P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 211; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
```

```
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 CGACTTCAT 14
    |||||
Db 10 CGGCTTCAT 2

RESULT 559
AAZ81164
ID AAZ81164 standard; DNA; 10 BP.
XX
AC AAZ81164;
XX
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #398.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
XX
PR 19-JUN-1998; 98US-0089997P.
XX
PR 19-JUN-1998; 98US-0090039P.
XX
PR 19-JUN-1998; 98US-0090040P.
XX
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 68; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
```

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 1 GTGAGCCAC 9

RESULT 560
AAZ83259
ID AAZ83259 standard; DNA; 10 BP.
XX AC AAZ83259;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #2493.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW anti-metastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX OS WO9965928-A2.
XX PN 23-DEC-1999.
XX PD 18-JUN-1999; 99WO-US013647.
XX PF 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 126; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 2 TACATCCTT 10

RESULT 561
AAZ84009/C
ID AAZ84009 standard; DNA; 10 BP.
XX AC AAZ84009;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #3243.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW anti-metastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX OS WO9965928-A2.
XX PN 23-DEC-1999.
XX PD 18-JUN-1999; 99WO-US013647.
XX PF 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 145; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

```
CC immunotherapy
XX Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCCTT 18
Db 10 TTCATCCAT 2

RESULT 562
AAZ86139
ID AAZ86139 standard; DNA; 10 BP.
XX AC AAZ86139;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5373.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WI WI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 201; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
```

```
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 2 GTGAGCTAC 10

RESULT 563
AAZ86325/C
ID AAZ86325 standard; DNA; 10 BP.
XX AC AAZ86325;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5599.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WI WI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 205; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
```


CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 | | | | |
 Db 10 CGTCATCCT 2

RESULT 564
 AAZ81317
 ID AAZ81317 standard; DNA; 10 BP.
 XX AC AAZ81317;
 XX DT 07-APR-2000 (first entry)
 XX DE Metastatic breast tumour cell upregulated transcript tag #551.
 XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX KW antimetastatic; vaccine; diagnosis; ss.
 XX OS Homo sapiens.
 XX PN WO9965928-A2.
 XX FD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US013647.
 XX PR 19-JUN-1998; 98US-0089853P.
 XX PR 19-JUN-1998; 98US-0089997P.
 XX PR 19-JUN-1998; 98US-0090039P.
 XX PR 19-JUN-1998; 98US-0090040P.
 XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.
 XX PA (ROBE/) ROBERTS B L.
 XX PA (SHAN/) SHANKARA S.
 XX PI Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 73; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 XX that are preferentially transcribed in the metastatic breast tumour
 XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 XX to AAZ86677 represent tags corresponding to distinct transcripts that are
 XX preferentially transcribed in the primary or non-metastatic breast tumour
 XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
 XX transcripts can be used for diagnosis, prognosis, monitoring and
 XX treatment of breast cancer, particularly where metastatic. Diagnosis is
 XX by standard immunoassays or hybridisation/amplification reactions.
 XX Compounds that modulate expression of the transcripts are potentially
 XX useful for treatment of (metastatic) breast cancer, while promoters from
 XX the transcripts are used to direct expression, in selected cell types, of
 XX e.g. therapeutic genes (also ribozymes or antisense sequences),
 XX particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 | | | | |
 Db 2 CTTTCATCCT 10

RESULT 565
 AAZ84870/C
 ID AAZ84870 standard; DNA; 10 BP.
 XX AC AAZ84870;
 XX DT 07-APR-2000 (first entry)
 XX DE Metastatic breast tumour cell downregulated transcript tag #4104.
 XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 XX KW antimetastatic; vaccine; diagnosis; ss.
 XX OS Homo sapiens.
 XX PN WO9965928-A2.
 XX FD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US013647.
 XX PR 19-JUN-1998; 98US-0089853P.
 XX PR 19-JUN-1998; 98US-0089997P.
 XX PR 19-JUN-1998; 98US-0090039P.
 XX PR 19-JUN-1998; 98US-0090040P.
 XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.
 XX PA (ROBE/) ROBERTS B L.
 XX PA (SHAN/) SHANKARA S.
 XX PI Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 168; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 XX that are preferentially transcribed in the metastatic breast tumour
 XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 XX to AAZ86677 represent tags corresponding to distinct transcripts that are
 XX preferentially transcribed in the primary or non-metastatic breast tumour
 XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
 XX transcripts can be used for diagnosis, prognosis, monitoring and
 XX treatment of breast cancer, particularly where metastatic. Diagnosis is
 XX by standard immunoassays or hybridisation/amplification reactions.
 XX Compounds that modulate expression of the transcripts are potentially
 XX useful for treatment of (metastatic) breast cancer, while promoters from
 XX the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATTCCTT 18
||| |||||
Db 10 TTCATTCCTT 2

RESULT 566
AAZ86235
ID AAZ86235 standard; DNA; 10 BP.

XX
XX AAZ86235;
XX
XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5469.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.
OS
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.

(GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX Claim 1; Page 203; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX

SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
||||| ||
Db 2 TGAGCGTCT 10

RESULT 567
AAZ84043
ID AAZ84043 standard; DNA; 10 BP.

XX
XX AAZ84043;
XX
XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #3277.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.
OS
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.

(GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX Claim 1; Page 146; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially

CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences).
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX
 SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 1 CTTTCATCCT 9
 ||| |||||
 ||| |||||

RESULT 568
 AAC74018
 ID AAC74018 standard; cDNA; 10 BP.
 AC AAC74018;
 XX
 XX 02-FEB-2001 (first entry)
 DT
 XX Human dendritic cell and monocyte expressed gene oligonucleotide #105.
 DE
 XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmunity disease; tumour; ss.
 KW
 XX Homo sapiens.
 OS
 XX W0200060074-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-JP002019.
 PF
 XX 01-APR-1999; 99JP-00095481.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Hashimoto S, Matsushima K, Suzuki T;
 PI
 XX WPI; 2000-619172/59.
 DR
 XX

Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune disease and tumors.
 PT
 XX Claim 10; Page 12; 95pp; Japanese.
 PS
 XX The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells; a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3', located most closely to the poly-A region. The sequences can be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers

XX
 SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 10 CGTCATCCT 2
 ||| |||||
 ||| |||||

CC and autoimmune diseases

XX
 SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCCGAC 9
 Db 2 GTGAGCCGAC 10
 ||||| |||
 ||||| |||

RESULT 569
 AAC74100/c
 ID AAC74100 standard; cDNA; 10 BP.
 AC AAC74100;
 XX
 XX 02-FEB-2001 (first entry)
 DT
 XX Human dendritic cell and monocyte expressed gene oligonucleotide #187.
 DE
 XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmunity disease; tumour; ss.
 KW
 XX Homo sapiens.
 OS
 XX W0200060074-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-JP002019.
 PF
 XX 01-APR-1999; 99JP-00095481.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Hashimoto S, Matsushima K, Suzuki T;
 PI
 XX WPI; 2000-619172/59.
 DR
 XX

Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune disease and tumors.
 PT
 XX Claim 10; Page 13; 95pp; Japanese.

The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells; a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3', located most closely to the poly-A region. The sequences can be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers and autoimmune diseases

XX
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 10 CGTCATCCT 2
 ||| |||||
 ||| |||||

RESULT 570
AAZ50020/c
ID AAZ50020 standard; DNA; 10 BP.
XX AC
XX AC AAZ50020;
XX DT
XX DT 25-APR-2000 (first entry)
XX DE Interleukin 2 enhancer for transcription regulation.
XX KW Enhancer; polyomavirus enhancer activator 3; PEA3; transformation;
KW tumorigenic; metastatic; cancer; neu-mediated cancer; ovarian cancer;
KW ras-mediated cancer; HER/neu promoter; anti-transformation therapy;
KW anti-cancer therapy; cytostatic; ds.
XX OS Unidentified.
XX PN WO200004153-A2.
XX PD 27-JAN-2000.
XX PF 15-JUL-1999; 99WO-US016142.
XX PR 15-JUL-1998; 98US-00116049.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Hung M;
XX DR WPI; 2000-171269/15.
XX PT Repression of cell transformation used to suppress tumor growth,
PT comprises contacting the cell with human polyomavirus enhancer activator
PT 3.
XX PS Disclosure; Page 16; 92pp; English.
XX CC The patent discloses methods for repressing transformation in a cell by
CC contacting it with polyomavirus enhancer activator 3 (PEA3) to inhibit a
CC transformed phenotype resulting in reduced tumorigenic or metastatic
CC potential of a cell. This is used in the treatment of various forms of
CC cancer, e.g. neu- or ras- mediated cancers. The nucleic acid is
CC introduced into the mammal through a vector or liposomal complex having
CC DOTMA, DOPE or DC-Chol. The present sequence is interleukin 2 enhancer
CC (NF-AT-1), a regulatory element containing ETS-binding site. This can
CC bind to E1f-1 to enhance transcriptional activity
XX SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX DT
XX DT 13-FEB-2001 (first entry)
XX DE Human B18Ag1 cDNA randomly chosen PCR primer.
XX KW Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO2000061753-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US009312.
XX PR 09-APR-1999; 99US-00289198.
XX PR 28-OCT-1999; 99US-00429755.
XX PR 23-MAR-2000; 2000US-00534825.
XX PA (CORI-) CORIXA CORP.
XX KW Enhancer; polyomavirus enhancer activator 3; PEA3; transformation;
KW tumorigenic; metastatic; cancer; neu-mediated cancer; ovarian cancer;
KW ras-mediated cancer; HER/neu promoter; anti-transformation therapy;
KW anti-cancer therapy; cytostatic; ds.

XX OS Unidentified.
XX PN WO200004153-A2.
XX PD 27-JAN-2000.
XX PF 15-JUL-1999; 99WO-US016142.
XX PR 15-JUL-1998; 98US-00116049.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Hung M;
XX DR WPI; 2000-171269/15.
XX PT Repression of cell transformation used to suppress tumor growth,
PT comprises contacting the cell with human polyomavirus enhancer activator
PT 3.
XX PS Disclosure; Page 16; 92pp; English.
XX CC The patent discloses methods for repressing transformation in a cell by
CC contacting it with polyomavirus enhancer activator 3 (PEA3) to inhibit a
CC transformed phenotype resulting in reduced tumorigenic or metastatic
CC potential of a cell. This is used in the treatment of various forms of
CC cancer, e.g. neu- or ras- mediated cancers. The nucleic acid is
CC introduced into the mammal through a vector or liposomal complex having
CC DOTMA, DOPE or DC-Chol. The present sequence is Ets-2 promoter, a
CC regulatory element containing ETS-binding site. This can bind to Ets-
CC 1/Ets-2 to enhance transcriptional activity
XX SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX DT
XX DT 13-FEB-2001 (first entry)
XX DE Human B18Ag1 cDNA randomly chosen PCR primer.
XX KW Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO2000061753-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US009312.
XX PR 09-APR-1999; 99US-00289198.
XX PR 28-OCT-1999; 99US-00429755.
XX PR 23-MAR-2000; 2000US-00534825.
XX PA (CORI-) CORIXA CORP.
XX KW Enhancer; polyomavirus enhancer activator 3; PEA3; transformation;
KW tumorigenic; metastatic; cancer; neu-mediated cancer; ovarian cancer;
KW ras-mediated cancer; HER/neu promoter; anti-transformation therapy;
KW anti-cancer therapy; cytostatic; ds.

DR WPI; 2000-628403/60.

XX An isolated polypeptide comprising an immunogenic portion of a breast

PT tumor protein used for inhibiting the development of cancer, especially

PT breast cancer, and monitoring cancer progression in a patient.

XX Example 1; Page 33; 187pp; English.

PS The present sequence is a PCR primer which was used in the isolation of

CC human breast tumour-specific antigens. Methods for the treatment and

CC diagnosis of breast cancer are disclosed. Nucleotide sequences that are

CC preferentially expressed in breast tumour tissue, and the polypeptides

CC encoded by such nucleotide sequences, are used in compositions and

CC vaccines to inhibit the development of cancer, especially breast cancer.

CC The progression of a cancer may be monitored by carrying out detection of

CC tumour-specific antigens at subsequent time points and comparing the

CC results from the different time points. CD4+ and/or CD8+ T-Cells isolated

CC from the cancer patient may be treated with tumour-specific polypeptides,

CC polynucleotides encoding the polypeptides or antigen presenting cells

CC expressing the polypeptides. The cells are then administered to the

CC patient to inhibit development of cancer

XX

SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCCT 17

Db 1 CTTCAACCT 9

RESULT 573

AA15249/C

ID AA15249 standard; DNA; 10 BP.

XX AC AA15249;

XX 04-SEP-2000 (first entry)

DE Primer MR14 for modified differential display of tumour antigens.

XX

XX Epitope; tumour specific epitope; antigen; vaccine; tumour regression;

KW cancer; infection; primer; ss.

XX Synthetic.

OS

XX WO200028016-A1.

PN

XX 18-MAY-2000.

PD

XX

XX 10-NOV-1998; 98WO-US024029.

PF

XX

XX 10-NOV-1998; 98WO-US024029.

PR

XX (UVRP) UNIV ROCHESTER.

PA

XX

XX Zauderer M;

PI

XX WPI; 2000-376533/32.

DR

XX

PT Novel method of identifying target epitopes or antigens specific for

PT human tumors, cancers and infected cells involving screening expression

PT library products of a cell expressing the target epitope.

XX

PS Disclosure; Page 68; 132pp; English.

XX

XX AA15239-50 represent arbitrary primers which are used for modified

CC differential display of tumour antigens, in the method of the invention.

CC The specification describes a method for identifying a target epitope.

CC The method comprises screening the products of an expression library from

CC a cell expressing the target epitope with cytotoxic T cells generated

CC

CC against the cell to identify DNA clones expressing the target epitope.

CC The method may also comprise providing a cytotoxic T cell specific for a

CC gene product differentially expressed by a cell and measuring the cross-

CC reactivity of the cytotoxic T cell. The methods are useful for

CC identifying tumour specific target epitopes and antigens which are useful

CC in immunogenic compositions or vaccines to induce the regression of

CC tumors, cancers or infections in mammals. The genes expressed in a panel

CC of tumour cells that are derived from single immortalised, non-

CC tumorigenic cell line are used to generate HLA restricted cytotoxic T

CC cells which are evaluated for activity against tumour cells. The method

CC is useful to identify potential antigens expressed not only by the

CC pathogen but also by the host cells whose gene expression is altered as a

CC result of infection. The differential gene expression strategies can be

CC applied to identify immunogenic molecules of cells infected with virus,

CC fungus or mycobacterium

XX

SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GACTTCATC 15

Db 9 GACTTGATC 1

RESULT 574

AA234683/C

ID AA234683 standard; DNA; 10 BP.

XX AC AA234683;

XX 15-FEB-2000 (first entry)

DE D14 randomer used in DDRT-PCR identification of ERAB.

XX

XX Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

KW Leydig cell; differential display RT-PCR; DDRT-PCR;

KW short chain alcohol dehydrogenase; SCAD; testis; marker; spermatogenesis;

KW primer; ss.

XX Synthetic.

OS

XX WO9954347-A2.

PN

XX 28-OCT-1999.

PD

XX

XX 19-APR-1999; 99WO-EP002610.

PF

XX

XX 17-APR-1998; 98US-0082257P.

PR

XX (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.

PA

XX Ivell R, Spiess A, Balvers M, Jaehner D, Hansis C;

PI

XX WPI; 2000-052699/04.

DR

XX Novel differential display reverse transcription PCR method used to

PT detect genes expressed in mutant tissues.

PT

XX Disclosure; Page 26; 40pp; English.

PS

XX This sequence represents decamer D14, which was used in a novel

CC differential display RT-PCR (DDRT-PCR) method of detecting genes

CC expressed in tissues, especially mutant tissue. RNA isolated from adult

CC male w/wv azoospermic mutant mice testis was subjected to reverse

CC transcription. 324 PCRs were performed on the resulting cDNA using 3'

CC clamp primers (see 23467-69) and variable decamer 5' primers D1-D26 (see

CC AA234670-95). Differentially expressed clones were used as probes in

CC northern hybridisation, and a novel gene product that was preferentially

CC upregulated in w/wv mouse testis was identified and termed Alzheimer-

CC associated beta-amyloid binding protein (ERAB, see AA232239)

```

XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 9 GACTTGATC 1

RESULT 575
AAC79078
ID AAC79078 standard; DNA; 10 BP.
XX AC AAC79078;
XX AC AC
XX DT 05-FEB-2001 (first entry)
XX DE Human lung tumour-specific antigen-related primer.
XX KW Lung tumour protein; lung cancer; cytostatic; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200060077-A2.
XX PD 12-OCT-2000.
XX PF 30-MAR-2000; 2000WO-US008560.
XX PR 02-APR-1999; 99US-00285323.
XX PR 09-AUG-1999; 99US-00370838.
XX PR 30-DEC-1999; 99US-00476235.
XX PR 03-MAR-2000; 2000US-00518809.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Lodes MJ, Mohamath R, Secrist H;
XX WPI; 2000-638466/61.
XX DT Novel lung tumor polypeptides and polynucleotides, useful for detecting,
PT monitoring or treating cancer, especially lung cancer.
XX PS Claim 1; Page 106; 243pp; English.
XX CC The present sequence is given in a specification relating to compounds
CC for therapy and diagnosis of lung cancer. Polypeptides comprising at
CC least an immunogenic part of a lung tumour protein are disclosed. The
CC polypeptides are useful for inhibiting the development of cancer,
CC especially lung cancer. Samples of T cells expressing the polypeptides
CC may be used to inhibit the development of cancer. The polypeptides are
CC also useful for detecting and monitoring the progression of cancer,
CC especially lung cancer
XX SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCAACT 9

RESULT 576
AAH44157/C
ID AAH44157 standard; DNA; 10 BP.
XX AC AAH44157;

XX SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACGTCATCC 2

RESULT 577
AAF30878/C
ID AAF30878 standard; DNA; 10 BP.
XX AC AAF30878;

```

```

XX DT 14-SEP-2001 (first entry)
XX DE Escherichia coli 16S RNA gene oligonucleotide #11.
XX KW Mycoplasma; 16S RNA gene; infection; biological probe; detection;
KW ribosomal RNA gene; prokaryote; ss.
XX OS Escherichia coli.
XX PN US6245509-B1.
XX PD 12-JUN-2001.
XX PF 14-SEP-1998; 98US-00152375.
XX PR 04-MAR-1985; 85US-00707725.
XX PR 06-MAY-1988; 88US-00191852.
XX PR 27-NOV-1991; 91US-00799856.
XX PR 19-FEB-1993; 93US-00020874.
XX PR 14-OCT-1993; 93US-00136723.
XX PR 06-JUN-1995; 95US-00469600.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Stanbridge EJ, Gobel UB;
XX WPI; 2001-416908/44.
XX DT Generating oligonucleotide probes, which are useful in DNA hybridization
PT techniques for detecting mycoplasmas or prokaryotes in general.
XX PS Disclosure; Col 2; 6pp; English.
XX CC The present invention describes a method for obtaining oligonucleotide
CC probes, comprising synthesising and isolating an oligonucleotide
CC comprising a sequence identical to a sequence identified as hybridisable
CC under predetermined conditions to a nucleotide sequence from one or more
CC target organisms. The oligonucleotide probes are hybridisable to a
CC nucleotide sequence contained by or specific to one or more target
CC organisms but not to one or more selected non-target organisms in a
CC sample. The target and non-target organisms do not have a cellular
CC nucleus or are no higher phylogenetically than prokaryotes. The method
CC comprises: (a) obtaining particular nucleotide sequence information of
CC one or more of the target organisms; (b) obtaining particular nucleotide
CC sequence information of one or more of the selected non-target organisms;
CC (c) comparing the target and non-target sequence information and
CC identifying from it at least one oligonucleotide sequence that is
CC hybridisable under the predetermined conditions to a nucleotide sequence
CC from the target organisms, but not to a nucleotide sequence of non-target
CC organisms; and (d) synthesising and isolating an oligonucleotide
CC comprising a sequence identical to the identified sequence. The method
CC can be used for generating oligonucleotide probes for detecting
CC mycoplasmas or prokaryotes in general. The present sequence represents an
CC Escherichia coli 16S RNA gene oligonucleotide which is given in the
CC exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACGTCATCC 2

RESULT 577
AAF30878/C
ID AAF30878 standard; DNA; 10 BP.
XX AC AAF30878;

```

XX .DT 09-JUL-2001 (first entry)
XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.
XX DE ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX KW hybridisation; detection; fluorescence; probe; ss.
XX KW Synthetic.
XX OS WO200131063-A1.
XX PN 03-MAY-2001.
XX PD 26-OCT-2000; 2000WO-US029786.
XX PF 26-OCT-1999; 99US-00428236.
XX PR (EPOC-) EPOCH BIOSCIENCES INC.
XX PA Dempcy RO, Afonina IA, Vermeulen NMJ;
XX PI WPI; 2001-328656/34.
XX DR Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX PT useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX PT mismatch discrimination.
XX XX Disclosure; Page 58; 105pp; English.
XX CC The present sequence is that of the oligonucleotide (ODN) component of an
XX CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX CC invention. MGBs bind in a non-intercalating manner to the minor groove of
XX CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX CC but in an intercalating manner, or lies in the minor groove, or is
XX CC oriented in some other way to the DNA molecule by MGB, such that it
XX CC becomes fluorescent (or its fluorescent properties change detectably).
XX CC The conjugates are used as hybridisation probes and amplification primers
XX CC for fluorescent detection of specifically hybridising sequences, for
XX CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX CC mismatch discrimination, target or signal amplification, array-based
XX CC assays and sequencing, including detection of double-stranded DNA by
XX CC triplex formation. Many different targets can be detected a single
XX CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX CC hybridisation-triggered fluorescence. Upon hybridisation to the
XX CC complementary target sequence there was an increase in fluorescence
XX CC yield, measured as the ratio of the fluorescence emitted by the hybrid
XX CC between the ODN-MGB-LF conjugate and its target sequence to the
XX CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX CC of 8.3
XX SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
Db 9 AGCAACTTC 1

RESULT 578
AAH64040/c
ID AAH64040 standard; cDNA; 10 BP.
XX AC AAH64040;
XX AC
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 880.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX OS WO200138577-A2.
XX PN 31-MAY-2001.
XX PD 21-NOV-2000; 2000WO-US031922.
XX PF 24-NOV-1999; 99US-00448480.
XX PR (UYJO) UNIV JOHNS HOPKINS.
XX PA Velculescu VE, Vogelstein B, Kinzler KW;
XX PI WPI; 2001-367706/38.
XX DR New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 59; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the
XX CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTCATCCT 17
Db 10 CTCTTCCT 2

RESULT 579
AAH64082/c
ID AAH64082 standard; cDNA; 10 BP.
XX AC AAH64082;
XX AC
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 922.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX OS WO200138577-A2.
XX PN 31-MAY-2001.
XX PD 21-NOV-2000; 2000WO-US031922.
XX PF 24-NOV-1999; 99US-00448480.
XX PR (UYJO) UNIV JOHNS HOPKINS.
XX PA Velculescu VE, Vogelstein B, Kinzler KW;
XX PI WPI; 2001-367706/38.
XX DR
XX KW

PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.

XX Claim 13; Page 60; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 580
AAH64081/c
ID AAH64081 standard; cDNA; 10 BP.
XX AAH64081;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 921.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.

XX Claim 13; Page 60; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 582
AAH63895/c
ID AAH63895 standard; cDNA; 10 BP.
XX AAH63895;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 735.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.

XX Claim 13; Page 66; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 582
AAH63895/c
ID AAH63895 standard; cDNA; 10 BP.
XX AAH63895;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 735.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.

Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 581
AAH64326/c
ID AAH64326 standard; cDNA; 10 BP.
XX AAH64326;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1166.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.

XX Claim 13; Page 66; 94pp; English.

XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 582
AAH63895/c
ID AAH63895 standard; cDNA; 10 BP.
XX AAH63895;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 735.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.

KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 XX cancer diagnosis; Cell specific gene expression; ss.
 XX Homo sapiens.
 XX WO200138577-A2.
 XX 31-MAY-2001.
 XX 21-NOV-2000; 2000WO-US031922.
 XX 24-NOV-1999; 99US-00448480.
 XX (UJJO) UNIV JOHNS HOPKINS.
 XX Velculescu VE, Vogelstein B, Kinzler KW;
 XX WPI; 2001-367706/38.
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX Claim 13; Page 56; 94pp; English.
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific. cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
 SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TGAGCGACT 10
 Db 10 TGAGAGACT 2
 |||||
 |||||
 RESULT 583
 AAS57303/C
 ID AAS57303 standard; DNA; 10 BP.
 XX AAS57303;
 XX 16-JAN-2002 (first entry)
 XX Human CHRN2 allele specific oligonucleotide PCR primer terminus #28.
 XX Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;
 KW CHRN2; memory disorder; Alzheimer's disease; epilepsy; learning;
 KW chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;
 KW ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ss;
 KW allele specific oligonucleotide; ASO; PCR primer.
 XX Homo sapiens.
 XX WO200174833-A2.
 XX 11-OCT-2001.
 XX 03-APR-2001; 2001WO-US010666.
 XX 03-APR-2000; 2000US-0194155P.
 XX 13-JUL-2000; 2000US-0217952P.
 XX (GENA-) GENAISANCE PHARM INC.

XX Choi JY, Klem SE, Koshy B, Lee HH, Sanchis A;
 XX WPI; 2001-626374/72.
 XX Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an
 PT individual involves determining for two copies of the gene, the identity
 PT of nucleotide pair at polymorphic sites selected from PSI-24.
 XX Claim 17; Page 15; 82pp; English.
 XX The invention relates to genotyping/haplotyping the cholinergic receptor,
 CC nicotinic, beta-polypeptide 2 (neuronal) (CHRN2) gene of an individual,
 CC comprising determining for the two copies of the CHRN2 gene present in
 CC the individual, the identity of the nucleotide pair at one or more
 CC polymorphic sites selected from PSI-24. Also include are oligonucleotides
 CC for performing the method and the nucleotide sequence of the polymorphic
 CC variants of CHRN2. The method is useful for detecting novel CHRN2
 CC polymorphisms and for determining if an individual has a haplotype or
 CC haplotype pairs defined in the specification and to validate CHRN2 as a
 CC candidate agent for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity (e.g. a memory disorder, Alzheimer's
 CC disease, epilepsy, a learning disorder, schizophrenia, attention
 CC deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal
 CC frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials of
 CC candidate drugs for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity. The method is useful to screen for
 CC compounds targeting CHRN2 to treat a specific conditions or disease
 CC associated with CHRN2 activity. The polymorphic nucleic acids are useful
 CC in studying the expression and function of CHRN2, and in expressing
 CC CHRN2 protein for use in screening for candidate drugs to treat diseases
 CC related to CHRN2 activity and are useful for therapeutic purposes. The
 CC CHRN2 gene is located on chromosome 1q21. The present sequence is an
 CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for
 CC performing the method of the invention
 XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
 SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GAGCGACTT 11
 Db 9 GAGGGACTT 1
 |||||
 |||||
 RESULT 584
 AAD23153
 ID AAD23153 standard; DNA; 10 BP.
 XX AAD23153;
 XX 26-FEB-2002 (first entry)
 XX Human lung tumour-specific cDNA synthesising random RT-PCR primer.
 XX Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
 KW antisense-therapy; vaccine; immune response; lung cancer; RT-PCR primer;
 KW ss.
 XX Homo sapiens.
 XX WO200172295-A2.
 XX 04-OCT-2001.
 XX 28-MAR-2001; 2001WO-US009991.
 XX 29-MAR-2000; 2000US-00538037.
 XX 05-JUN-2000; 2000US-00588937.
 XX 18-AUG-2000; 2000US-00640878.
 XX 22-SEP-2000; 2000US-0234517P.


```
PA (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 30; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 2.9e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
Db 1 GACGTCATC 9
|||||
|
RESULT 587
AAAF42074/C
ID AAF42074 standard; DNA; 10 BP.
XX AAF42074;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8813.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX
```

```
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 314; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 2.9e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TGAGCGACT 10
Db 10 TCACGGACT 2
|||||
|
RESULT 588
AAAF35238/C
ID AAF35238 standard; DNA; 10 BP.
XX AAF35238;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1977.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
```

```
PD 21-DEC-2000.
XX
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
XX
PR 16-JUN-1999; 99US-00335032.
XX
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 70; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTATCCT 17
Db 9 CATCATCCT 1
| | | | |
| | | | |
RESULT 589
AAF33485
ID AAF33485 standard; DNA; 10 BP.
XX
XX
AC AAF33485;
XX
XX
DT 23-MAR-2001 (first entry)
XX
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:224.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation: cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX
PD 21-DEC-2000.
XX
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
XX
PR 16-JUN-1999; 99US-00335032.
XX
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 70; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 3 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTATCCT 17
Db 9 CATCATCCT 1
| | | | |
| | | | |
RESULT 590
AAF35943/C
ID AAF35943 standard; DNA; 10 BP.
XX
XX
AC AAF35943;
XX
XX
DT 23-MAR-2001 (first entry)
XX
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2682.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation: cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW serial analysis of gene expression; antifungal; tag; identification;
KW
```

linker; PCR primer; ds.
Saccharomyces cerevisiae.
WO200077214-A2.
21-DEC-2000.
14-JUN-2000; 2000WO-US016223.
16-JUN-1999; 99US-00335032.
(UYJO) UNIV JOHNS HOPKINS.
Velulescu V, Vogelstein B, Kinzler K;
WPI; 2001-061874/07.
Yeast gene coding sequences comprising NORF genes with serial analysis of
gene expression (SAGE) tags, useful for studying, monitoring and
affecting phases of the cell cycle.
Example; Page 95; 419pp; English.
The present invention describes an isolated DNA molecule comprising a
coding sequence of a yeast gene selected from a group of 745 NORF (not
previously assigned open reading frame; or nonannotated ORF) genes
comprising a SAGE (serial analysis of gene expression) tag. Also
described are: (1) a method (M1) of using NORF genes to affect the cell
cycle comprising administering a NORF gene whose expression varies by at
least 10% between any two phases of the cell cycle selected from log
phase, S phase and G2/M; (2) a method (M2) for screening candidate
antifungal drugs comprising: (a) contacting a test substance with a yeast
cell; and (b) monitoring expression of a NORF gene whose expression
varies as in M1, where a test substance which modifies the expression of
the yeast gene is a candidate antifungal drug; (3) a method (M3) for
identifying human genes which are involved in cell cycle progression
comprising contacting human DNA with a probe which comprises at least 10
contiguous nucleotides of a NORF gene whose expression varies as in M1;
and (4) a method (M4) for identifying a candidate drug as a member of a
class of drugs having a characteristic effect on gene expression in a
yeast cell comprising contacting a yeast cell with a candidate drug and
monitoring expression in the yeast cell of at least 1 NORF gene whose
expression is affected by the class of drugs. The NORF genes may be used
to study, monitor and affect phases of the cell cycle, the differentially
expressed genes may be used as markers of phases of the cell cycle. The
methods may be used to identify candidate drugs which affect the cell
cycle and for identification of antifungal drugs. AAF33268 to AAF4064.
represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GACTTCATC 15
DB 9 GAATTCATC 1

RESULT 591
AAF35079
ID AAF35079 standard; DNA; 10 BP.
XX
AC AAF35079;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1818.
XX

Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
nor previously assigned open reading frame; nonannotated ORF; SAGE;
serial analysis of gene expression; antifungal; tag; identification;
linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX WO200077214-A2.
XX PN 21-DEC-2000.
XX PD 14-JUN-2000; 2000WO-US016223.
XX PF 16-JUN-1999; 99US-00335032.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 64; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064.
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CGACTTCAT 14
DB 2 CGACTACAT 10

RESULT 592
AAF36262/c
ID AAF36262 standard; DNA; 10 BP.
XX
AC AAF36262;
XX
DT 23-MAR-2001 (first entry)
XX

```

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3001.
XX
XX
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX OS Saccharomyces cerevisiae.
XX
XX PN WO200077214-A2.
XX
XX PD 21-DEC-2000.
XX
XX PF 14-JUN-2000; 2000WO-US016223.
XX
XX PR 16-JUN-1999; 99US-00335032.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX PS Example; Page 107; 419pp; English.
XX
XX CC The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 2.9e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 9 CTTTCATCCT 17
XX | | | | |
XX 9 CATCATCCT 1
XX
XX Db
XX
XX RESULT 593
XX AAF39042/C
XX ID AAF39042 standard; DNA; 10 BP.
XX

```

```

AAAF39042;
23-MAR-2001 (first entry)
Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5781.
Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
nor previously assigned open reading frame; nonannotated ORF; SAGE;
serial analysis of gene expression; antifungal; tag; identification;
linker; PCR primer; ds.
Saccharomyces cerevisiae.
WO200077214-A2.
21-DEC-2000.
14-JUN-2000; 2000WO-US016223.
16-JUN-1999; 99US-00335032.
(UYJO ) UNIV JOHNS HOPKINS.
Velculescu V, Vogelstein B, Kinzler K;
WPI; 2001-061874/07.
Yeast gene coding sequences comprising NORF genes with serial analysis of
gene expression (SAGE) tags, useful for studying, monitoring and
affecting phases of the cell cycle.
Example; Page 206; 419pp; English.
The present invention describes an isolated DNA molecule comprising a
coding sequence of a yeast gene selected from a group of 745 NORF (not
previously assigned open reading frame; or nonannotated ORF) genes
comprising a SAGE (serial analysis of gene expression) tag. Also
described are: (1) a method (M1) of using NORF genes to affect the cell
cycle comprising administering a NORF gene whose expression varies by at
least 10% between any two phases of the cell cycle selected from log
phase, S phase and G2/M; (2) a method (M2) for screening candidate
antifungal drugs comprising: (a) contacting a test substance with a yeast
cell; and (b) monitoring expression of a NORF gene whose expression
varies as in M1, where a test substance which modifies the expression of
the yeast gene is a candidate antifungal drug; (3) a method (M3) for
identifying human genes which are involved in cell cycle progression
comprising contacting human DNA with a probe which comprises at least 10
contiguous nucleotides of a NORF gene whose expression varies as in M1;
and (4) a method (M4) for identifying a candidate drug as a member of a
class of drugs having a characteristic effect on gene expression in a
yeast cell comprising contacting a yeast cell with a candidate drug and
monitoring expression in the yeast cell of at least 1 NORF gene whose
expression is affected by the class of drugs. The NORF genes may be used
to study, monitor and affect phases of the cell cycle, the differentially
expressed genes may be used as markers of phases of the cell cycle. The
methods may be used to identify candidate drugs which affect the cell
cycle and for identification of antifungal drugs. AAF33268 to AAF4064
represent SAGE tags used in the exemplification of the present invention.
AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
method, in the exemplification of the present invention
Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CGACTTCAT 14
| | | | |
Db 10 CCATTCAT 2
| | | | |
RESULT 594

```

```

AAF40204/c
ID AAF40204 standard; DNA; 10 BP.
XX
AC AAF40204;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6943.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UVOJ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 248; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAF40585/c
ID AAF40585 standard; DNA; 10 BP.
XX
AC AAF40585;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7324.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UVOJ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 261; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAAF40585/c
ID AAAF40585 standard; DNA; 10 BP.
XX
AC AAAF40585;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7324.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UVOJ) UNIV JOHNS HOPKINS.
XX
PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 261; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention.
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 CGACTTCAT 14
Db 9 CGACTTCAT 1

```

```
Qy      6 CGACTTCAT 14
Db      10 CGACTTCGT 2

RESULT 596
AAF42897
ID  AAF42897 standard; DNA; 10 BP.
XX
AC  AAF42897;
XX
DT  23-MAR-2001 (first entry)
XX
DE  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11036.
XX
KW  Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
OS  Saccharomyces cerevisiae.
XX
FN  WO200077214-A2.
XX
PD  21-DEC-2000.
XX
PP  14-JUN-2000; 2000WO-US016223.
XX
PR  16-JUN-1999; 99US-00335032.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Velculescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
PT  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
PS  Example; Page 344; 419pp; English.
XX
CC  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
SQ  Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
    Query Match      41.1%; Score 7.4; DB 1; Length 10;
```

```
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CGACTTCAT 14
Db      2 CGACTACAT 10

RESULT 597
AAF36542/C
ID  AAF36542 standard; DNA; 10 BP.
XX
AC  AAF36542;
XX
DT  23-MAR-2001 (first entry)
XX
DE  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3281.
XX
KW  Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
OS  Saccharomyces cerevisiae.
XX
FN  WO200077214-A2.
XX
PD  21-DEC-2000.
XX
PP  14-JUN-2000; 2000WO-US016223.
XX
PR  16-JUN-1999; 99US-00335032.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Velculescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
PT  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
PS  Example; Page 117; 419pp; English.
XX
CC  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
```


SQ Sequence 10 BP; 3 A; 1 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GACTTCATC 15
| | | | | | | |
Db 9 GAATTCATC 1

RESULT 598
AAF40379
ID AAF40379 standard; DNA; 10 BP.
XX AC AAF40379;
DT 23-MAR-2001 (first entry)
XX DT
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7118.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WPT; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Example; Page 254; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ACTTCATCC 16
| | | | | | | |
Db 1 ATTTCATCC 9

RESULT 599
AAF37254/C
ID AAF37254 standard; DNA; 10 BP.
XX AC AAF37254;
XX DT 23-MAR-2001 (first entry)
XX DT
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3993.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WPT; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Example; Page 142; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.

CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 CGACTTCAT 14
Db 9 CGTCTTCAT 1
RESULT 600
AAAF33972
ID AAF33972 standard; DNA; 10 BP.
XX
AC AAF33972;
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:711.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 400; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 10 TTCATCCTT 18
Db 1 TTCACCCCTT 9
RESULT 601
AAAF34658/C
ID AAF34658 standard; DNA; 10 BP.
XX
AC AAF34658;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1397.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
FN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 49; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 7 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCAATCCTT 18
 |||||
 Db 9 TTTATCCTT 1

RESULT 602
 AAF37149
 ID AAF37149 standard; DNA; 10 BP.

XX AC AAF37149;

XX DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3888.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 138; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGCGACTT 11
 |||||
 Db 2 GAGCGAATT 10

RESULT 603

AAF37919/C

ID AAF37919 standard; DNA; 10 BP.

XX AC AAF37919;

XX DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4558.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 166; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGACTTCA 13
 ||| |||||
 Db 10 GCGCCTCA 2

RESULT 604
 AAF34682
 ID AAF34682 standard; DNA; 10 BP.
 XX
 AC AAF34682;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1421.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 50; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44084
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GACTTCATC 15
 ||| |||||
 Db 1 GATTTCATC 9

RESULT 605
 AAF42044/C
 ID AAF42044 standard; DNA; 10 BP.
 XX
 AC AAF42044;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8783.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 313; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 10 CCTCATCCT 2

RESULT 606
AAF36972/c
ID AAF36972 standard; DNA; 10 BP.
XX
AC AAF36972;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3711.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 132; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 9 CTTTCATCTT 1

RESULT 607
AAF42155/c
ID AAF42155 standard; DNA; 10 BP.
XX
AC AAF42155;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8894.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 132; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a

PS Example; Page 317; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC identifies human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15

Db 9 GTCTTCATC 1

RESULT 608

AAF33706/c

ID AAF33706 standard; DNA; 10 BP.

XX

AC AAF33706;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:445.

XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

XX 21-DEC-2000.

XX

PP 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

XX (UYJO) UNIV JOHNS HOPKINS.

XX

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

DR

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

PS Claim 1; Page 391; 419pp; English.

XX

CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC identifies human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17

Db 9 CTTTCATCTT 1

RESULT 609

AAF36501/c

ID AAF36501 standard; DNA; 10 BP.

XX

AC AAF36501;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3240.

XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

XX 21-DEC-2000.

XX

PP 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

XX (UYJO) UNIV JOHNS HOPKINS.

XX

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

DR

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

```

DR WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 115; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCTATCCTT 18
Db ||| |||||
10 TTCTATCCTT 2

RESULT 610
AAF36973/c
ID AAF36973 standard; DNA; 10 BP.
XX
XX AAF36973;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3712.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
PD
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
XX
XX 16-JUN-1999; 99US-00335032.
PR
XX
XX (UWJO ) UNIV JOHNS HOPKINS.
PA

```

```

XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 132; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17
Db ||| |||||
9 CTTCATCCT 1

RESULT 611
AAF39329/c
ID AAF39329 standard; DNA; 10 BP.
XX
XX AAF39329;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6068.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
PD
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
XX
XX 14-JUN-2000; 2000WO-US016223.
PR
XX
XX
PA

```

```
PR 16-JUN-1999; 99US-00335032.
XX
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 216; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 9 CTTTCATCTT 17
Db 9 CTTTCATCTT 1
|||||
|
RESULT 612
AAF39819/c
ID AAF39819 standard; DNA; 10 BP.
XX
XX AAF39819;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6558.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
```

```
XX 14-JUN-2000; 2000WO-US016223.
XX
XX
PR 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 234; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 TGAGCCGACT 10
Db 9 TGAGCCCACT 1
|||||
|
RESULT 613
AAF34234/c
ID AAF34234 standard; DNA; 10 BP.
XX
XX AAF34234;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:973.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX OS
```



```

PN WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 34; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 2.9e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 7 GACTTCATC 15
XX 10 GACTTCACC 2
XX
XX RESULT 614
XX AAF35014
XX ID AAF35014 standard; DNA; 10 BP.
XX AC AAF35014;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1753.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.

```

```

XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 62; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 10;
XX Best Local Similarity 88.9%; Pred. No. 2.9e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 10 TTCATCCTT 18
XX 1 TTCACCTT 9
XX
XX RESULT 615
XX ABL88455/c
XX ID ABL88455 standard; DNA; 10 BP.
XX AC ABL88455;
XX
XX 16-MAY-2002 (first entry)
XX
XX Pain regulated gene related PCR primer Dekal4.
XX Pain; analgesic; gene therapy; neurological disorder;

```

KW neurodegenerative disease; primer; ss.
XX Synthetic.
OS
XX WO200212338-A2.
PN
XX
XX 14-FEB-2002.
PD
XX
XX 03-AUG-2001; 2001WO-EP009011.
PP
XX
XX 03-AUG-2000; 2000DE-01037759.
PR
XX
XX (CHEF) GRUENENTHAL GMBH.
PA
XX
XX Gillen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;
PI WPI; 2002-257469/30.
XX
XX Identifying pain-regulating compounds, useful for treating chronic pain
DR and for diagnosis, by measuring binding of compounds to specific peptides
XX and proteins.
XX
XX Example 1; Page 62; 213pp; German.
PS
XX The invention relates to identifying pain-regulating substances (A)
CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABL8411-ABL88441) that encode proteins (B, ABB85006-
CC ABB85037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a PCR primer, used in examples of the
CC invention
XX
XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 9 GACTTGATC 1

RESULT 616
AAS18735
ID AAS18735 standard; DNA; 10 BP.
XX
AC AAS18735;
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Primer-extension oligonucleotide #23 to detect human SCYA3 polymorphisms.
DE
XX Human; single nucleotide polymorphism; SNP; SCYA3; chromosome 17q11-q21;
XX small inducible cytokine A3; haplotyping; genotyping; primer; ss;
XX inflammatory disorder.
KW
XX Homo sapiens.
OS
XX WO200179217-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US010595.
PP
XX
XX 14-APR-2000; 2000US-0197830P.
PR

XX (GENA-) GENAISSANCE PHARM INC.
PA Chew A, Choi JY, Koshiy B, Stephens JC;
PI WPI; 2002-055247/07.
XX
XX New polymorphic variants comprising small inducible cytokine A3 (SCYA3)
PT isogene, useful in expressing SCYA3 protein for use in screening for
PT candidate drugs to treat diseases related to SCYA3 activity, e.g.
PT inflammatory disorders.
XX
XX Claim 17; Page 15; 67pp; English.
PS
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on
CC chromosome 17q11-q21, and methods for haplotyping and/or genotyping the
CC SCYA3 gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA3 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for (developing)
CC treatment of diseases associated with SCYA3 activity, such as
CC inflammatory disorders e.g. atopic dermatitis, rheumatoid arthritis,
CC multiple sclerosis, pulmonary fibrosis and sarcoidosis. AAS18713-AAS18742
CC represent primer-extension oligonucleotides for detecting human SYCA3
CC gene polymorphisms
XX
XX Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
Db 2 AGCGACCTC 10

RESULT 617
ABL01193/c
ID ABL01193 standard; DNA; 10 BP.
XX
AC ABL01193;
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Human AKR1B1 gene polymorphism detection primer SEQ ID NO:90.
DE
XX Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
XX AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
XX allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
KW
XX Homo sapiens.
OS
XX WO200179223-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 12-APR-2001; 2001WO-US011944.
PF
XX
XX 12-APR-2000; 2000US-0196315P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Choi JY, Nandabalan K, Rounds E, Sanchis A;
PI WPI; 2002-075056/10.
XX
XX Novel polymorphic variants of aldo-keto reductase family 1, member b1
PT gene useful in studying expression and function of the protein, useful
PT for screening drugs to treat diseases e.g. diabetes.
XX
XX Claim 18; Page 15; 103pp; English.
PS

XX The present invention describes an isolated polynucleotide (I) comprising
 CC a sequence which is a polymorphic variant (PV) of a reference sequence
 CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
 CC fragment, having the 2214 base pair sequence given in ABL01105. AKR1B1
 CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
 CC used in the treatment of diabetes. The human AKR1B1 gene is located on
 CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific
 CC oligonucleotide (ASO) probes used in the detection of polymorphisms in
 CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
 CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
 CC ABL01221 represent preferred primers used in the detection of
 CC polymorphisms in the human AKR1B1 gene

XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCCGAC 9
 Db 10 GTGAGCCAC 2

RESULT 618

AAS98881
 ID AAS98881 standard; DNA; 10 BP.

AC AAS98881;

XX 26-MAR-2002 (first entry)

XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #247.

XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytostatic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; primer;
 KW primer extension; ss.

XX Homo sapiens.

XX WO200179225-A2.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US012044.

XX 12-APR-2000; 2000US-0196411P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Choi JY, Koshy B;

XX WPI; 2002-075058/10.

XX Novel polymorphic variants of colony stimulating factor 1 receptor useful
 PT in studying expression and function of the protein, useful for screening
 PT candidate drugs to treat diseases e.g. inflammatory disorders.

XX Claim 17; Page 18; 164pp; English.

XX The invention describes a novel isolated polynucleotide (I) comprising a
 CC sequence which is a polymorphic variant (PV) of a reference sequence for
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
 CC polypeptide are useful for improving the discovery and development of
 CC drugs for treating diseases associated with CSF1R activity, e.g.,
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
 CC and the haplotypes can be used to validate CSF1R as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is

CC useful in studying the expression and function of CSF1R, and in
 CC expressing CSF1R protein for use in screening for candidate drugs to
 CC treat diseases related to CSF1R activity and in studying the effect of
 CC the variation on the biological activity of CSF1R as well as on the
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A transgenic animal is useful in studying expression of the
 CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against CSF1R protein, and for testing the efficacy of
 CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
 CC are useful as probes and primers, and for assaying a polymorphism in the
 CC target region. Without requiring any a priori knowledge of the phenotypic
 CC effect of any particular CSF1R or haplotype the invention provides a
 CC method for identifying lead compounds that are more likely to show
 CC efficacy in clinical trials. This sequence is a primer used to detect
 CC CSF1R gene polymorphisms by primer extension, described in the method of
 CC the invention

XX SQ Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTCATCCT 17
 Db 1 CTCCTCCT 9

RESULT 619

AAS99671
 ID AAS99671 standard; DNA; 10 BP.

AC AAS99671;

XX 12-MAR-2002 (first entry)

XX Breast tumour-specific cDNA B18Agl, PCR primer #1.

XX Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
 KW tumour; vaccine; immunogenic.

XX Homo sapiens.

XX WO200190152-A2.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US016776.

XX 24-MAY-2000; 2000US-00577505.

XX 08-JUN-2000; 2000US-00590583.

XX 26-OCT-2000; 2000US-00699295.

XX 16-MAR-2001; 2001US-00810936.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;

XX Wang A, Skeiky YAW, Harlocker SL, Day CH;

XX WPI; 2002-089919/12.

XX New breast tumor proteins and polynucleotides encoding them, useful for
 PT treating and/or preventing cancer, particularly breast cancer, and for
 PT eliciting humoral and/or cellular immune response.

XX Example 1; Page 93; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC particularly humoral and/or cellular immune response. The polynucleotides

CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and PCR
 CC primers of the invention
 CC
 XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
 |||||
 Db 1 CTTTCACCT 9

RESULT 620
 ABL42924/c
 ID ABL42924 standard; cDNA; 10 BP.

XX ABL42924;
 XX
 DT 12-APR-2002 (first entry)
 DE Human maturation/activation dendritic cell expression gene tag #298.

XX Human; maturation/activation dendritic cell expression gene; tag;
 KW maturation; activation; dendritic cell; ss.
 XX Homo sapiens.

XX JP2001327293-A.
 XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.
 XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.
 XX Claim 19; Page 17; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC activation DC. Also described are: (1) a protein expressed by the above
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention
 XX
 XX Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TTTCATCCTT 18
 |||||
 Db 10 TTTCATCAT 2

RESULT 621
 ABL60201/c

ID ABL60201 standard; DNA; 10 BP.
 XX
 AC ABL60201;
 XX
 DT 22-JUL-2002 (first entry)
 DE Human MUC1 PCR primer SEQ ID NO 45.

XX Human; mucin 1; MUC1; transmembrane protein; SNP; cancer; cytostatic;
 KW single nucleotide polymorphism; haplotyping; genotyping; drug;
 XX antiinflammatory; PCR; primer; ss.

OS Homo sapiens.
 XX
 PN WO200226765-A2.
 XX

PD 04-APR-2002.

XX 25-SEP-2001; 2001WO-US030151.

XX 28-SEP-2000; 2000US-0236113P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Koshiy B;

XX WPI; 2002-405042/43.

XX New genetic variants of mucin 1, Transmembrane gene, useful in studying
 PT expression and function of protein encoded by the gene and for screening
 PT drugs to treat diseases e.g. cancer.

XX Claim 16; Page 14; 75pp; English.

XX The invention relates to a polynucleotide (ABL60158, ABL60159) encoding
 CC mucin 1/MUC1 (AB077476), Transmembrane isogene. The invention describes
 CC novel genetic variants of the MUC1 gene. The invention is useful for
 CC haplotyping/genotyping the MUC1 gene in an individual and identifying an
 CC association between a trait and at least one of the haplotypes or
 CC haplotype pairs of MUC1 gene. MUC1 is useful for studying the expression
 CC and function of MUC1 and expressing MUC1 protein for use in screening for
 CC candidate drugs to treat diseases related to MUC1 activity and in
 CC studying the effect of the variation on the biological activity of MUC1
 CC as well as on the binding affinity of candidate drugs targeting MUC1 for
 CC the treatment of e.g. cancer. MUC1 is further used by the pharmaceutical
 CC research scientist to validate MUC1 as a candidate target for and in
 CC design of clinical trials of candidate drugs for, treating a specific
 CC condition drugs or disease predicted to be associated with MUC1 activity.
 CC MUC1 antibodies are useful in a variety of diagnostic and prognostic
 CC formats and therapeutic methods. The present sequence is that of a PCR
 CC primer for detecting MUC1 polymorphisms, useful to the invention

XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ACTTCATCC 16
 |||||
 Db 9 ACTTCAGCC 1

RESULT 622
 AAS96188/c
 ID AAS96188 standard; DNA; 10 BP.

XX AAS96188;

XX 26-FEB-2002 (first entry)

XX Human Acetylcholinesterase gene ASO primer extension primer #6.

KW Human; ss; PCR primer; allele specific oligonucleotide; ASO; ACHC;
 KW acetylcholinesterase; polymorphic variant; haplotyping; genotyping;
 KW neurological disease; Parkinson's disease; Alzheimer's disease; cancer;
 KW leukaemia; tumour; chromosome 7q22; primer extension.
 XX Homo sapiens.
 XX WO200179219-A2.
 XX 25-OCT-2001.
 XX 11-APR-2001; 2001WO-US011853.
 XX 14-APR-2000; 2000US-0197173P.
 XX (GENA-) GENA/ISSANCE PHARM INC.
 XX (KAZE/) KAZEMI A.
 XX Bentivegna SC, Chew A, Choi JY, Koshy B;
 XX WPI; 2002-055248/07.
 XX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
 PT useful in expressing ACHE protein for use in screening for candidate
 PT drugs to treat diseases related to ACHE activity, e.g. neurological
 PT diseases or cancer.
 XX Claim 18; Page 14; 79pp; English.
 XX The invention relates to a polynucleotide comprising a polymorphic
 CC variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
 CC complement, the variant comprising an ACHE isogene defined by a haplotype
 CC selected from haplotypes 1-20 listed in the specification. Also included
 CC are methods for haplotyping and genotyping the ACHE gene of an
 CC individual, a method for predicting a haplotype pair for the ACHE gene of
 CC an individual, a method for identifying an association between a trait
 CC and at least one haplotype or haplotype pair of ACHE gene, recombinant
 CC nonhuman organisms transformed or transfected with the polynucleotide
 CC where the organism expresses ACHE protein encoded by the first nucleotide
 CC sequence or encoded by the polymorphic variant sequence, an isolated
 CC antibody specific for and immunoreactive with ACHE, a method of screening
 CC for drugs targeting the polypeptide contacting ACHE polymorphic variant
 CC with a candidate agent and assaying for binding activity, a computer
 CC system for storing and analysing polymorphism data for ACHE gene and a
 CC genome anthology for ACHE gene which comprises ACHE isogenes defined by
 CC haplotypes 1-20 given in the specification. The Polymorphisms are useful
 CC for studying the biological function of ACHE as well as in identifying
 CC drugs targeting this protein for the treatment of disorder related to its
 CC abnormal expression or function. The polymorphic variants may also be
 CC used in screening for compounds targeting ACHE to treat a specific
 CC condition or disease predicted to be associated with ACHE activity e.g.
 CC neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
 CC cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
 CC 7q22. The present sequence is the allele specific (ASO) portion of a PCR
 CC primer used in a primer extension experiment to detect the polymorphic
 CC ACHE variants of the invention
 XX
 SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTTCATCCTT 18
 Db 10 TTTCACCTT 2
 RESULT 623
 ABK46715
 ID ABK46715 standard; DNA; 10 BP.
 XX
 AC ABK46715;

XX 05-JUN-2002 (first entry)
 XX Human breast tumour-specific cDNA B18Ag1, RT-PCR primer.
 DE Human; breast tumour-specific protein; vaccine; breast cancer; primer;
 KW ss.
 KW Homo sapiens.
 XX OS
 XX US6344550-B1.
 XX 05-FEB-2002.
 PD 17-APR-1998; 98US-00062451.
 XX 01-JAN-1996; 96US-00585392.
 XX 20-AUG-1996; 96US-00700014.
 PR 10-JAN-1997; 97WO-US000485.
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 XX (CORI-) CORIXA CORP.
 XX Frudakis TN, Smith JM, Reed SG;
 PI WPI; 2002-215084/27.
 DR
 XX Polynucleotide encoding breast-specific tumor polypeptides useful as
 PT vaccine for preventing and treating breast cancer in a subject.
 XX Example 1; Col 85; 128pp; English.
 CC The invention relates to an isolated DNA molecule (I) encoding breast-
 CC tumour-specific polypeptides. (I) is useful as a vaccine for preventing
 CC and treating breast cancer in a subject. The polypeptide encoded by (I)
 CC is used for production of compounds such as antibodies useful in
 CC diagnosing and monitoring the progression of breast cancer. ABK46614-
 CC ABK46999 represent human breast tumour-specific coding sequences and
 CC related PCR primers of the invention
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTTTCATCCT 17
 Db 1 CTTTCACCT 9
 RESULT 624
 ABN80636
 ID ABN80636 standard; DNA; 10 BP.
 XX
 AC ABN80636;
 XX 19-JUL-2002 (first entry)
 DT Human P450(cytochrome) oxidoreductase ASO primer extension oligo #24.
 DE Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
 XX single nucleotide polymorphism; flavoprotein; enzyme;
 KW primer extension oligonucleotide; ss.
 XX Homo sapiens.
 XX WO200226768-A2.
 XX 04-APR-2002.
 XX 01-OCT-2001; 2001WO-US030877.

XX 29-SEP-2000; 2000US-0236449P.
PR (GENA-) GENAISSANCE PHARM INC.
PA Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;
PI WPI; 2002-394236/42.
XX
XX
XX New genetic variants comprising haplotypes of the P450 (cytochrome)
PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
PT screening protocols for compounds targeting POR.
XX
XX
XX Claim 16; Page 15; 141pp; English.
XX
XX The present invention provides the protein, gene and cDNA sequences of
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC polymorphisms (SNPs) identified therein. The sequences can be used to
CC haplotype the POR gene of an individual, and to establish whether POR is
CC a suitable target for drugs to treat cancer and disorders associated with
CC impaired protein synthesis in cells. The present sequence is an allele
CC specific primer extension oligonucleotide for the coding sequences of the
CC invention
XX
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGAGCGAC 9
DB 1 GTGAGCGGC 9

RESULT 625
ABV78534/c
ID ABV78534 standard; cDNA; 10 BP.
XX
AC ABV78534;
XX
XX 29-NOV-2002 (first entry)
DT Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:245.
XX
XX SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
XX Homo sapiens.
XX
XX JP2002186482-A.
XX
XX 02-JUL-2002.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX 19-DEC-2000; 2000JP-00385816.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-594261/64.
XX
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
PT
XX
XX Claim 19; Page 12; 60pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif

CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in Th1
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
CC compared with Th2 cells
XX
XX
SQ Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
DB 10 CTTCTTCCT 2

RESULT 626
ABV84676
ID ABV84676 standard; cDNA; 10 BP.
XX
AC ABV84676;
XX
XX 12-DEC-2002 (first entry)
DT Human amino acid transporter 2 SAGE tag #486.
XX
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; ss.
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
PT
XX
XX Claim 37; Page 24; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences

CC ABV84591-ABV84690 are SAGE tags representing the 100 most highly expressed genes out of those genes which are overexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue

XX Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTTCATCCT 9

RESULT 627
ABK23661
ID ABK23661 standard; DNA; 10 BP.
XX AC
XX ABK23661;
XX XX
DT 09-APR-2002 (first entry)
DE Transcript tag DNA sequence #250 induced or suppressed by N-myc.
XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX Homo sapiens.
XX OS
XX WO200185941-A2.
XX PN
XX 15-NOV-2001.
XX PD
XX 11-MAY-2001; 2001WO-NL000361.
XX PF
XX 11-MAY-2000; 2000EP-00201698.
XX PR
XX 29-JUN-2000; 2000EP-00202284.
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX PI Versteeg R, Caron HN;
XX WPI; 2002-066603/09.
XX A new nucleic acid library of myc-dependent downstream genes capable of supporting a neoplastic characteristic of cancer is useful to find new therapies and diagnoses for cancer.
XX Disclosure; Page 55; 69pp; English.
XX The present invention relates to a nucleic acid library comprising myc-dependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to find new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABK23412-ABK23828 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma
XX Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCCTCCTT 18
Db 1 TTCCTCCTT 9

RESULT 628
ABK23547
ID ABK23547 standard; DNA; 10 BP.
XX AC
XX ABK23547;
XX XX
DT 09-APR-2002 (first entry)
DE Transcript tag DNA sequence #136 induced or suppressed by N-myc.
XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX Homo sapiens.
XX OS
XX WO200185941-A2.
XX PN
XX 15-NOV-2001.
XX PD
XX 11-MAY-2001; 2001WO-NL000361.
XX PF
XX 11-MAY-2000; 2000EP-00201698.
XX PR
XX 29-JUN-2000; 2000EP-00202284.
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX PI Versteeg R, Caron HN;
XX WPI; 2002-066603/09.
XX A new nucleic acid library of myc-dependent downstream genes capable of supporting a neoplastic characteristic of cancer is useful to find new therapies and diagnoses for cancer.
XX Disclosure; Page 52; 69pp; English.
XX The present invention relates to a nucleic acid library comprising myc-dependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to find new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABK23412-ABK23828 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma
XX Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 2 CGTCATCCT 10

RESULT 629
ABK23602
ID ABK23602 standard; DNA; 10 BP.
XX AC
XX ABK23602;
XX XX
DT 09-APR-2002 (first entry)
DE Transcript tag DNA sequence #191 induced or suppressed by N-myc.
XX Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.

```

XX OS Homo sapiens.
XX PN WO200185941-A2.
XX PD 15-NOV-2001.
XX PF 11-MAY-2001; 2001WO-NL000361.
XX PR 11-MAY-2000; 2000EP-00201698.
XX PR 29-JUN-2000; 2000EP-00202284.
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX PI Versteeg R, Caron HN;
XX PX WPI; 2002-066603/09.
XX PT A new nucleic acid library of myc-dependent downstream genes capable of
XX PT supporting a neoplastic characteristic of cancer is useful to find new
XX PT therapies and diagnoses for cancer.
XX PS Disclosure; Page 54; 69pp; English.
XX CC The present invention relates to a nucleic acid library comprising myc-
XX CC dependent downstream genes or their functional fragments essentially
XX CC capable of supporting a neoplastic character of cancer such as growth,
XX CC invasion or spread. These myc target or tag sequences are identified by
XX CC SAGE (serial analysis of gene expression). The library is useful to find
XX CC new diagnoses and treatments for cancer. The invention is also useful to
XX CC enhance production of recombinant proteins in a production system with
XX CC high expression of endogenous or transfected myc oncogenes. ABK23412-
XX CC ABK23828 represent transcript tag DNA sequences that are activated or
XX CC repressed by N-myc in human neuroblastoma
XX SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTTTCATCCT 17
DB 1 CTTTCATCCT 9

RESULT 630
ABK23710/C
ID ABK23710 standard; DNA; 10 BP.
AC ABK23710;
XX
XX 09-APR-2002 (first entry)
XX DE Transcript tag DNA sequence #299 induced or suppressed by N-myc.
XX MYC-dependent downstream gene; neoplastic; cancer; growth; invasion;
XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;
XX myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX OS Homo sapiens.
XX PN WO200185941-A2.
XX PD 15-NOV-2001.
XX PF 11-MAY-2001; 2001WO-NL000361.
XX PR 11-MAY-2000; 2000EP-00201698.
XX PR 29-JUN-2000; 2000EP-00202284.
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX

```

```

PI Versteeg R, Caron HN;
XX WPI; 2002-066603/09.
XX A new nucleic acid library of myc-dependent downstream genes capable of
XX PT supporting a neoplastic characteristic of cancer is useful to find new
XX PT therapies and diagnoses for cancer.
XX XX Disclosure; Page 57; 69pp; English.
XX CC The present invention relates to a nucleic acid library comprising myc-
XX CC dependent downstream genes or their functional fragments essentially
XX CC capable of supporting a neoplastic character of cancer such as growth,
XX CC invasion or spread. These myc target or tag sequences are identified by
XX CC SAGE (serial analysis of gene expression). The library is useful to find
XX CC new diagnoses and treatments for cancer. The invention is also useful to
XX CC enhance production of recombinant proteins in a production system with
XX CC high expression of endogenous or transfected myc oncogenes. ABK23412-
XX CC ABK23828 represent transcript tag DNA sequences that are activated or
XX CC repressed by N-myc in human neuroblastoma
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGCGGACT 10
DB 10 TGAGGAGACT 2

RESULT 631
ABK23658
ID ABK23658 standard; DNA; 10 BP.
AC ABK23658;
XX
XX 09-APR-2002 (first entry)
XX DE Transcript tag DNA sequence #247 induced or suppressed by N-myc.
XX MYC-dependent downstream gene; neoplastic; cancer; growth; invasion;
XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;
XX myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX OS Homo sapiens.
XX PN WO200185941-A2.
XX PD 15-NOV-2001.
XX PF 11-MAY-2001; 2001WO-NL000361.
XX PR 11-MAY-2000; 2000EP-00201698.
XX PR 29-JUN-2000; 2000EP-00202284.
XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX PI Versteeg R, Caron HN;
XX PX WPI; 2002-066603/09.
XX A new nucleic acid library of myc-dependent downstream genes capable of
XX PT supporting a neoplastic characteristic of cancer is useful to find new
XX PT therapies and diagnoses for cancer.
XX XX Disclosure; Page 55; 69pp; English.
XX CC The present invention relates to a nucleic acid library comprising myc-
XX CC dependent downstream genes or their functional fragments essentially
XX CC capable of supporting a neoplastic character of cancer such as growth,
XX CC invasion or spread. These myc target or tag sequences are identified by

```


CC SAGE (serial analysis of gene expression). The library is useful to find
 CC new diagnoses and treatments for cancer. The invention is also useful to
 CC enhance production of recombinant proteins in a production system with
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-
 CC ABK23828 represent transcript tag DNA sequences that are activated or
 CC repressed by N-myc in human neuroblastoma

XX Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 10 TTCTCTCTT 18
 Db 1 TTCTCTCTT 9

RESULT 632
 ABL52033/c
 ID ABL52033 standard; DNA; 10 BP.
 XX
 AC ABL52033;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:81.
 XX
 KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
 KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
 KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
 KW haplotyping; genotyping; respiratory inflammatory disease;
 KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200222652-A2.
 XX
 PD 21-MAR-2002.
 XX
 PP 17-SEP-2001; 2001WO-US042217.
 XX
 PR 15-SEP-2000; 2000US-0232895P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Han J, Klien SE, Sausker EA;
 XX
 DR WPI; 2002-393942/42.
 XX
 PT Novel genetic variants of soluble carrier family 18 (vesicular
 PT monoamine), member 2 gene useful for screening drugs to treat diseases
 PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.
 XX
 PS Claim 19; Page 15; 183pp; English.

CC The present invention describes an isolated polynucleotide (I) having a
 CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
 CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
 CC sequence (S2) of 4023 bp (see ABL51954), and defined by a corresponding
 CC set of polymorphisms whose locations and identities are given in the
 CC specification; or a sequence (S2) complementary to (S1). (I) has
 CC antiinflammatory and neuroleptic activities, and can be used in gene
 CC therapy. Methods from the present invention can be used for haplotyping
 CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
 CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying
 CC the expression and function of SLC18A2, and in expressing the SLC18A2
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to SLC18A2 activity and in studying the effect of the variation
 CC on the biological activity of SLC18A2 as well as on the binding affinity
 CC of candidate drugs targeting SLC18A2 for the treatment of respiratory
 CC inflammatory diseases such as neuropsychiatric disorders involving
 CC monoaminergic brain systems. The present sequence represents a preferred

CC oligonucleotide primer for human SLC18A2, which is given in the present
 CC invention

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TGAGCGACT 10
 Db 10 TGAGCGACT 2

RESULT 633
 ABX09674/c
 ID ABX09674 standard; DNA; 10 BP.
 XX
 AC ABX09674;
 XX
 DT 22-JAN-2003 (first entry)
 XX
 DE Arteriosclerosis-detecting probe from NF1 #64.
 XX
 KW Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy;
 KW mutation; probe; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200272882-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 13-MAR-2002; 2002WO-EP002780.
 XX
 PR 13-MAR-2001; 2001DE-01011925.
 XX
 PA (OGHA-) OGHAM GMBH.
 XX
 PI Cullen P, Seedorf U;
 XX
 DR WPI; 2002-723374/78.
 XX
 PT Determining genetic risk of arteriosclerosis, for clinical diagnosis,
 PT comprises hybridizing patient nucleic acid with an array of probes
 PT derived from risk-associated reference genes and their mutations.
 XX
 PS Example 1; Page 140; 146pp; German.

CC This invention describes a novel method for determining the genetic risk
 CC of arteriosclerosis both for clinical diagnosis and for population
 CC studies. The method comprises: (i) selecting risk-associated reference
 CC nucleic acid sequences, including their functionally characterizing
 CC mutations; (ii) applying probes from these sequences, or their
 CC complements, to a carrier; (iii) hybridising the probes with a nucleic
 CC acid from (or synthesised from) a patient sample; and (iv) detecting and
 CC evaluating the hybridisation pattern. The method provides a quick,
 CC inexpensive and informative diagnosis, and makes possible a
 CC multifactorial analysis for detecting e.g. synergism between different
 CC mutations or mutations that when present alone carry no risk but are risk
 CC -associated in presence of other mutations. The results may be combined
 CC with known risk-assessment methods to provide a more reliable diagnosis,
 CC especially important with new therapeutic methods (e.g. gene therapy)
 CC that are directed against specific genes. All relevant mutations in a
 CC reference sequence can be screened for in a single test and the method is
 CC well suited to automation. ABX09147-ABX09676 represent probes used to
 CC illustrate the method of the invention

XX
 SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
 XX

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ID XX ABK14439 standard; DNA; 10 BP.
 XX AC ABK14439;
 XX DT 08-MAY-2002 (first entry)
 XX DE ASO oligo primer #6, used to detect human HMGL gene polymorphisms.
 XX KW Human; 3-hydroxy-3-methylglutaryl coenzyme A lyase; HMGL; primer; ss;
 XX KW single nucleotide polymorphism; SNP; haplotyping; genotyping; ASO.
 XX OS Homo sapiens.
 XX PN WO200198315-A2.
 XX PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-US019834.
 XX PR 20-JUN-2000; 2000US-0212782P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Duda A, Kliem SE, Koshy B, Parks KE;
 XX DR WPI; 2002-130786/17.
 XX PT Novel genetic variants of 3-hydroxy-3-methylglutaryl coenzyme A lyase
 XX PT useful in screening drugs to treat disease associated with the protein
 XX PT e.g. 3-hydroxy-3-methylglutaryl coenzyme A deficiency.
 XX PS Claim 19; Page 13; 84pp; English.
 XX CC The present invention relates to a new polynucleotide having a sequence
 XX CC comprising a 3-hydroxy-3-methylglutaryl coenzyme A lyase (HMGL) isogene,
 XX CC selected from 6 isogenes, and defined by a corresponding set of
 XX CC polymorphisms whose locations and identities are given in the
 XX CC specification. The method of the invention is useful for haplotyping the
 XX CC HMGL gene in an individual and in design of clinical trials of candidate
 XX CC drugs for treating a specific condition or disease predicted to be
 XX CC associated with HMGL activity and is useful for genotyping HMGL gene of
 XX CC an individual. The method of the invention is also useful for identifying
 XX CC an association between a trait and at least one haplotype or haplotype
 XX CC pair of HMGL gene. ASO is useful as probes and primers and for assaying
 XX CC a polymorphism in the target region. The invention is useful for
 XX CC genotyping and/or haplotyping the HMGL gene in an individual. Without
 XX CC requiring any a prior knowledge of the phenotypic effect of any
 XX CC particular HMGL haplotype or haplotype pair, the method of the invention
 XX CC provides the scientist with a tool to identify lead compounds that are
 XX CC more likely to show efficacy in clinical trials. The present nucleic acid
 XX CC sequence represents one of a collection of ASO oligonucleotide primers
 XX CC (ABK14434-ABK14445) that were used in the invention to detect
 XX CC polymorphisms in the human HMGL gene
 XX SQ Sequence 10 BP; 1 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTGATCCCT 18
 Db 2 TTGATCCCT 10
 RESULT 637
 ABL91868
 ID ABL91868 standard; DNA; 10 BP.
 XX AC ABL91868;
 XX DT 11-JUL-2002 (first entry)
 XX

DE Human LIPG gene primer extension oligonucleotide 7.
 XX Human; ss; primer; extension oligonucleotide;
 XX KW single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
 XX KW drug screening; atherosclerosis; cardiovascular disorder;
 XX KW LIPG haplotyping; LIPG genotyping.
 XX OS Homo sapiens.
 XX PN WO200216397-A2.
 XX PD 28-FEB-2002.
 XX PF 17-AUG-2001; 2001WO-US026639.
 XX PR 25-AUG-2000; 2000US-0227825P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Duda A, Kazemi A, Kliem SE, Messer C;
 XX DR WPI; 2002-292055/33.
 XX PT Novel genetic variants of Lipase, Endothelial isogenes, useful for
 XX PT improving efficiency and reliability in drug development for treating
 XX PT diseases associated with LIPG activity, e.g. atherosclerosis.
 XX PS Claim 18; Page 14; 134pp; English.
 XX CC The invention comprises the DNA and amino acid sequence of the human
 XX CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
 XX CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
 XX CC LIPG coding sequence and protein are useful for screening drugs that can
 XX CC be used to treat atherosclerosis and other cardiovascular disorders. The
 XX CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
 XX CC gene of an individual. The DNA sequences ABL91862 - ABL91901 represent
 XX CC LIPG gene primer extension oligonucleotides
 XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TGAGCGACT 10
 Db 1 TGAGCAACT 9
 RESULT 638
 AAD31792/c
 ID AAD31792 standard; DNA; 10 BP.
 XX AC AAD31792;
 XX DT 18-JUN-2002 (first entry)
 XX DE MR 14 arbitrary primer used for modified differential display.
 XX KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
 XX KW vaccine; immune response; cytostatic; primer; ss.
 XX OS Unidentified.
 XX PN US2002018785-A1.
 XX PD 14-FEB-2002.
 XX PF 02-APR-2001; 2001US-00822250.
 XX PR 22-SEP-1997; 97US-00935377.
 XX PA (UYRP) UNIV ROCHESTER.

XX Zauderer M;
 XX WPI; 2002-239252/29.
 XX Representational Difference Analysis method for identification of
 PT antigens recognized by cytotoxic T cells and specific for human tumors,
 PT comprises improved selection of genes encoding target antigens.
 XX
 XX Example 4; Page 19; 54pp; English.
 XX
 CC The present invention relates to novel methods for the identification of
 CC antigens recognised by cytotoxic T cells (CTLs) and specific for human
 CC tumours, cancers and infected cells. The method involves screening the
 CC products of an expression library generated from DNA/RNA of a cell
 CC expressing a target epitope with cytotoxic T cells generated against the
 CC cell to identify DNA clones expressing target epitope or providing
 CC cytotoxic T cells specific for a gene product differentially expressed by
 CC a cell and measuring the cross-reactivity of the cytotoxic T cells for
 CC cells expressing a target epitope in which the target epitope is
 CC identified as a gene product inducing cytotoxic T cells. The method is
 CC useful for identifying a target epitope or antigen specific for a tumour
 CC cell. The target epitope is also useful for identifying target antigens
 CC in other target cells against which it is desirable to induce cell-
 CC mediated immunity. The antigen identified by the method is useful in
 CC immunogenic compositions and vaccine preparations to induce the
 CC regression of tumours, cancers and infections in mammals. The invention
 CC also relates to vaccinia viral vectors which are useful for treating
 CC tumour-bearing mammals, including humans to generate immune response
 CC against the tumour cells. They are also useful for immunising or
 CC vaccinating tumour-free subjects to prevent tumour formation. The present
 CC DNA sequence is an arbitrary primer which is used for modified
 CC differential display of genes encoding potential tumour immunogens. This
 CC primer is used in the exemplification of the invention
 XX
 XX Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 GACTTCATC 15
 Db 9 GACTTGCATC 1
 |||||
 |||||
 RESULT 639
 ABL45787
 ID ABL45787 standard; DNA; 10 BP.
 AC ABL45787;
 XX
 XX 03-MAY-2002 (first entry)
 DT
 XX Human MMP13 gene allele specific primer extension oligo SEQ ID NO: 75.
 DE
 XX Human; matrix metalloproteinase 13 (collagenase 3); MMP13; cancer;
 KW arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme;
 KW cystostatic; antiarthritic; gene therapy; chromosome 11q22.3; PCR primer;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200206294-A2.
 FN
 XX 24-JAN-2002.
 PD
 XX 13-JUL-2001; 2001WO-US022238.
 PF
 XX 13-JUL-2000; 2000US-0217950P.
 PR
 XX 17-AUG-2000; 2000WO-US022693.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.

XX Finkel K, Kliem SE, Messer C, Tanguay DA;
 XX WPI; 2002-171797/22.
 XX
 XX Novel genetic variants of matrix metalloproteinase 13 (collagenase 3)
 PT gene useful in studying expression and function of the protein, and for
 PT screening drugs to treat diseases e.g. cancer and arthritis.
 XX
 XX Claim 18; Page 15; 110pp; English.
 XX
 CC The present invention provides the cDNA, protein and gene fragments of
 CC the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also
 CC provided are single nucleotide polymorphisms (SNPs) identified within the
 CC sequences. The sequences can be used to haplotype an individual and in
 CC the treatment of cancer and arthritis, including metastatic cancers. The
 CC present sequence is a primer extension oligonucleotide for the MMP13
 CC gene, which is found on chromosome 11q22.3
 XX
 XX Sequence 10 BP; 4 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 ACTTCATCC 16
 Db 2 ACTTCATAC 10
 |||||
 |||||
 RESULT 640
 ABK29921/c
 ID ABK29921 standard; DNA; 10 BP.
 XX
 XX ABK29921;
 AC
 XX 23-APR-2002 (first entry)
 DT
 XX Human epidermal growth factor receptor 2, repressor sequence.
 DE
 XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW transgenic; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200194600-A2.
 PN
 XX 13-DEC-2001.
 PD
 XX 06-JUN-2001; 2001WO-US018343.
 PF
 XX 06-JUN-2000; 2000US-0209549P.
 PR
 XX (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 XX Kim JF, Starr DB, Tam AW, Laurance ME, Michelotti EF;
 PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 PI Lim WY, Bruice TW;
 XX
 XX WPI; 2002-130595/17.
 DR
 XX New nucleic acid regulatory sequences, which are able to regulate
 PT

PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 XX immunological diseases.

PS Claim 15; Page 56; 95pp; English.

XX The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vhh gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a primer used in the invention to
 CC determine the functions of regions within the selected promoters,
 CC described in the method of the invention

XX SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
 |||||
 Db 9 ACTTCATTC 1

RESULT 641

ABL36403
 ID ABL36403 standard; DNA; 10 BP.

XX ABL36403;

XX 22-APR-2002 (first entry)

XX Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 39.

XX Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
 KW lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
 KW Hodgkin's disease; HD; acid phosphatase deficiency;
 KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
 KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.

XX WO200194362-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018457.

XX 07-JUN-2000; 2000US-0210047P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Klien SE, Messer C, Tanguay DA;

XX

DR WPI; 2002-154563/20.

XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene
 PT useful in studying expression and function of the protein, and for
 PT screening drugs to treat diseases e.g. Hodgkin's disease.

XX Claim 19; Page 15; 109pp; English.

XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
 CC nucleic acid and protein sequences. Specifically, the invention relates
 CC to the discovery of 22 novel polymorphic sites within the APC2 gene. The
 CC invention also comprises methods for haplotyping and genotyping the ACP2
 CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
 CC lysosomal-specific enzyme that catalyses the hydrolysis of
 CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
 CC protein are pharmaceutically important in the treatment of Hodgkin's
 CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
 CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.
 CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing
 CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
 CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
 CC useful for ACP2 genotyping, which can also be used to develop diagnostic
 CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of
 CC the invention are useful in the production of a transgenic animal which
 CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are
 CC useful in the production of allele-specific oligonucleotides designed to
 CC genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320
 CC represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-
 CC ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic
 CC acids ABL36365-ABL36408 represent claimed ACP2 primer-extension
 CC oligonucleotides

XX SQ Sequence 10 BP; 1 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17
 |||||
 Db 1 CTCCATCCT 9

RESULT 642

AAAD51164/c

ID AAD51164 standard; DNA; 10 BP.

XX AAD51164;

XX 02-APR-2003 (first entry)

XX Decoder binding site #3 used to prepare LEAE labelled detection probes.

XX Genetic analysis; allelic analysis; ds.

XX Unidentified.

XX WO200279496-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002WO-US009928.

XX 28-MAR-2001; 2001US-00821694.

XX (MIND-) APPLIED MINDS INC.

XX Hallis WD;

XX WPI; 2003-046825/04.

XX Obtaining information on target nucleic acid analyte, by hybridizing

PT target with oligonucleotide probes complementary, or complementary except

PT at position of interest to target and analyzing probe hybridization.
 XX Example 4; Page 47; 66pp; English.
 XX The invention relates to a method of obtaining information on a target
 CC nucleic acid analyte containing a target segment. The method involves
 CC hybridizing target nucleic acid analyte with at least two oligonucleotide
 CC probes, where each probe comprises a sequence fully complementary, or
 CC complementary except at a position of interest or variable position, to
 CC the target nucleic acid analyte and analysing whether all, some or none
 CC of the probes hybridise. The method is useful for sequencing and for
 CC obtaining information on a number of target nucleic acid sequence
 CC segments, where information comprises the determination of a nucleotide
 CC at a position of interest. It is also useful for genetic or allelic
 CC analysis of genomic DNA or cDNA. The present sequence is decoder binding
 CC site used to prepare LEAE (longer emission acridinium ester) labelled
 CC detection probes. This sequence is used to illustrate the method of the
 CC invention
 XX SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GACTTCATC 15
 Db 10 GACTTCTTC 2
 RESULT 643
 AAD51168
 ID AAD51168 standard; DNA; 10 BP.
 XX
 AC AAD51168;
 XX
 XX 02-APR-2003 (first entry)
 XX
 DE Decoder probe #3 used to illustrate the method of the invention.
 XX
 XX Genetic analysis; allelic analysis; ss.
 XX
 XX Unidentified.
 XX
 PH Key Location/Qualifiers
 FT modified_base 10
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Optionally linked to NH2 linker and LEAE
 FT labelled"
 XX
 XX WO200279496-A2.
 XX
 XX 10-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-US009928.
 XX
 XX 28-MAR-2001; 2001US-00821694.
 XX
 XX (MIND-) APPLIED MINDS INC.
 XX
 XX Hillis WD;
 XX
 XX WPI; 2003-046825/04.
 XX
 XX Obtaining information on target nucleic acid analyte, by hybridizing
 XX target with oligonucleotide probes complementary, or complementary except
 XX at position of interest to target and analyzing probe hybridization.
 XX
 XX Example 4; Page 47; 66pp; English.
 XX The invention relates to a method of obtaining information on a target
 CC nucleic acid analyte containing a target segment. The method involves

CC hybridising target nucleic acid analyte with at least two oligonucleotide
 CC probes, where each probe comprises a sequence fully complementary, or
 CC complementary except at a position of interest or variable position, to
 CC the target nucleic acid analyte and analysing whether all, some or none
 CC of the probes hybridise. The method is useful for sequencing and for
 CC obtaining information on a number of target nucleic acid sequence
 CC segments, where information comprises the determination of a nucleotide
 CC at a position of interest. It is also useful for genetic or allelic
 CC analysis of genomic DNA or cDNA. The present sequence is decoder probe
 CC used to illustrate the method of the invention
 XX SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GACTTCATC 15
 Db 1 GACTTCTTC 9
 RESULT 644
 ADA11182
 ID ADA11182 standard; DNA; 10 BP.
 XX
 AC ADA11182;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 DE Differential display random PCR primer #17.
 XX
 KW ss; PCR; breast cancer; cytostatic; tumour; gene therapy; primer;
 KW differential display.
 XX
 OS Synthetic.
 XX
 XX US2002165371-A1.
 XX
 XX 07-NOV-2002.
 XX
 XX 07-AUG-2001; 2001US-00924400.
 XX
 XX 11-JAN-1996; 96US-00585392.
 XX
 XX 10-JAN-1997; 97WO-US000485.
 XX
 XX 09-APR-1997; 97US-00838762.
 XX
 XX 11-DEC-1997; 97US-00991789.
 XX
 XX 17-APR-1998; 98US-00062451.
 XX
 XX 09-APR-1999; 99US-00289198.
 XX
 XX 28-OCT-1999; 99US-00429755.
 XX
 XX 23-MAR-2000; 2000US-00534825.
 XX
 XX 24-MAY-2000; 2000US-00577505.
 XX
 XX 08-JUN-2000; 2000US-00590583.
 XX
 XX 26-OCT-2000; 2000US-00692995.
 XX
 XX 16-MAR-2001; 2001US-00810936.
 XX
 XX (FRUD/) FRUDAKIS T N.
 XX
 XX (REED/) REED S G.
 XX
 XX (SMIT/) SMITH J M.
 XX
 XX (MISH/) MISHNER L E.
 XX
 XX (DILL/) DILLON D C.
 XX
 XX (RETT/) RETTER M W.
 XX
 XX (WANG/) WANG A.
 XX
 XX (SKEI/) SKEIKY Y A W.
 XX
 XX (HARL/) HARLOCKER S L.
 XX
 XX (DAYC/) DAY C H.
 XX
 XX (LISX/) LI S X.
 XX
 XX (DENG/) DENG T.
 XX
 XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 XX Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
 XX WPI; 2003-247262/24.

XX New breast tumor proteins nucleic acids encoding such proteins, useful in
 PT diagnosing, preventing and/or treating diseases such as cancer,
 PT particularly breast cancer, and as markers for detecting the presence of
 PT a cancer.

XX Example 1; Page 70; 190pp; English.

XX The invention relates to a breast tumour polynucleotide selected from one
 CC of the 275 fully defined nucleotide sequences (a) given in the
 CC specification, including their complements, sequences consisting of at
 CC least 20 contiguous residues of a sequence in (a), sequences that
 CC hybridise to a sequence in (a) under moderately stringent conditions,
 CC sequences having at least 75% or 90% identity to a sequence in (a), or
 CC degenerate variants of a sequence in (a). Also included are an isolated
 CC polypeptide (II) (comprising an amino acid sequence selected from
 CC sequences encoded by (a), sequences having at least 70% or 90% identity
 CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
 CC sequences (c), and sequences having at least 70% or 90% identity to a
 CC sequence in (c)), expression vectors comprising (a), a host cell
 CC transformed or transfected with the expression vector, an isolated
 CC antibody or its antigen-binding fragment that specifically binds to (II),
 CC a method for detecting the presence of a cancer in a patient, a fusion
 CC protein comprising at least one polypeptide (II), an oligonucleotide that
 CC hybridises to (a), under moderately stringent conditions, a method for
 CC stimulating and/or expanding T cells specific for a tumour protein (by
 CC contacting T cells with at least one component selected from (a), (II)
 CC and antigen-presenting cells that express (II)), an isolated T cell
 CC population comprising T cells prepared from as detailed above, a method
 CC for stimulating an immune response or treating cancer in a patient by
 CC administering a composition comprising (a), (II), the vector, cells or
 CC the antibodies, and a method for inhibiting the development of a cancer
 CC in a patient. The polynucleotides may be used in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in tumour cells. The breast tumour proteins are
 CC useful as markers to indicate the presence or absence of a cancer, such
 CC as breast cancer, and in the detection of other cancers. Compositions
 CC comprising the breast tumour proteins are useful in diagnosing,
 CC preventing and/or treating diseases such as cancer, particularly breast
 CC cancer. The present sequence is a differential display random PCR primer
 CC used in the isolation of breast cancer specific cDNAs of the invention.

XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCACTCT 17
 ||||| |||||
 Db 1 CTTCACTCT 9

RESULT 645

ID ABV76219
 XX ABV76219 standard; DNA; 10 BP.

AC ABV76219;

XX 28-MAR-2003 (first entry)

XX Primer for detecting nicotinamide N-methyltransferase polymorphism.

XX Human; nicotinamide N-methyltransferase; NNMT; enzyme; haplotyping;
 KW genotyping; Parkinson's disease; cachexia; antiparkinsonian;
 KW single nucleotide polymorphism; SNP; PCR; primer; ss.

XX Homo sapiens.

XX WO200290512-A2.

XX 14-NOV-2002.

XX

PF 07-MAY-2002; 2002WO-US014538.

XX 07-MAY-2001; 2001US-0289335P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Gilson CR, Kazemi A, Koshy B;

XX WPI; 2003-120539/11.

XX New isolated polynucleotide having nicotinamide N-methyltransferase

XX (NNMT) gene, useful for treating diseases associated with NNMT activity,

XX e.g. Parkinson's disease and cancer cachexia.

XX Claim 33; Page 13; 57pp; English.

XX The present sequence is a preferred primer for detecting the PS2
 CC polymorphic site in the human nicotinamide N-methyltransferase (NNMT)
 CC gene (see also ABV76204) by the primer extension method. The invention is
 CC based on the discovery of 3 novel polymorphic sites (PS1-PS3) in the NNMT
 CC gene. The identity of the alleles at these sites were determined in a
 CC human reference population of 79 unrelated individuals self-identified as
 CC belonging to African descent, Asian, Caucasian and Hispanic/Latino
 CC population groups. The invention provides a method, composition and kit
 CC for genotyping the NNMT gene in an individual. A genotyping kit
 CC composition comprises a probe or primer designed to specifically
 CC hybridise to a target region containing, or adjacent to, one of the NNMT
 CC polymorphic sites. A genotyping kit comprises a set of oligonucleotides
 CC designed to genotype each of the NNMT polymorphic sites. The invention
 CC also provides a method for haplotyping the NNMT gene. This is useful for
 CC improving the development of drugs metabolised by NNMT or drugs for
 CC treating diseases associated with NNMT activity, e.g. Parkinson's disease
 CC and cancer cachexia (claimed). The invention is also useful for screening
 CC compounds that target NNMT, and for identifying associations between a
 CC trait and a NNMT genotype, haplotype or haplotype pair for one or more of
 CC the novel polymorphic sites

XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
 ||||| |||||
 Db 1 GACTTCATC 9

RESULT 646

ID ACC85187
 XX ACC85187 standard; DNA; 10 BP.

AC ACC85187;

XX 18-SEP-2003 (first entry)

XX Human COX1 gene DSNP assay probe #2.

XX Crab; human; selective cleavage; nuclease; duplex nucleic acid;
 KW polymorphism; PCR; primer; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT /mod_base= modified by Fluorescein

FT modified_base 10

FT /*tag= b

FT /mod_base= modified by Dabcy1

XX WO2003048378-A2.

XX

```
PD 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-US038808.
XX
XX 04-DEC-2001; 2001US-0337125P.
PR 02-JUL-2002; 2002US-0393699P.
XX
XX (EURE-) EUREGEN LLC.
XX
XX Lukyanov S, Rebrikov DV, Shagin DA;
XX WPI; 2003-505300/47.
XX
XX Selectively cleaving DNA molecules in duplex nucleic acids in a complex
XX nucleic acid sample by contacting the sample with a nuclease under DSN
XX conditions for the duplex nucleic acids in the sample to be selectively
XX cleaved.
XX
XX Disclosure; Page 64; 102pp; English.
XX
XX The present invention relates to a method of selectively cleaving DNA
XX molecules in duplex nucleic acids in a complex nucleic acid sample, which
XX comprises contacting the sample with a nuclease under duplex-specific
XX nuclease conditions for a period of time for the duplex nucleic acids in
XX the sample to be selectively cleaved. The method is useful for
XX selectively cleaving DNA molecules in duplex nucleic acids in a complex
XX nucleic acid sample. The present sequence is a PCR primer/probe used in
XX the exemplification of the invention
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
Db 1 GTGAGCTAC 9
RESULT 647
ACC85186
ID ACC85186 standard; DNA; 10 BP.
AC ACC85186;
XX
XX 18-SEP-2003 (first entry)
XX
XX Human COX1 gene DSNP assay probe #1.
XX
XX Crab; human; selective cleavage; nuclease; duplex nucleic acid;
XX polymorphism; PCR; primer; probe; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /tag= a
XX /mod_base= modified by Fluorescein
XX modified_base 10
XX /tag= b
XX /mod_base= modified by Dabcyl
XX
XX WO2003048378-A2.
XX
XX 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-US038808.
XX
XX 04-DEC-2001; 2001US-0337125P.
PR 02-JUL-2002; 2002US-0393699P.
XX
XX (EURE-) EUREGEN LLC.
XX
```

```
XX Lukyanov S, Rebrikov DV, Shagin DA;
XX WPI; 2003-505300/47.
XX
XX Selectively cleaving DNA molecules in duplex nucleic acids in a complex
XX nucleic acid sample by contacting the sample with a nuclease under DSN
XX conditions for the duplex nucleic acids in the sample to be selectively
XX cleaved.
XX
XX Disclosure; Page 64; 102pp; English.
XX
XX The present invention relates to a method of selectively cleaving DNA
XX molecules in duplex nucleic acids in a complex nucleic acid sample, which
XX comprises contacting the sample with a nuclease under duplex-specific
XX nuclease conditions for a period of time for the duplex nucleic acids in
XX the sample to be selectively cleaved. The method is useful for
XX selectively cleaving DNA molecules in duplex nucleic acids in a complex
XX nucleic acid sample. The present sequence is a PCR primer/probe used in
XX the exemplification of the invention
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCGAC 9
Db 1 GTGAGCTAC 9
RESULT 648
ADB81028
ID ADB81028 standard; DNA; 10 BP.
XX
XX ADB81028;
XX
XX 04-DEC-2003 (first entry)
XX
XX LINE retro-position related TRAS1 oligo, SEQ ID No 42.
XX
XX RNA retro-position; 3' UTR; LINE; APE domain; retro-transposition;
XX endonuclease domain; chromosome; gene therapy; gene transfer; ss.
XX
XX Unidentified.
XX
XX WO2003064644-A1.
XX
XX 07-AUG-2003.
XX
XX 26-NOV-2002; 2002WO-JF012317.
XX
XX 31-JAN-2002; 2002JP-00024226.
XX
XX (DNAV-) DNAVEC RES INC.
XX
XX Fujiwara H, Takahashi H, Hasegawa M;
XX WPI; 2003-627609/59.
XX
XX LINE retro-position by trans-complementation for transferring targeted,
XX specific gene or nucleic acid of e.g. endonuclease domain via
XX substitution to chromosome using virus vector, applicable in gene
XX therapy.
XX
XX Example 8; Fig 6; 96pp; Japanese.
XX
XX The invention relates to a novel RNA retro-position comprising the
XX transcription of an RNA containing a 3' UTR fragment of a LINE in cells;
XX and trans-positioning the ORF protein of such LINE after expressing from
XX other than the RNA. The invention further comprises a similar method in
XX which the transcription of an RNA containing a 3' UTR fragment of an APE
```


CC domain-carrying type site-specific LINE in cells, and expressing the ORF
 CC protein of the LINE in such cells; or transcribing of an RNA containing
 CC 3' UTR fragment of a LINE in cells, and expressing ORF protein in such
 CC cells thereby modifying a retro-transposition target site of a LINE by
 CC substituting the endonuclease domain of the LINE by that of another LINE
 CC via ORF protein of such LINE. The invention also includes a retro-
 CC transposition vector with RNA encoding the 3' UTR fragment of a LINE but
 CC not expressing the encoded ORF of the LINE; a vector encoding a protein
 CC for substitution of the endonuclease domain of an encoded ORF protein in
 CC the site-specific LINE by the endonuclease domain of the encoded ORF
 CC protein in another LINE; and a kit for gene transfer through retro-
 CC transposition of an RNA. The method is useful for transferring targeted,
 CC specific genes or nucleic acids of an endonuclease domain via
 CC substitution to a chromosome using a virus vector, which is applicable in
 CC gene therapy. The retro-transposition in the host is highly efficient by
 CC targeting specifically at LINE, and with little damage to the host due to
 CC the gene transfer. This polynucleotide sequence represents an
 CC oligonucleotide used in the exemplification of the invention.

XX
 SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGCGACTT 11
 |||||
 Db 2 GAGTGACTT 10

RESULT 649
 ADC15155
 ID ADC15155 standard; DNA; 10 BP.
 XX
 AC ADC15155;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human breast tumour protein primer, SEQ ID 103.
 XX
 KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003013431-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 05-AUG-2002; 2002WO-US024917.
 XX
 PR 07-AUG-2001; 2001US-00924400.
 PR 20-FEB-2002; 2002US-00079137.
 PR 02-AUG-2002; 2002US-00212679.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
 PI Kalos MD;
 XX
 XX WPI; 2003-342398/32.
 XX
 XX New polynucleotide, useful for preparing a composition for diagnosing,
 PT treating or preventing cancer.
 PT
 XX Example 1; SEQ ID NO 103; 308pp; English.

XX The present invention relates to compositions and methods for the therapy
 CC and diagnosis of cancer, particularly breast cancer. The method for
 CC detecting the presence of a cancer in a patient comprises: obtaining a
 CC biological sample from the patient; contacting the biological sample with
 CC a binding agent that binds to the polypeptide; detecting in the sample an
 CC amount of the polypeptide that binds to the binding agent; and comparing

CC the amount of the polypeptide to a predetermined cut-off value. Treating
 CC breast cancer comprises administering a composition comprising breast
 CC tumour proteins and nucleic acids, which simulates and/or expands T cells
 CC specific for the tumour protein. The present sequence was used to
 CC illustrate the invention.

SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 |||||
 Db 1 CTTCAAGCT 9

RESULT 650
 ADD07264/c
 ID ADD07264 standard; DNA; 10 BP.

XX
 AC ADD07264;

XX
 DT 01-JAN-2004 (first entry)

XX
 DE Mouse differential display RT-PCR primer #15.

XX
 KW PCR; ss; interferon regulatory factor; IRF-1; IRF-2; herpes; antiviral;
 KW transcription factor; virucide; vaccine; interferon; mouse; primer;
 KW differential display; RT-PCR; reverse transcriptase PCR.

XX
 OS Mus musculus.

XX
 PN US2003104356-A1.

XX
 PD 05-JUN-2003.

XX
 PF 26-MAR-2002; 2002US-00108164.

XX
 PR 22-NOV-1999; 99US-00424348.

XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
 PI Berger SL;

XX
 PN WPI; 2003-801223/75.

XX
 PT Treating infection or reactivation caused by Herpes virus comprises using
 PT antagonist of Herpes Simplex virus polynucleotide sequence and interferon
 PT regulatory factor-1.

XX
 XX Example 3; SEQ ID NO 112; 53pp; English.

XX The invention relates to treating viral infection or reactivation
 CC comprising contacting an individual with an antagonist of the interaction
 CC between a Herpes Simplex virus (HSV) polynucleotide sequence appearing as
 CC ADD07153 and interferon regulatory factor-1 (IRF-1, a transcription
 CC factor of the interferon regulatory pathway). Also included are an
 CC isolated HSV polynucleotide comprising ADD07153, a composition comprising
 CC a HSV polypeptide involved in viral infection or reactivation, screening
 CC for compounds capable of inhibiting specific binding of IRF-1 to a
 CC polynucleotide, screening for compounds capable of inhibiting specific
 CC binding of IRF-1 to IRF-1:IRF-BP (undefined) complex, a compound capable
 CC of agonising or antagonising any compound in IRF-1 and/or interferon
 CC genetic regulatory pathway and a composition for comprising an HSV IRF-1
 CC binding site consensus sequence. The method is useful for treating
 CC infection or reactivation caused by Herpes virus, e.g., HSV-1 or HSV-2
 CC infections and for cytomegalovirus, Epstein Barr virus and zoster virus
 CC infection. The HSV polypeptide and polynucleotides may also be useful as
 CC antiviral vaccines. An experiment was performed where cDNA from the
 CC transgenimal ganglia of mice infected with HSV was isolated by
 CC differential display reverse transcriptase PCR (DDRT-PCR). The present
 CC sequence is a DDRT-PCR primer used in the experiment.

```
XX SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 9 GACTTGATC 1

RESULT 651
ADD66356
ID ADD66356 standard; DNA; 10 BP.
XX AC
XX AC ADD66356;
XX DT 15-JAN-2004 (first entry)
XX DE Human lung tumour-specific DNA related primer, SEQ ID No 48.
XX KW expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
XX KW human; lung tumour-specific; PCR; primer; ss.
XX OS Homo sapiens.
XX PN WO200292001-A2.
XX PD 21-NOV-2002.
XX PF 10-MAY-2002; 2002WO-US014975.
XX PR 11-MAY-2001; 2001US-00854133.
XX PA (CORI-) CORIXA CORP.
XX PI Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;
XX WPI; 2003-120592/11.
XX DR New polynucleotide and polypeptide, useful for preparing a composition
XX FT for diagnosing, treating or preventing cancer.
XX PS Example 1; SEQ ID NO 48; 494pp; English.
XX CC The invention relates to a novel isolated polynucleotide comprising one
XX CC of 32 47-6080 base pair sequences, given in the specification, or their
XX CC complements or degenerate variants, at least 20 contiguous residues of a
XX CC sequence in, or having at least 75 or 90 % identity with the isolated
XX CC polynucleotide, or that hybridise with the polynucleotide. The invention
XX CC further comprises: an isolated polypeptide; an expression vector
XX CC comprising the polynucleotide operably linked to an expression control
XX CC sequence; a host cell transformed or transfected with the expression
XX CC vector; an isolated antibody or its antigen-binding fragment that
XX CC specifically binds to the polypeptide; a method for detecting the
XX CC presence of a cancer in a patient; a fusion protein comprising the
XX CC polypeptide; an oligonucleotide that hybridises to the isolated
XX CC polynucleotide under moderately stringent conditions; a method for
XX CC stimulating and/or expanding T cells specific for a tumour protein; an
XX CC isolated T cell population; a composition comprising a first component
XX CC consisting of carriers and immunostimulants and a second component; a
XX CC method for stimulating an immune response in a patient; a method for
XX CC treating cancer in a patient; a method for determining cancer in a
XX CC patient; a diagnostic kit comprising at least one oligonucleotide or
XX CC antibody and a detection reagent comprising a reporter group; and a
XX CC method for inhibiting the development of cancer in a patient. The
XX CC compositions of the invention have cytostatic activity and can be used to
XX CC create a vaccine. The isolated polynucleotide is useful for preparing a
XX CC composition for diagnosing, treating or preventing cancer. This
XX CC polynucleotide sequence represents a primer relating to the human lung
XX CC tumour-specific cDNA sequences of the invention.
```

```
XX SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
SQ Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTTCACCT 9

RESULT 652
ADE87610
ID ADE87610 standard; DNA; 10 BP.
XX AC
XX AC ADE87610;
XX DT 29-JAN-2004 (first entry)
XX DE Human lung tumour antigen cDNA PCR primer #2.
XX KW Human; lung tumour antigen; PCR; ss; cancer; lung cancer; CD4+; CD8+;
XX KW T cell; immune response; immunostimulant; cytostatic; primer.
XX OS Homo sapiens.
XX PN US2003118599-A1.
XX PD 26-JUN-2003.
XX PF 10-MAY-2002; 2002US-00144649.
XX PR 02-APR-1999; 99US-00285323.
XX PR 09-AUG-1999; 99US-00370838.
XX PR 30-DEC-1999; 99US-00476235.
XX PR 03-MAR-2000; 2000US-00518809.
XX PR 29-MAR-2000; 2000US-00538037.
XX PR 05-JUN-2000; 2000US-00588937.
XX PR 18-AUG-2000; 2000US-00640878.
XX PR 20-SEP-2000; 2000US-00667170.
XX PR 01-NOV-2000; 2000US-00704512.
XX PR 14-DEC-2000; 2000US-00738973.
XX PR 11-MAY-2001; 2001US-00854133.
XX PA (CORI-) CORIXA CORP.
XX PI Algate PA, Lodes MJ, Wang T, Fan L, Mcneill PD;
XX DR WPI; 2003-897103/82.
XX PS New polynucleotides encode lung tumor antigens and are useful to
XX FT stimulate an immune response or detect or treat a cancer in a patient,
XX XX particularly lung cancer.
XX PS Example 1; SEQ ID NO 48; 63pp; English.
XX CC The invention relates to polynucleotides encoding lung tumour antigens.
XX CC The invention also relates to the polypeptides encoded by the
XX CC polynucleotides, isolated antibodies or antigen-binding fragments that
XX CC specifically bind the polypeptides and a method for detecting cancer in a
XX CC patient, comprising obtaining a biological sample from the patient,
XX CC contacting the sample with a binding agent that binds a polypeptide of
XX CC the invention, detecting in the sample an amount of polypeptide that
XX CC binds to the binding agent, and comparing the amount of polypeptide to a
XX CC predetermined cut-off value. T cells specific for a tumour protein can be
XX CC stimulated and/or expanded by contacting the T cells with a polypeptide,
XX CC polypeptide or an antigen-presenting cell that expresses a
XX CC polypeptide. Cancer development can be inhibited by incubating CD4+
XX CC and/or CD8+ T cells isolated from a patient with a polypeptide,
XX CC polynucleotide or an antigen-presenting cell that expresses a
XX CC polypeptide, so that the T cells proliferate. The invention is used to
XX CC stimulate an immune response or to detect or treat a cancer in a patient,
XX CC particularly lung cancer. This sequence represents a PCR primer used to
```

CC amplify human lung tumour antigen cDNA of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCAACT 9

RESULT 653
AAQ69869
ID AAQ69869 standard; DNA; 11 BP.
XX
AC AAQ69869;
XX
DT 25-MAR-2003 (revised)
DT 07-MAR-1995 (first entry)
XX
DE Sample distamycin target sequence.
XX
KW DNA protein-binding assay; test sequence; screening sequence; promoter;
KW target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9;
KW transcription factor; TFIID: ds.
XX
OS Synthetic.
XX
PN WO9414980-A1.
XX
PD 07-JUL-1994.
XX
PF 20-DEC-1993; 93WO-US012388.
XX
PR 23-DEC-1992; 92US-00996783.
PR 17-SEP-1993; 93US-00123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX WPI; 1994-234711/28.
XX
DR
XX
XX Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
XX as molecular reagents.
XX
PS Example 13.E.; Page 522; 587pp; English.
XX
XX A DNA protein-binding assay is provided, useful for screening libraries
XX of synthetic or biological cpds. for their ability to bind DNA test
XX sequences. The assay is versatile in that any number of test sequences
XX can be tested by placing the test sequence adjacent to a defined protein-
XX binding screening sequence. Binding of mols. to these test sequences
XX changes the binding characteristics of the protein mol. to its cognate
XX binding sequence. When such a mol. binds the test sequence, the
XX equilibrium of the DNA:protein complexes is disturbed, generating changes
XX in the concentration of free DNA probe. One application of this method is
XX to eucaryotic general transcription factors (e.g. TFIID), where the
XX target region is typically selected from DNA sequences adjacent to the
XX binding site for the eucaryotic transcription factor. Numerous exemplary
XX test sequences are given: the sequences in AAQ69251-731 and AAQ69850
XX correspond to promoter targets (typically, TATA box-contg. sites) for
XX human genes and the sequences in AAQ69732-849 correspond to promoter
XX targets for viral genes. The test sequences may also be randomly
XX generated. DNA:protein interaction may be used for screening purposes,
XX e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see
XX AAQ69851-52, AAQ69865 and AAQ69891). Example 13 describes a method for
XX selecting target sites for DNA- binding mols. that are dimers or trimers

CC of distamycin. A sequence was identified from the medically significant
CC target site database that contains the sequence given in AAQ69869, which
CC is a subset of the group of sequences represented by the sequence given
CC in AAQ69870. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

RESULT 654
AAT49573
ID AAT49573 standard; DNA; 11 BP.
XX
AC AAT49573;
XX
DT 25-MAR-2003 (revised)
DT 17-MAR-1997 (first entry)
XX
DE NFAT-1 binding site.
XX
KW Duplex DNA; target region; binding characteristic; DNA binding protein;
KW TFIID; transcription factor; binding site; inhibition; enhance; cancer;
KW inherited genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN US5578444-A.
XX
PD 26-NOV-1996.
XX
PF 20-DEC-1993; 93US-00171389.
XX
PR 27-JUN-1991; 91US-00723618.
PR 23-DEC-1992; 92US-00996783.
PR 17-SEP-1993; 93US-00123936.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX WPI; 1997-020402/02.
XX
XX Altering binding characteristics of DNA binding proteins to duplex DNA -
XX by attaching specific small cpd. to target region close to the protein's
XX binding site, useful in treatment of viral disease, cancer etc.
XX
XX Example 13; Col 417; 264pp; English.
XX
XX The sequences given in AAT49573-74 represent DNA's which act as target
XX regions in the method of the invention. These sequences overlap the
XX binding site for a transcription factor, nuclear factor of activated T
XX cells (NFAT-1), which is a major regulatory factor in the induction of
XX interleukin 2 expression early in the T cell activation response. These
XX sequences represent target sites for distamycin. The method of the
XX invention comprises altering the binding characteristics of a DNA-binding
XX protein to duplex DNA. The method comprises contacting the duplex DNA
XX with a small molecule which binds sequence-specifically to a target
XX region, where, when the small molecule is bound to the target region, it
XX is adjacent to, but not overlapping by more than 4 bp, a binding site for
XX a DNA-binding protein. The small molecule is added at a concentration
XX effective to alter the binding of the DNA binding protein, pref. TFIID,
XX to its binding site on the duplex DNA. The binding of the small molecule
XX may inhibit or enhance the binding of the DNA-binding protein to its
XX binding site. The compounds isolated using this method are potentially
XX useful as therapeutic agents for treatment of any disease which involves
XX a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.

CC (see also AAT63713-4312). (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;

SQ Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 10 TTTCATCCTT 18
Db 1 TTCTCCTT 9

RESULT 655
AAZ18694/C
ID AAZ18694 standard; DNA; 11 BP.

XX AAZ18694;
AC AAZ18694;
XX 22-OCT-1999 (first entry)
DT Murine C57BL/6 SAGE tag 3054865.
DE Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
XX healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
KW
XX Mus sp.
OS
XX WO9941364-A2.
PN 19-AUG-1999.
XX 12-FEB-1999; 99WO-US002962.
XX 13-FEB-1998; 98US-0074737P.
PR 26-AUG-1998; 98US-0097937P.
XX 28-SEP-1998; 98US-0102051P.
XX (WIST-) WISTAR INST.
PA Heber-Katz E;
XX WPI; 1999-494533/41.
XX New mammalian model for enhanced wound healing - useful for identifying enhanced wound healing genes.
PT Claim 13; Page 55; 136pp; English.
XX This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying DNA microsatellite markers which can distinguish healer mice from non-healer mice and identifying microsatellite markers which segregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and gene products involved in enhanced wound healing, and to provide methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags from C57BL/6 and MRL mice which are used to illustrate the method of the invention

XX Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTGAGCGAC 9
Db 9 GTGAGCGAC 1

RESULT 656
AAZ19007/C
ID AAZ19007 standard; DNA; 11 BP.

XX AAZ19007;
AC AAZ19007;
XX 22-OCT-1999 (first entry)
DT Murine MRL SAGE tag 3054867.
DE Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
XX healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
KW
XX Mus sp.
OS
XX WO9941364-A2.
PN 19-AUG-1999.
XX 12-FEB-1999; 99WO-US002962.
XX 13-FEB-1998; 98US-0074737P.
PR 26-AUG-1998; 98US-0097937P.
XX 28-SEP-1998; 98US-0102051P.
XX (WIST-) WISTAR INST.
PA Heber-Katz E;
XX WPI; 1999-494533/41.
XX New mammalian model for enhanced wound healing - useful for identifying enhanced wound healing genes.
PT Claim 13; Page 74; 136pp; English.
XX This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying DNA microsatellite markers which can distinguish healer mice from non-healer mice and identifying microsatellite markers which segregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and gene products involved in enhanced wound healing, and to provide methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags from C57BL/6 and MRL mice which are used to illustrate the method of the invention

XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

SQ Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTGAGCGAC 9
Db 9 GTGAGCGAC 1

```

RESULT 657
AAZ18957/c
ID AAZ18957 standard; DNA; 11 BP.
XX
XX
AC AAZ18957;
XX
XX DT 22-OCT-1999 (first entry)
XX
XX DE Murine MRL SAGE tag 1236433.
XX
XX KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX OS Mus sp.
XX
XX PN WO9941364-A2.
XX
XX PD 19-AUG-1999.
XX
XX PF 12-FEB-1999; 99WO-US002962.
XX
XX PR 13-FEB-1998; 98US-0074737P.
XX
XX PR 26-AUG-1998; 98US-0097937P.
XX
XX PR 28-SEP-1998; 98US-0102051P.
XX
XX PA (WIST-) WISTAR INST.
XX
XX PI Heber-Katz E;
XX
XX DR WPI; 1999-494533/41.
XX
XX PT New mammalian model for enhanced wound healing - useful for identifying
XX enhanced wound healing genes.
XX
XX PS Claim 13; Page 73; 136pp; English.
XX
XX This invention describes a novel non-MRL healer mouse (M) having at least
XX one quantitative trait locus selected from those given in the
XX specification, exhibiting an enhanced healing response to a wound
XX compared to mice (m) without the locus. The invention describes a novel
XX method of identifying a gene involved in enhanced wound healing by
XX identifying DNA microsatellite markers which can distinguish healer
XX from non-healer mice and identifying microsatellite markers which
XX segregate with enhanced wound healing in progeny of the mice, where a
XX chromosomal locus containing at least one enhanced wound healing gene is
XX identified. A method of treating a wound in a mammal is also disclosed.
XX The new methods are useful for treating wounds, especially central and
XX peripheral nerve wound. The methods of the invention are useful for
XX restoring function after nerve injury in a mammal. (M) is useful as a
XX mammalian model of enhanced wound healing, useful for identifying genes
XX and gene products involved in enhanced wound healing, and to provide
XX methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
XX from C57BL/6 and MRL mice which are used to illustrate the method of the
XX invention
XX
XX SQ Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

RESULT 658
AAZ18853/c
ID AAZ18853 standard; DNA; 11 BP.
XX
XX AC AAZ18853;
XX
XX DT 24-MAR-1999 (first entry)
XX
XX DE Triple helix third strand of 23S rRNA gene nucleotides 459-469.
XX
XX KW Triplex formation; DNA detection; triple helix; identification; bacteria;

```

```

XX DT 22-OCT-1999 (first entry)
XX
XX DE Murine MRL SAGE tag 3054865.
XX
XX KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX OS Mus sp.
XX
XX PN WO9941364-A2.
XX
XX PD 19-AUG-1999.
XX
XX PF 12-FEB-1999; 99WO-US002962.
XX
XX PR 13-FEB-1998; 98US-0074737P.
XX
XX PR 26-AUG-1998; 98US-0097937P.
XX
XX PR 28-SEP-1998; 98US-0102051P.
XX
XX PA (WIST-) WISTAR INST.
XX
XX PI Heber-Katz E;
XX
XX DR WPI; 1999-494533/41.
XX
XX PT New mammalian model for enhanced wound healing - useful for identifying
XX enhanced wound healing genes.
XX
XX PS Claim 13; Page 71; 136pp; English.
XX
XX This invention describes a novel non-MRL healer mouse (M) having at least
XX one quantitative trait locus selected from those given in the
XX specification, exhibiting an enhanced healing response to a wound
XX compared to mice (m) without the locus. The invention describes a novel
XX method of identifying a gene involved in enhanced wound healing by
XX identifying DNA microsatellite markers which can distinguish healer
XX from non-healer mice and identifying microsatellite markers which
XX segregate with enhanced wound healing in progeny of the mice, where a
XX chromosomal locus containing at least one enhanced wound healing gene is
XX identified. A method of treating a wound in a mammal is also disclosed.
XX The new methods are useful for treating wounds, especially central and
XX peripheral nerve wound. The methods of the invention are useful for
XX restoring function after nerve injury in a mammal. (M) is useful as a
XX mammalian model of enhanced wound healing, useful for identifying genes
XX and gene products involved in enhanced wound healing, and to provide
XX methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
XX from C57BL/6 and MRL mice which are used to illustrate the method of the
XX invention
XX
XX SQ Sequence 11 BP; 3 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 659
AAZ14903
ID AAZ14903 standard; DNA; 11 BP.
XX
XX AC AAZ14903;
XX
XX DT 24-MAR-1999 (first entry)
XX
XX DE Triple helix third strand of 23S rRNA gene nucleotides 459-469.
XX
XX KW Triplex formation; DNA detection; triple helix; identification; bacteria;

```

KW oncogene; virus; ss.
 XX Synthetic.
 OS Clostridium pasteurianum.
 XX
 XX US5861244-A.
 XX
 XX 19-JAN-1999.
 PD
 XX 22-DEC-1993; 93US-00173489.
 PF
 XX 29-OCT-1992; 92US-00968436.
 XX
 XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
 PA
 XX Hepburn AG, Wang C;
 FI
 XX WPI; 1999-130384/11.
 DR
 XX Assay of genetic sequences based on triplex formation from double
 XX stranded analyte - and hybrid of anchor and reporter sequences, with
 PT reporter released if triplex formation occurs, used e.g. to identify
 PT bacteria.
 XX
 XX Disclosure; Col 23-24; 160pp; English.
 PS
 XX The present sequence represents a polynucleotide that is able to form a
 CC triple helix with a double stranded sequence. Cytosine bases in the
 CC present can be replaced with 5-methylcytosine for increased triplex
 CC stability. The present sequence is used in the assay of the invention,
 CC where it can be part of the anchor DNA or reporter DNA sequence. The
 CC assay comprises adding a sample containing double-stranded DNA test
 CC sequences to an aqueous medium containing at least one complex of anchor
 CC DNA, attached to a solid support, and reporter DNA, where either a part
 CC of the anchor DNA or reporter DNA is designed to form a triple-strand
 CC structure with part of the test sequence. Triplex formation results in
 CC displacement of the reporter DNA which is detected as an indication of
 CC the presence of the DNA test sequence. The method is used to detect DNA
 CC sequences, particularly for identification of bacteria (by detecting
 CC genes for ribosomal RNA) in clinical samples, but also detection of
 CC oncogenes and Hepatitis B virus
 XX
 SQ Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTTCATCCTT 18
 Db 2 TTCTCCTT 10
 RESULT 660
 AAX17619
 ID AAX17619 standard; DNA; 11 BP.
 XX
 XX AAX17619;
 AC
 XX 06-MAY-1999 (first entry)
 DT
 XX Distamycin sample target sequence.
 DE
 XX Test sequence; DNA-binding molecule; screening sequence; distamycin;
 KW nucleic acid amplification; target; HSV; viral; ss.
 XX
 XX Synthetic.
 OS
 XX US5869241-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 07-JUN-1995; 95US-00475228.
 PF

XX 27-JUN-1991; 91US-00723618.
 PR 23-DEC-1992; 92US-00996783.
 PR 17-SEP-1993; 93US-00123936.
 PR 20-DEC-1993; 93US-00171389.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 XX Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
 PI
 XX WPI; 1999-152755/13.
 DR
 XX Determination of DNA sequence preference of a DNA-binding molecule -
 PT based on inhibition of binding of protein to oligonucleotide sequence
 PT attached to test sequence.
 PT
 XX Disclosure; Col 419; 270pp; English.
 PS
 XX The invention relates to a method of determining the DNA sequence
 CC preference of a DNA-binding molecule. The method comprises: (i) adding a
 CC test molecule and a DNA-binding protein to a mixture of duplex DNA test
 CC oligonucleotides, each of the test oligonucleotides having a test
 CC sequence adjacent to a screening sequence, where the screening sequence
 CC binds to the DNA-binding protein with a binding affinity that is
 CC independent of the DNA sequence of the test sequence, and where the
 CC mixture of duplex DNA test oligonucleotides includes several test
 CC sequences; (ii) incubating the test molecule, the mixture of duplex DNA
 CC test oligonucleotides and the DNA-binding protein for a time sufficient
 CC to permit binding of the test molecule to test sequences in the duplex
 CC DNA; (iii) separating unbound test oligonucleotides from test
 CC oligonucleotides bound to binding protein; (iv) amplifying the unbound
 CC test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating
 CC the amplified test oligonucleotides; and (vii) sequencing the isolated
 CC test oligonucleotides. The invention provides test sequences AAX17001-
 CC AAX17481 and AAX17500 that correspond to promoter targets for human genes
 CC and test sequences AAX17482-X17599 that correspond to promoter targets
 CC for viral genes. The present sequence represents a sample distamycin
 CC target sequence
 XX
 SQ Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTTCATCCTT 18
 Db 1 TTCTCCTT 9
 RESULT 661
 AAX77659
 ID AAX77659 standard; DNA; 11 BP.
 XX
 XX AAX77659;
 AC
 XX 09-AUG-1999 (first entry)
 DT
 XX N11 active EGS 23.
 DE
 XX External guide sequence; EGS; target mRNA; identification; diagnostic;
 KW inactivation; essential gene; therapy; ss.
 XX
 XX Synthetic.
 OS
 XX WO9927135-A2.
 PN
 XX 03-JUN-1999.
 PD
 XX 20-NOV-1998; 98WO-US024854.
 PF
 XX 21-NOV-1997; 97US-00976220.
 XX
 PR 30-MAR-1998; 98US-0079851P.
 PR

XX PA (INNO-) INNOVIR LAB INC.
 XX FI Nilsen TW, Robertson HD, Kindt TJ;
 XX DR WPI; 1999-357853/30.
 XX FT Identifying and inhibiting functional nucleic acid molecules in cells.
 XX PS Example 3; Page 28; 58pp; English.
 XX CC This invention describes a novel method allowing essential or functional
 CC genes to be rapidly identified and inactivated. The method is able to
 CC firstly identify most of the essential genes in an organism (i.e. a
 CC bacteria or a eukaryote) needed for survival, and secondly it provides
 CC for reducing or inactivating their expression. The method is able to
 CC identify functional oligonucleotide molecules able to be used as
 CC diagnostic reagents and therapeutics. The method provides a means for
 CC identifying essential genes whose sequence is known only as part of a
 CC genome with unknown function, as well as a means for identifying
 CC functional oligonucleotide molecules. The method involves the use of a
 CC nucleic acid molecule comprising (a) a first reporter gene encoding a
 CC fusion protein comprising a protein of interest (itself translated from
 CC an RNA of interest) and a reporter protein, a second reporter gene
 CC encoding a second reporter protein, and (c) a targeting gene encoding a
 CC functional oligonucleotide molecule such as an external guide sequence
 CC (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest
 CC at a site on the first reporter gene able to encode the RNA of interest
 XX
 SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTGAGCGAC 9
 ||| |||||
 Db 2 GTAAGCGAC 10
 RESULT 662
 AAF82242/C
 ID AAF82242 standard; DNA; 11 BP.
 XX AC AAF82242;
 XX DT 14-JUN-2001 (first entry)
 XX DE DNA sequence that forms complex with alphaPNA CCTCC(b2) .
 XX KW AlphaPNA; alpha-helical peptide nucleic acid; alphaPNA.DNA complex;
 KW solid-phase peptide synthesis; molecular switching; diagnosis; therapy;
 KW backbone 2; b2; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc_binding 4..8
 FT /+tag= a
 FT /bound_moiety= "Alpha-helical peptide nucleic acid shown
 FT in AAB74015"
 FT /note= "this region hybridises to the five nucleotides
 FT attached to the peptide backbone represented in AAB74015"
 XX PN WO200114398-A1.
 XX PD 01-MAR-2001.
 XX PF 11-AUG-2000; 2000WO-US021845.
 XX PR 25-AUG-1999; 99US-0150637P.
 XX PA (GARN/) GARNER P P.

XX FI Garner PP;
 XX DR WPI; 2001-265835/27.
 XX FT New peptide-based nucleic acid surrogate (PNAs) for use in therapeutic,
 XX diagnostic and molecular switching applications e.g. alpha-PNA chips.
 XX PS Example; Page 12; 32pp; English.
 XX CC The present sequence is a DNA sequence which hybridises to an alpha-
 CC helical peptide nucleic acid (alphaPNA). The invention relates to novel
 CC peptide-based nucleic acid surrogates comprising a secondary structure
 CC and a subunit with the sequence (AAB-aa)n, where: AA = hydroxyl-amino
 CC acid; B = nucleobase; aa = amino acid; n and m = greater than or equal to
 CC 1. Resin-bound PNAs are formed by solid-phase peptide synthesis and the
 CC resin is then cleaved from the PNAs. The PNAs are useful in therapeutic,
 CC diagnostic and molecular switching applications. The present sequence
 CC binds to nucleotides attached to the alphaPNA to form an alphaPNA.DNA
 CC complex
 XX
 SQ Sequence 11 BP; 7 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 10 TTCATCCTT 18
 ||| |||||
 Db 10 TTCTCTCTT 2
 RESULT 663
 ABQ86387/C
 ID ABQ86387 standard; cDNA; 11 BP.
 XX AC ABQ86387;
 XX DT 10-SEP-2002 (first entry)
 XX DE Human skin stress/ageing related EST SEQ ID NO 142.
 XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253773-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015178.
 XX PR 03-JAN-2001; 2001DE-01000121.
 XX PA (HENK) HENKEL KGAA.
 XX FH Petersohn D, Conradt M, Hofmann K;
 FT WPI; 2002-528865/56.
 XX FT Identifying genes involved in skin stress and aging, useful e.g. in
 FT screening for cosmetic or therapeutic agents, based on differential gene
 FT expression.
 XX PS Claim 8; Page 43; 325pp; German.
 XX CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining

```
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 11 GACTTCAAC 3

RESULT 664
ABQ87456
ID ABQ87456 standard; cDNA; 11 BP.
XX
XX
AC ABQ87456;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 1211.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015178.
XX
XX 03-JAN-2001; 2001DE-01000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX Claim 8; Page 87; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 3 TGAGCAACT 11

RESULT 666
ABQ86495
ID ABQ86495 standard; cDNA; 11 BP.
XX
XX
AC ABQ86495;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 250.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX
```

```
RESULT 665
ABQ86343/C
ID ABQ86343 standard; cDNA; 11 BP.
XX
XX
AC ABQ86343;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 98.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015178.
XX
XX 03-JAN-2001; 2001DE-01000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX Claim 8; Page 41; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGGCACTTC 12
Db 9 AGGCACTGC 1

RESULT 666
ABQ86495
ID ABQ86495 standard; cDNA; 11 BP.
XX
XX
AC ABQ86495;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human skin stress/ageing related EST SEQ ID NO 250.
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253773-A2.
XX
XX
```



```

PD 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015178.
XX
XX 03-JAN-2001; 2001DE-01000121.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX Claim 8; Page 47; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 0 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 9 CTTGCTCT 17
XX Db 2 CTTGCTCT 10
XX
XX RESULT 667
XX ABQ87002/c
XX ID ABQ87002 standard; cDNA; 11 BP.
XX
XX AC ABQ87002;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 757.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX

```

```

PS Claim 8; Page 68; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 5 GCGACTTCA 13
XX Db 11 GCGCTTCA 3
XX
XX RESULT 668
XX ABQ87571/c
XX ID ABQ87571 standard; cDNA; 11 BP.
XX
XX AC ABQ87571;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 1326.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX PS Claim 8; Page 92; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 5 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
XX

```

```

Query Match          41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCAATCCTT 18
Db 10 TTCAATCCAT 2
      |||||
      |||||

RESULT 669
ABV65752/c
ID ABV65752 standard; cDNA; 11 BP.
XX
AC ABV65752;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3538.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 123; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match          41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGACCGACT 10
Db 11 TGACCGACT 3
      |||||
      |||||

RESULT 670
ABV67491
ID ABV67491 standard; cDNA; 11 BP.
XX

```

```

AC ABV67491;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 5277.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 171; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match          41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCAATCCT 17
Db 2 CGTCAATCCT 10
      |||||
      |||||

RESULT 671
ABV68393/c
ID ABV68393 standard; cDNA; 11 BP.
XX
AC ABV68393;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6179.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.

```

XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 196; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGAGCGACT 10
 Db 10 TGAGAGACT 2
 |||||
 |||||
 RESULT 672
 ABV70831/c
 ID ABV70831 standard; cDNA; 11 BP.
 XX AC ABV70831;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 8617.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 196; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGAGCGACT 10
 Db 10 TGAGAGACT 2
 |||||
 |||||
 RESULT 672
 ABV70831/c
 ID ABV70831 standard; cDNA; 11 BP.
 XX AC ABV70831;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 8617.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 276; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTGAGCGAC 9
 Db 9 GTGAGCCAC 1
 |||||
 |||||
 RESULT 673
 ABV71968
 ID ABV71968 standard; cDNA; 11 BP.
 XX AC ABV71968;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 9754.
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
 KW immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 316; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin

XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Claim 24; Page 246; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 XX Sequence 11 BP; 5 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 CTTTCATCCT 17
 DB 11 CTTTCATCCT 3
 RESULT 677
 ABV71538/C
 ID ABV71538 standard; cDNA; 11 BP.
 AC
 XX ABV71538;
 AC
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 9324.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 KW Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX

PR 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 PA
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Claim 24; Page 300; 1345pp; German.
 PS
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 XX Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTGAGCCGAC 9
 DB 9 GTGAGCCGAC 1
 RESULT 678
 ABV66548/C
 ID ABV66548 standard; cDNA; 11 BP.
 AC
 XX ABV66548;
 AC
 XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 4334.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 KW Homo sapiens.
 OS
 XX WO200253774-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 20-DEC-2001; 2001WO-EP015179.
 PF
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Conradt M, Hofmann K;
 PI
 XX WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Disclosure; Page 144; 1345pp; German.
 PS

```
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
      Query Match      41.1%; Score 7.4; DB 1; Length 11;
      Best Local Similarity 88.9%; Pred. No. 3.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 9 CTTTCATCCT 17
      DB 11 CTTTACCCT 3
      RESULT 679
      ABV69063/C
      ID ABV69063 standard; cDNA; 11 BP.
      AC ABV69063;
      XX
      XX 21-OCT-2002 (first entry)
      DE Human skin EST 6849.
      XX
      XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
      KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
      KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
      XX
      XX Homo sapiens.
      OS
      XX WO200253774-A2.
      FN
      XX 11-JUL-2002.
      PD
      XX 20-DEC-2001; 2001WO-EP015179.
      PF
      XX 03-JAN-2001; 2001DE-01000127.
      PR
      XX (HENK ) HENKEL KGAA.
      PA
      XX Petersohn D, Conradt M, Hofmann K;
      PI
      XX WPI; 2002-590638/63.
      DR
      XX In vitro identification of skin-expressed genes, useful for determining
      PT homeostasis and identifying cosmetic or pharmaceutical agents against
      PT e.g. skin cancer.
      XX
      XX Disclosure; Page 215; 1345pp; German.
      XX
      XX The invention relates to in vitro identification (M1) of genes expressed
      CC in the skin of humans or animals by subjecting a mixture of genetically
      CC encoded factors from skin, to serial analysis of gene expression (SAGE)
      CC so as to identify skin-expressed genes and quantify their expression.
      CC (M1) is useful for identifying genes involved in skin homeostasis; to
      CC determine skin homeostasis and to test agent (A) that maintains or
      CC promotes skin homeostasis or that can be used for treating skin
      CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
      CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
      CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
      CC skin. The present sequence is that of a human expressed sequence tag
      CC (EST) of the invention
      XX
      XX SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
      Query Match      41.1%; Score 7.4; DB 1; Length 11;
      Best Local Similarity 88.9%; Pred. No. 3.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 9 CTTTCATCCT 17
      DB 11 CTTTACCCT 3
      RESULT 679
      ABV69063/C
      ID ABV69063 standard; cDNA; 11 BP.
      AC ABV69063;
      XX
      XX 21-OCT-2002 (first entry)
      DE Human skin EST 6849.
      XX
      XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
      KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
      KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
      XX
      XX Homo sapiens.
      OS
      XX WO200253774-A2.
      FN
      XX 11-JUL-2002.
      PD
      XX 20-DEC-2001; 2001WO-EP015179.
      PF
      XX 03-JAN-2001; 2001DE-01000127.
      PR
      XX (HENK ) HENKEL KGAA.
      PA
      XX Petersohn D, Conradt M, Hofmann K;
      PI
      XX WPI; 2002-590638/63.
      DR
      XX In vitro identification of skin-expressed genes, useful for determining
      PT homeostasis and identifying cosmetic or pharmaceutical agents against
      PT e.g. skin cancer.
      XX
      XX Disclosure; Page 215; 1345pp; German.
      XX
      XX The invention relates to in vitro identification (M1) of genes expressed
      CC in the skin of humans or animals by subjecting a mixture of genetically
      CC encoded factors from skin, to serial analysis of gene expression (SAGE)
      CC so as to identify skin-expressed genes and quantify their expression.
      CC (M1) is useful for identifying genes involved in skin homeostasis; to
      CC determine skin homeostasis and to test agent (A) that maintains or
      CC promotes skin homeostasis or that can be used for treating skin
      CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
      CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
      CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
      CC skin. The present sequence is that of a human expressed sequence tag
      CC (EST) of the invention
      XX
      XX SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
      Query Match      41.1%; Score 7.4; DB 1; Length 11;
      Best Local Similarity 88.9%; Pred. No. 3.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 7 GACTTCATC 15
      DB 11 GACTTCAAC 3
      RESULT 680
      ABV62527/C
      ID ABV62527 standard; cDNA; 11 BP.
      AC ABV62527;
      XX
      XX 21-OCT-2002 (first entry)
      DE Human skin EST 313.
      XX
      XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
      KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
      KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
      XX
      XX Homo sapiens.
      OS
      XX WO200253774-A2.
      FN
      XX 11-JUL-2002.
      PD
      XX 20-DEC-2001; 2001WO-EP015179.
      PF
      XX 03-JAN-2001; 2001DE-01000127.
      PR
      XX (HENK ) HENKEL KGAA.
      PA
      XX Petersohn D, Conradt M, Hofmann K;
      PI
      XX WPI; 2002-590638/63.
      DR
      XX In vitro identification of skin-expressed genes, useful for determining
      PT homeostasis and identifying cosmetic or pharmaceutical agents against
      PT e.g. skin cancer.
      XX
      XX Disclosure; Page 34; 1345pp; German.
      XX
      XX The invention relates to in vitro identification (M1) of genes expressed
      CC in the skin of humans or animals by subjecting a mixture of genetically
      CC encoded factors from skin, to serial analysis of gene expression (SAGE)
      CC so as to identify skin-expressed genes and quantify their expression.
      CC (M1) is useful for identifying genes involved in skin homeostasis; to
      CC determine skin homeostasis and to test agent (A) that maintains or
      CC promotes skin homeostasis or that can be used for treating skin
      CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
      CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
      CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
      CC skin. The present sequence is that of a human expressed sequence tag
      CC (EST) of the invention
      XX
      XX SQ Sequence 11 BP; 5 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
      Query Match      41.1%; Score 7.4; DB 1; Length 11;
      Best Local Similarity 88.9%; Pred. No. 3.1e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 9 CTTTCATCCT 17
      DB 11 CTTTCACTT 3
      RESULT 681
```


XX WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
PS Disclosure; Page 193; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 AGCGACTTC 12
Db 9 AGCGACTGC 1
|||||||
RESULT 684
ABV69658
ID ABV69658 standard; cDNA; 11 BP.
XX
AC ABV69658;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7444.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
PS Claim 24; Page 234; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
Db 2 GGCTTCATC 10
|||||||
RESULT 685
ABV70010/C
ID ABV70010 standard; cDNA; 11 BP.
XX
AC ABV70010;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7796.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
PS Claim 24; Page 248; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 6 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;


```

XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 158; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TGAGCGACT 10
Db 3 TGAGCGACT 11
|||||
|||||

RESULT 689
ABV70101
ID ABV70101 standard; cDNA; 11 BP.
XX AC ABV70101;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 7887.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX XX 11-JUL-2002.
XX XX 20-DEC-2001; 2001WO-EP015179.
XX XX 03-JAN-2001; 2001DE-01000127.
XX XX (HENK ) HENKEL KGAA.
XX PA Petersohn D, Conradt M, Hofmann K;
XX PI WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX XX e.g. skin cancer.
XX XX Disclosure; Page 26; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 5 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TTTCATCCT 17
Db 2 TTTCATCCT 10
|||||
|||||

RESULT 690
ABV62237
ID ABV62237 standard; cDNA; 11 BP.
XX AC ABV62237;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 23.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX XX 11-JUL-2002.
XX XX 20-DEC-2001; 2001WO-EP015179.
XX XX 03-JAN-2001; 2001DE-01000127.
XX XX (HENK ) HENKEL KGAA.
XX PA Petersohn D, Conradt M, Hofmann K;
XX PI WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX XX e.g. skin cancer.
XX XX Disclosure; Page 26; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

```

CC rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
 | |||||
 Db 2 GGCTTCATC 10

RESULT 691
 ABV65606/C
 ID ABV65606 standard; cDNA; 11 BP.

XX AC ABV65606;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 3392.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX FN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 119; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 5 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 | |||||
 Db 10 CTTTCATCCT 2

RESULT 692
 ABV62589/C

ID ABV62589 standard; cDNA; 11 BP.

XX AC ABV62589;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 375.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX FN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 36; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 6 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
 | |||||
 Db 11 TTCATCCTT 3

RESULT 693
 ABV64245/C

ID ABV64245 standard; cDNA; 11 BP.

XX AC ABV64245;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 2031.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;

KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
OS Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 81; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTGAGCCGAC 9
Db 9 GTGAGCCAC 1
RESULT 694
ABV68075
ID ABV68075 standard; cDNA; 11 BP.
XX AC ABV68075;
XX 21-OCT-2002 (first entry)
XX Human skin EST 5861.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
OS Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 203; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed

PA (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 187; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
CC Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGCGACTT 11
Db 1 GAGCGACTT 9
RESULT 695
ABV68618/c
ID ABV68618 standard; cDNA; 11 BP.
XX AC ABV68618;
XX 21-OCT-2002 (first entry)
XX Human skin EST 6404.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
OS Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 203; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression (SAGE)
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 10 CGTCATCCT 2
 |||||

RESULT 696
 ABV69016/c
 ID ABV69016 standard; cDNA; 11 BP.

AC ABV69016;

DT 21-OCT-2002 (first entry)

DE Human skin EST 6802.

Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

PN WO200253774-A2.

PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-EP015179.

PR 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

FA Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Disclosure; Page 214; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression (SAGE)
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX

SQ Sequence 11 BP; 2 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
 Db 11 ACTTCATCC 3
 |||||

RESULT 697

ABV65379

ID ABV65379 standard; cDNA; 11 BP.

AC ABV65379;

DT 21-OCT-2002 (first entry)

DE Human skin EST 3165.

Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 immunosuppressive; antinflammatory; cyostatic; SAGE; neurodermatitis;
 psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

PN WO200253774-A2.

PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-EP015179.

PR 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Disclosure; Page 113; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression (SAGE)
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX

SQ Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 1 CTTTCATCCT 9
 |||||

RESULT 698

ABV68327

ID ABV68327 standard; cDNA; 11 BP.

```
XX AC ABV68327;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 6113.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e-g. skin cancer.
XX XX Disclosure; Page 194; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX CC Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX CC Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX Qy 9 CTCATCCT 17
XX Db 2 CTTCGTCT 10
XX RESULT 699
XX ABV69550/c
XX ID ABV69550 standard; cDNA; 11 BP.
XX AC ABV69550;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 7336.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e-g. skin cancer.
XX XX Disclosure; Page 194; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX CC Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX CC Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX Qy 9 CTCATCCT 17
XX Db 2 CTTCGTCT 10
XX RESULT 699
XX ABV69550/c
XX ID ABV69550 standard; cDNA; 11 BP.
XX AC ABV71666;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 9452.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
```

```
PN WO200253774-A2.
PD 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e-g. skin cancer.
XX XX Disclosure; Page 230; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
XX CC Query Match 41.1%; Score 7.4; DB 1; Length 11;
XX CC Best Local Similarity 88.9%; Pred. No. 3.1e+02;
XX CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX Qy 9 CTCATCCT 17
XX Db 10 CTTCCTCCT 2
XX RESULT 700
XX ABV71666/c
XX ID ABV71666 standard; cDNA; 11 BP.
XX AC ABV71666;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 9452.
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
```

XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 305; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGAGCCGAC 9
|||||
DB 9 GTGAGCCAC 1
|||||
RESULT 701
ABV63410/C
ID ABV63410 standard; cDNA; 11 BP.
XX
AC ABV63410;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 1196.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 58; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGAGCCGAC 9
|||||
DB 9 GTGAGCCAC 1
|||||
RESULT 702
ABV64117/C
ID ABV64117 standard; cDNA; 11 BP.
XX
AC ABV64117;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 1903.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 77; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 703
ABV67192
ID ABV67192 standard; cDNA; 11 BP.
XX AC
XX ABV67192;
XX 21-OCT-2002 (first entry)
XX Human skin EST 4978.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Disclosure; Page 162; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX Sequence 11 BP; 2 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 2 ACCTCATCC 10

RESULT 704
ABV72053
ID ABV72053 standard; cDNA; 11 BP.
XX AC
XX ABV72053;
XX 21-OCT-2002 (first entry)
XX

```

```

DE Human skin EST 9839.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK ) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX Claim 24; Page 320; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCA 13
Db 2 GCAACTTCA 10

RESULT 705
ABV69454
ID ABV69454 standard; cDNA; 11 BP.
XX AC
XX ABV69454;
XX 21-OCT-2002 (first entry)
XX Human skin EST 7240.
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.

```



```

XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX
XX Disclosure; Page 227; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e-02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 10 TTCATCCTT 18
Db 3 TTCCTCCTT 11
RESULT 706
ABK83110
ID ABK83110 standard; DNA; 11 BP.
AC ABK83110;
XX
XX 27-AUG-2002 (first entry)
XX
XX DNA binding molecule screening method test sequence #619.
XX
XX DNA binding molecule screening; inhibition of transcription; infection;
XX KW human immunodeficiency virus; HIV; parasite; cancer; cardiovascular;
XX KW respiratory; gastrointestinal; endocrine; metabolic; rheumatic;
XX KW immunological; haematological; neurological; psychiatric; dermatological;
XX KW ophthalmological; musculo-skeletal; urogenital disorder; ss.
XX OS Synthetic.
XX
XX US6384208-B1.
XX
XX 07-MAY-2002.
XX
XX 15-JUL-1999; 99US-00354947.
XX
XX 27-JUN-1991; 91US-00723618.
XX PR 23-DEC-1992; 92US-00996783.
XX PR 17-SEP-1993; 93US-00123936.
XX PR 20-DEC-1993; 93US-00171389.
XX PR 07-JUN-1995; 95US-00482080.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX

```

```

DR WPI; 2002-442819/47.
XX
XX Decreasing transcriptional activity of genes for treating infections or
XX PT cancer, by administration of an agent that binds to two non-overlapping
XX PT regions of the gene.
XX
XX Example 13; SEQ ID NO 619; 98pp; English.
XX
XX The invention relates to a method of decreasing transcriptional activity
XX CC in a duplex deoxyribonucleic acid (DNA) template (T1) comprising
XX CC contacting (T1) with a binding agent comprising at least one small duplex
XX CC DNA-binding molecule (T2) coupled to at least one other small duplex-
XX CC binding molecule that binds to a non-overlapping region of target
XX CC sequence (TS). The method is useful for inhibiting transcription of a
XX CC range of disease-related genes for treating infections (by viruses,
XX CC including human immunodeficiency virus, bacteria, fungi, protozoa and
XX CC parasites), cancer, cardiovascular, respiratory, gastrointestinal,
XX CC endocrine/metabolic, rheumatic/immunological, haematological, musculo-
XX CC neurological, psychiatric, dermatological, ophthalmological,
XX CC skeletal, genetic or urogenital disorders. The method provides sequence-
XX CC specific inhibition of transcription of pathological genes without
XX CC affecting transcription of cellular genes regulated by the same
XX CC transcription factor, and can be applied to regulation of any gene.
XX CC ABK82492-ABK83155 represent DNA binding molecule test sequences used in
XX CC the method of the invention
XX
XX Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e-02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9
RESULT 707
AAD34601/C
ID AAD34601 standard; DNA; 11 BP.
XX
XX AAD34601;
XX
XX 16-JUL-2002 (first entry)
XX
XX Human CYP2C19 gene polymorphic site 1060 detecting antisense A variant.
XX
XX Human; CYP2C19 gene; cytochrome P450 2C19; S-mephenytoin-4'-hydroxylase;
XX KW drug metabolism; diagnosis; detection; xenobiotic; variant; SNP;
XX KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH variation replace(6, G)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX
XX WO200218639-A2.
XX
XX 07-MAR-2002.
XX
XX 28-AUG-2001; 2001WO-IB001552.
XX
XX 30-AUG-2000; 2000GB-00021286.
XX PR (GEMI-) GEMINI GENOMICS PLC.
XX
XX Risinger C, Andersson MK, Lewander T, Oliasson E;
XX
XX WPI; 2002-339661/37.
XX
XX Determining a human's capacity to metabolize a substrate of CYP2C19
XX PT

```

PT enzyme, useful for predicting a subject's likely response to drug or
 PT variations in drug response, comprises detecting polymorphisms within the
 PT region of the CYP2C19 gene.

XX Claim 2; Page 17; 35pp; English.

XX The invention relates to detection of certain polymorphisms in the 5'
 CC regulatory region of the gene encoding cytochrome P450 2C19 (CYP2C19)
 CC also known as S-mephenytoin-4'-hydroxylase. CYP2C19 enzymes are involved
 CC in the metabolism of many different xenobiotics. Human CYP2C19 gene is
 CC located on chromosome 10. The method is useful for predicting variations
 CC in an individual's ability to metabolise certain drugs. This is
 CC particularly useful for diagnosing or predicting an individual's likely
 CC response to drug, which is a CYP2C19 substrate, and in selecting subjects
 CC for clinical trials of such drugs. The present sequence is an antisense
 CC variant used for detecting human CYP2C19 gene 5' flanking region single
 CC nucleotide polymorphism (SNP)

XX Sequence 11 BP; 4 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
 |||||
 Db 10 ACTTATCC 2

RESULT 708

ID AAD34581
 XX AAD34581 standard; DNA; 11 BP.
 AC AAD34581;
 XX 16-JUL-2002 (first entry)
 XX Human CYP2C19 gene 5' flanking region polymorphic site 1060, T variant.
 XX Human; CYP2C19 gene; cytochrome P450 2C19; S-mephenytoin-4'-hydroxylase;
 KW drug metabolism; diagnosis; detection; xenobiotic; enzyme; polymorphism;
 KW chromosome 10; variant; ds.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT variation replace(6, C)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 XX
 XX WO200218639-A2.

XX 07-MAR-2002.

XX 28-AUG-2001; 2001WO-IB001552.

XX 30-AUG-2000; 2000GB-00021286.

XX (GEMINI-) GEMINI GENOMICS PLC.

XX Risinger C, Andersson MK, Lewander T, Oliasson E;

XX WPI; 2002-339661/37.

XX Determining a human's capacity to metabolize a substrate of CYP2C19
 PT enzyme, useful for predicting a subject's likely response to drug or
 PT variations in drug response, comprises detecting polymorphisms within the
 PT region of the CYP2C19 gene.

XX Claim 2; Page 14; 35pp; English.

XX The invention relates to detection of certain polymorphisms in the 5'
 CC regulatory region of the gene encoding cytochrome P450 2C19 (CYP2C19)

CC also known as S-mephenytoin-4'-hydroxylase. CYP2C19 enzymes are involved
 CC in the metabolism of many different xenobiotics. Human CYP2C19 gene is
 CC located on chromosome 10. The method is useful for predicting variations
 CC in an individual's ability to metabolise certain drugs. This is
 CC particularly useful for diagnosing or predicting an individual's likely
 CC response to drug, which is a CYP2C19 substrate, and in selecting subjects
 CC for clinical trials of such drugs. The present sequence is a variant of
 CC human CYP2D6 gene 5' flanking region containing polymorphic site

XX Sequence 11 BP; 3 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
 |||||
 Db 2 ACTTATCC 10

RESULT 709

ACC97178/c
 ID ACC97178 standard; RNA; 11 BP.
 XX
 AC ACC97178;
 XX 28-AUG-2003 (first entry)
 XX Consensus 16S rRNA related ribosomal oligonucleotide SEQ ID NO:189.
 DE 16S rRNA; molecular interaction site; ribosomal RNA; ribozyme;
 KW secondary structure; screening; combinatorial library; drug;
 KW agricultural chemical; industrial chemical; prokaryotic cell growth;
 KW research reagent; detection; naturally occurring molecule; diagnostic;
 KW therapeutic; agricultural; industrial; ss.
 XX Synthetic.
 OS
 XX WO2003018828-A2.
 XX 06-MAR-2003.
 XX 19-AUG-2002; 2002WO-US026212.
 XX 21-AUG-2001; 2001US-0313890P.
 XX (ISIS-) ISIS PHARM INC.
 XX Ecker DJ;
 XX WPI; 2003-312891/30.

XX New polynucleotides comprising molecular interaction sites of 16S rRNA,
 PT useful for virtually or actually screening combinatorial libraries of
 PT compounds, e.g. novel drug or industrial chemicals, that bind to the
 PT polynucleotides.

XX Claim 90; Page 66; 232pp; English.

XX The present invention describes polynucleotides comprising molecular
 CC interaction sites of 16S rRNA that have particular secondary structure.
 CC Also described are compositions comprising the polynucleotides described
 CC above. The polynucleotides are useful for virtually or actually screening
 CC combinatorial libraries of compounds, e.g. novel drug, agricultural
 CC chemicals or industrial chemicals, that bind to the polynucleotides,
 CC which modulates the activity of 16S rRNA to inhibit or stimulate
 CC prokaryotic cell growth. The polynucleotides are also useful as research
 CC reagents to detect, e.g. naturally occurring molecules that bind the
 CC molecular interaction sites, or as decoys to compete with naturally
 CC occurring molecular interaction sites within a cell for research,
 CC diagnostic, therapeutic, agricultural or industrial applications.
 CC ACC96990 to ACC97191 represent oligonucleotide sequences used in the
 CC exemplification of the present invention

```
XX SQ Sequence 11 BP; 2 A; 2 C; 5 G; 0 T; 1 U; 1 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 11 GACGTCNTCC 2

RESULT 710
ADE80649
ID ADE80649 standard; DNA; 11 BP.
XX AC
AC ADE80649;
XX DT
XX 29-JAN-2004 (first entry)
XX DE
XX Duplex oligonucleotide for DNA protein binding assay seq id 619.
XX KW DNA-binding; duplex DNA test oligonucleotide; DNA protein binding;
XX library screening; promoter target; human; ds.
XX OS
XX Unidentified.
XX OS
XX US2003124530-A1.
XX FN
XX 03-JUL-2003.
XX PD
XX 13-NOV-2001; 2001US-00993346.
XX PF
XX 27-JUN-1991; 91US-00723618.
XX PR
XX 23-DEC-1992; 92US-00996783.
XX PR
XX 17-SEP-1993; 93US-00123936.
XX PR
XX 20-DEC-1993; 93US-00171389.
XX PR
XX 07-JUN-1995; 95US-00482080.
XX PR
XX 15-JUL-1999; 99US-00354947.
XX PA
(GENE-) GENELABS TECHNOLOGIES INC.
XX ED
Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX WPI; 2004-031270/03.
XX PT
Screening for sequence-directed DNA-binding molecules comprises adding a
test molecule to a test system composed of a DNA-binding protein and a
duplex DNA test oligonucleotide having adjacent screening and test
sequences.
XX PS
Disclosure; SEQ ID NO 619; 283pp; English.
XX CC
The invention describes a method for screening for molecules capable of
binding to a selected test sequence in a duplex DNA. The above method
comprises: constructing a duplex DNA test oligonucleotide having a
screening sequence adjacent to a selected test sequence, where a DNA-
binding protein is effective to bind to the screening sequence with a
binding affinity that is substantially independent of such test sequence,
but where DNA protein binding to the screening sequence is sensitive to
binding of test molecules to such test sequence; adding a test molecule
to be screened to a test system composed of the DNA-binding protein and
the duplex DNA test oligonucleotide having the screening and test
sequences adjacent one another; incubating the molecule in the test
system for a period sufficient to permit binding of the molecule being
tested to the test sequence in the duplex DNA; and comparing the amount
of binding protein bound to the duplex DNA before and after the adding.
The method is useful in screening libraries of synthetic or biological
compounds for their ability to bind DNA test sequences. The method may
also be used in characterizing the preferred binding sequences of any
selected DNA-binding molecule. This sequence represents a test sequence
corresponding to a promoter target of a human gene.
XX
```

```
SQ Sequence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

RESULT 711
AAA81052
ID AAA81052 standard; DNA; 8 BP.
XX AC
AC AAA81052;
XX DT
XX 24-NOV-2000 (first entry)
XX DE
XX A. thaliana primer walking octamer SEQ ID NO: 365.
XX KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX OS
XX Arabidopsis thaliana.
XX FN
XX US6083695-A.
XX PD
XX 04-JUL-2000.
XX PF
XX 21-MAY-1997; 97US-00859954.
XX PR
XX 15-APR-1996; 96US-00632782.
XX PA
(UYHO-) UNIV HOUSTON.
XX (HARD/) HARDIN S H.
XX PI
Hardin PE, Hardin SH, Homayouni R;
XX WPI; 2000-474852/41.
XX PT
Sequencing an unknown DNA molecule for the polymerase chain reaction and
other primer processes comprises primer walking of octamer
oligonucleotides.
XX PS
Example 8; Col 209-210; 161pp; English.
XX CC
This invention describes a novel method for sequencing an unknown DNA
molecule which comprises selecting a library primer from an octamer
oligonucleotide library consisting of 48 8-bp sequences and corresponding
complementary sequences, where the library primer is complementary to a
known sequence adjacent to the unknown sequence or is complementary to a
sequence in a known extension product. The method is useful for DNA
nucleotide sequencing, in PCR, and in other processes which make use of
primers. The octamers are used to identify coding sequences. Primer
walking using the octamer libraries is advantageous over other sequencing
methods because it does not require multiple cloning steps nor subsequent
template preparations, and it is a directed and methodical approach.
XX CC
AAA80688-A81253 represent the octamer primers used in the primer walking
method of the invention
XX SQ Sequence 8 BP; 1 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 2 CATCCTT 8

RESULT 712
AAA80772
```

```

ID  AAA80772 standard; DNA; 8 BP.
XX  AC
XX  AAA80772;
XX  DT 24-NOV-2000 (first entry)
XX  DE A. thaliana primer walking octamer SEQ ID NO: 85.
XX  KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX  OS Arabidopsis thaliana.
XX  PN US6083695-A.
XX  PD 04-JUL-2000.
XX  PF 21-MAY-1997; 97US-00859954.
XX  PR 15-APR-1996; 96US-00632782.
XX  PA (UYHO-) UNIV HOUSTON.
XX  PI (HARD/) HARDIN S H.
XX  PI Hardin PE, Hardin SH, Homayouni R;
XX  DR WPI; 2000-474852/41.
XX  PD Sequencing an unknown DNA molecule for the polymerase chain reaction and
XX  PF other primer processes comprises primer walking of octamer
XX  PR oligonucleotides.
XX  PR Example 8; Col 67-68; 161pp; English.
XX  CC This invention describes a novel method for sequencing an unknown DNA
XX  CC molecule which comprises selecting a library primer from an octamer
XX  CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
XX  CC complementary sequences, where the library primer is complementary to a
XX  CC known sequence adjacent to the unknown sequence or is complementary to a
XX  CC sequence in a known extension product. The method is useful for DNA
XX  CC nucleotide sequencing, in PCR, and in other processes which make use of
XX  CC primers. The octamers are used to identify coding sequences. Primer
XX  CC walking using the octamer libraries is advantageous over other sequencing
XX  CC methods because it does not require multiple cloning steps nor subsequent
XX  CC template preparations, and it is a directed and methodical approach.
XX  CC AAA80688-A81253 represent the octamer primers used in the primer walking
XX  CC method of the invention
XX  SQ Sequence 8 BP; 1 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
XX  Query Match 38.9%; Score 7; DB 1; Length 8;
XX  Best Local Similarity 100.0%; Pred. No. 2.4e+03;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 CTTTCATC 15
Db 2 CTTTCATC 8

RESULT 713
AAA80798
ID AAA80798 standard; DNA; 8 BP.
XX AC
XX AAA80798;
XX DT 24-NOV-2000 (first entry)
XX DE A. thaliana primer walking octamer SEQ ID NO: 111.
XX KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX OS Arabidopsis thaliana.
XX PN US6083695-A.

```

```

XX 04-JUL-2000.
XX PD
XX PF 21-MAY-1997; 97US-00859954.
XX PR 15-APR-1996; 96US-00632782.
XX PA (UYHO-) UNIV HOUSTON.
XX PI (HARD/) HARDIN S H.
XX PI Hardin PE, Hardin SH, Homayouni R;
XX DR WPI; 2000-474852/41.
XX PD Sequencing an unknown DNA molecule for the polymerase chain reaction and
XX PF other primer processes comprises primer walking of octamer
XX PR oligonucleotides.
XX PR Example 8; Col 81-82; 161pp; English.
XX  CC This invention describes a novel method for sequencing an unknown DNA
XX  CC molecule which comprises selecting a library primer from an octamer
XX  CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
XX  CC complementary sequences, where the library primer is complementary to a
XX  CC known sequence adjacent to the unknown sequence or is complementary to a
XX  CC sequence in a known extension product. The method is useful for DNA
XX  CC nucleotide sequencing, in PCR, and in other processes which make use of
XX  CC primers. The octamers are used to identify coding sequences. Primer
XX  CC walking using the octamer libraries is advantageous over other sequencing
XX  CC methods because it does not require multiple cloning steps nor subsequent
XX  CC template preparations, and it is a directed and methodical approach.
XX  CC AAA80688-A81253 represent the octamer primers used in the primer walking
XX  CC method of the invention
XX  SQ Sequence 8 BP; 1 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
XX  Query Match 38.9%; Score 7; DB 1; Length 8;
XX  Best Local Similarity 100.0%; Pred. No. 2.4e+03;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 CATCCTT 18
Db 2 CATCCTT 8

RESULT 714
AAA28773/c
ID AAA28773 standard; DNA; 9 BP.
XX AC
XX AAA28773;
XX DT 04-SEP-2000 (first entry)
XX DE Tethered probe CF13M for V520F CFTR gene detection.
XX KW Cystic fibrosis; CFTR; mutation; Q493X; nucleic acid analysis; DNA array;
XX KW DNA chip; probe; ss.
XX OS Homo sapiens.
XX FH Key modified_base 1 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "derivatized to carry a primary amino group which
XX FT covalently binds to epoxysilanized glass"
XX PN WO200026412-A1.
XX PD 11-MAY-2000.
XX PF 02-NOV-1999; 99WO-US025693.
XX PR 02-NOV-1998; 98US-0106655P.

```

```

XX PA (BEAT/) BEATTIE K L.
XX PA (RODR/) MALDONADO RODRIGUEZ R.
XX PI Beattie KL, Maldonado Rodriguez R;
XX DR WPI; 2000-365647/31.
XX DR WPI; 2000-365647/31.
XX PT Analyzing nucleic acids, used to analyze genomic variations and gene
XX PT expression levels, comprises mixing heat-denatured nucleic acid with a
XX PT labeled probe and a surface tethered capture probe.
XX PS Example 1; Page 42; 129pp; English.
XX CC Each of four possible cystic fibrosis (CF) mutations in a 138 bp target
XX CC (see AAB28762) amplified from exon 10 of the CFTR gene were represented
XX CC on a glass slide by a pair of probes, one complementary to the wild-type
XX CC allele and the other complementary to the mutant allele. Auxiliary
XX CC oligonucleotides were designed to produce a partially duplex structure
XX CC across the target fragment. The target molecules were hybridized to
XX CC oligonucleotide probe arrays tethered to the glass slides. The mutation
XX CC was detected using a novel method of nucleic acid analysis. The method
XX CC comprises mixing a heat-denatured nucleic acid sample with a molar excess
XX CC of at least one labeled oligonucleotide probe, hybridizing the mixture to
XX CC an array of oligonucleotide capture probes, surface-tethered to a solid
XX CC phase support, and analyzing the binding pattern on the support. The
XX CC length and sequence of the labeled probe is selected to anneal a unique
XX CC position in a target nucleic acid. The capture probes bind to the target
XX CC nucleic acid in tandem with the labeled probe. The hybridization
XX CC conditions are selected so that the capture probe can only bind to the
XX CC target strand when hybridized in tandem with the labeled probe, forming a
XX CC stable, contiguously stacked labeled probe/capture probe duplex structure
XX CC with no base mismatches, at, or near the junction of the two probes. The
XX CC method can be used for directly analyzing sequence variations between two
XX CC or more samples of genomic DNA by acquiring a quantitative hybridization
XX CC pattern for the DNA and comparing the patterns. The patterns can be used
XX CC to analyze gene expression at the transcription level in different
XX CC cellular samples
XX SQ Sequence 9 BP; 3 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 715
AAF91646
ID AAF91646 standard; DNA; 9 BP.
XX AC AAF91646;
XX XX
DT 10-MAY-2001 (first entry)
XX DE Breast-cancer associated protein isoform BPI-48 preferred probe #1.
XX KW Human; breast cancer; breast cancer associated protein isoform; BPI;
XX KW breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
XX OS Homo sapiens.
XX XX
XX FN WO200113117-A2.
XX XX
XX PD 22-FEB-2001.
XX XX
XX PF 14-AUG-2000; 2000WO-GB003143.
XX XX
XX PR 13-AUG-1999; 99GB-00019258.
XX PR 30-MAR-2000; 2000GB-00007754.

XX PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX PA Herath HMC;
XX PI WPI; 2001-211252/21.
XX DR
XX PT Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
XX PT of serum or plasma by two dimensional electrophoresis to detect the
XX PT presence or level of a breast cancer-associated feature.
XX PS Claim 138; Page 41; 146pp; English.
XX CC The present invention describes a method for the screening, diagnosis or
XX CC prognosis of breast cancer (BC), determining the stage or severity of BC,
XX CC and monitoring the effect of therapy administered to a subject having BC,
XX CC comprising analysing a sample of body fluid by two dimensional
XX CC electrophoresis to generate a two-dimensional array of features,
XX CC comprising a chosen feature whose abundance correlates with BC or
XX CC predicts the onset or course of BC. The method (I) involves: (a)
XX CC analysing a sample of body fluid from the subject by two-dimensional
XX CC electrophoresis to generate a two-dimensional array of features,
XX CC comprising a chosen feature whose relative abundance correlates with BC
XX CC or predicts the onset of BC; and (b) comparing the abundance of each
XX CC chosen feature in the sample with the abundance of that chosen feature in
XX CC the body fluid from one or more persons free from BC, or with a
XX CC previously determined reference range for that feature in subjects free
XX CC from BC, or with the abundance of an expression reference feature (ERF)
XX CC in the test sample. The method is useful for screening, diagnosis or
XX CC prognosis of breast cancer, determining the stage or severity of BC,
XX CC monitoring the effect of therapy administered to a subject having BC, and
XX CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
XX CC represents breast cancer associated protein isoform (BPI) peptide
XX CC sequences, and AAF91643 to AAF91848 represent BPI probes used in the
XX CC exemplification of the present invention
XX SQ Sequence 9 BP; 2 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12
Db 3 CGACTTC 9

RESULT 716
AAD21036/c
ID AAD21036 standard; DNA; 9 BP.
XX AC AAD21036;
XX XX
DT 15-JAN-2002 (first entry)
XX DE Human CFTR gene exon 10 fragment mutation detecting CF13M probe.
XX KW Human; CFTR; sequence-targeted tandem hybridisation; gene expression;
XX KW detection; genetic complexity; probe; ss.
XX OS Homo sapiens.
XX XX
XX FN modified_base 1
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Guanosine is derivatised to a primary amino group
XX FT which covalently binds to epoxysilicised glass"
XX XX
XX PN US6268147-B1.
XX XX
XX PD 31-JUL-2001.
XX XX

```

```

PF 02-NOV-1999; 99US-004332020.
PR
XX
PR 02-NOV-1998; 98US-0106555P.
XX
XX (BEATTIE) BEATTIE K L.
PA (RODRIGUEZ) RODRIGUEZ R M.
XX
XX Beattie KL, Rodriguez RM;
XX
XX WPI; 2001-647055/74.
DR
XX
XX Analyzing nucleic acid samples of high genetic complexity, comprises
PT employing sequence-targeted tandem hybridization, in which
PT oligonucleotides are preannealed to target nucleic acid to form duplex
PT target molecule.
XX
XX Example 1; Col 21; 50pp; English.
PS
XX The invention relates to a method for analysing nucleic acids samples.
CC The method comprises employing a sequence-targeted tandem hybridisation,
CC where oligonucleotides that are preannealed to the single-stranded target
CC nucleic acid form a partially duplex target molecule. The methods are
CC useful for analysing nucleic acid samples of high genetic complexity, for
CC profiling gene expression using numerous oligonucleotide probes targetted
CC to mRNA species. The method provides an efficient identification of
CC species, strains and individuals using DNA probe arrays designed to
CC hybridise with numerous unique nucleotide sequences. The method directly
CC analyses nucleic acid samples without the use of additional steps of
CC target sequence amplification, single strand isolation and labelling. The
CC present sequence is a probe used for detecting mutation in human CFTR
CC gene exon 10 fragment used in the exemplification of the invention
XX
XX Sequence 9 BP; 3 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 717
ABQ72179/C
ID ABQ72179 standard; DNA; 9 BP.
XX
XX AC ABQ72179;
XX
XX DT 28-AUG-2002 (first entry)
XX
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:2477.
XX
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FN WO200242459-A2.
XX
XX PD 30-MAY-2002.
XX
XX PF 20-NOV-2001; 2001WO-US043438.
XX
XX PR 20-NOV-2000; 2000US-00716637.
XX
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX PI Liu Q;
XX
XX DR WPI; 2002-500284/53.
XX
XX PT New zinc finger protein that binds to target site, useful in studying
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 63; 81pp; English.

PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 63; 81pp; English.
PS
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (W) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutic methods to
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
XX invention
XX
XX Sequence 9 BP; 3 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
Db 9 TTCATCC 3

RESULT 718
ABQ72174/C
ID ABQ72174 standard; DNA; 9 BP.
XX
XX AC ABQ72174;
XX
XX DT 28-AUG-2002 (first entry)
XX
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:2472.
XX
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FN WO200242459-A2.
XX
XX PD 30-MAY-2002.
XX
XX PF 20-NOV-2001; 2001WO-US043438.
XX
XX PR 20-NOV-2000; 2000US-00716637.
XX
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX PI Liu Q;
XX
XX DR WPI; 2002-500284/53.
XX
XX PT New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 63; 81pp; English.

```

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (i); (2) a polynucleotide (III) encoding (i) or (ii); and
 CC (3) designing (M) (i) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (i), (ii) or (iii) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 XX
 CC Sequence 9 BP; 3 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 TTCATCC 16
 Db 9 TTCATCC 3
 RESULT 719
 AAD44140/c
 ID AAD44140 standard; DNA; 9 BP.
 AC AAD44140;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE PCR primer #5 designed to bind human MMP PPR region.
 XX
 KW Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;
 KW propeptide region; PPR; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6277571-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 30-SEP-1998; 98US-00163485.
 XX
 PR 03-OCT-1997; 97US-00943162.
 PR 03-OCT-1997; 97US-0108152P.
 XX
 PA (UUVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 XX
 PI Fillmore H, Broadus W, Gillies G;
 XX
 DR WPI; 2002-412824/44.
 XX
 PT Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.
 XX
 PS Example; Col 12; 19pp; English.
 XX
 CC The invention relates to a method of sequential consensus region-directed

CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is a PCR
 CC primer designed to bind to human matrix metalloproteinase (MMP)
 CC propeptide region (PPR). This primer is used to illustrate the method of
 CC the invention
 XX
 SQ Sequence 9 BP; 4 A; 0 C; 4 G; 0 T; 0 U; 1 Other;
 Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.1e+03;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 CTCATCCT 17
 Db 9 TTCATCCT 1
 RESULT 720
 ADA64501/c
 ID ADA64501 standard; DNA; 9 BP.
 AC ADA64501;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Zinc finger target sequence DNA #959.
 XX
 KW ds; target sequence; zinc finger protein;
 KW multi-finger zinc finger protein; improved affinity;
 KW improved specificity; enhanced biological activity.
 XX
 OS Synthetic.
 XX
 PN US2003068675-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 20-NOV-2001; 2001US-00990186.
 XX
 PR 24-MAR-1999; 99US-0126238P.
 PR 24-MAR-1999; 99US-0126239P.
 PR 30-JUL-1999; 99US-0146595P.
 PR 30-JUL-1999; 99US-0146615P.
 PR 23-MAR-2000; 2000US-00535008.
 PR 20-NOV-2000; 2000US-00716837.
 XX
 PA (LIUQ/) LIU Q.
 XX
 PI Liu Q;
 XX
 DR WPI; 2003-567233/53.
 XX
 PT Designing zinc finger protein that has three zinc fingers from N-terminus
 PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
 PT site, by selecting zinc fingers that bind their respective subsites.
 XX
 PS Disclosure; Page 27; 34pp; English.
 XX
 CC The invention relates to a method of designing a zinc finger protein. The
 CC method is useful for designing a zinc finger protein. The method provides
 CC multi-finger zinc finger proteins with improved affinity and specificity
 CC for their target sequences, as well as enhanced biological activity. The
 CC present sequence represents a zinc finger protein DNA target sequence.
 XX
 SQ Sequence 9 BP; 3 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      10  TTCATCC 16
      |||||
Db      9  TTCATCC 3

RESULT 721
ADA64506/C
ID  ADA64506 standard; DNA; 9 BP.
XX
XX  ADA64506;
AC
XX
XX  20-NOV-2003 (first entry)
XX
XX  Zinc finger target sequence DNA #964.
XX
XX  ds; target sequence; zinc finger protein;
KW  multi-finger zinc finger protein; improved affinity;
KW  improved specificity; enhanced biological activity.
XX
XX  Synthetic.
XX
XX  US2003068675-A1.
XX
XX  10-APR-2003.
XX
XX  20-NOV-2001; 2001US-00990186.
XX
XX  24-MAR-1999; 99US-0126238P.
XX  24-MAR-1999; 99US-0126239P.
PR  30-JUL-1999; 99US-0146595P.
PR  30-JUL-1999; 99US-0146615P.
PR  23-MAR-2000; 2000US-00535008.
PR  20-NOV-2000; 2000US-00716637.
XX
XX  (LIUQ)/ LIU Q.
XX
XX  Liu Q;
PI
XX  WPI; 2003-567233/53.
XX
XX  Designing zinc finger protein that has three zinc fingers from N-terminus
PT  and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT  site, by selecting zinc fingers that bind their respective subsites.
XX
XX  Disclosure; Page 27; 34pp; English.
XX
XX  The invention relates to a method of designing a zinc finger protein. The
CC  method is useful for designing a zinc finger protein. The method provides
CC  multi-finger zinc finger proteins with improved affinity and specificity
CC  for their target sequences, as well as enhanced biological activity. The
CC  present sequence represents a zinc finger protein DNA target sequence.
XX
XX  Sequence 9 BP; 3 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
SQ

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10  TTCATCC 16
      |||||
Db      9  TTCATCC 3

RESULT 722
AAQ88357/C
ID  AAQ88357 standard; DNA; 10 BP.
XX
XX  AAQ88357;
AC
XX
XX  18-DEC-1995 (first entry)
XX
XX  Set of probes for CFTR gene analysis.
DE
XX
XX  WO9531574-A1.

KW  Tiling strategy; immobilised nucleic acid probe array; CFTR gene;
KW  cystic fibrosis transmembrane conductance regulator; hybridisation;
KW  biological chip; interrogation position; ss.
XX
XX  Synthetic.
XX
XX  Key      Location/Qualifiers
FT  misc_difference 4
FT  /*tag= a
FT  /note= "N is A, T, C or G, i.e. the sequence represents a
FT  set of 4 probes"
XX
XX  WO9511995-A1.
XX
XX  04-MAY-1995.
XX
XX  26-OCT-1994; 94WO-US012305.
XX
XX  26-OCT-1993; 93US-00143312.
PR  02-AUG-1994; 94US-00284064.
XX
XX  (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX  Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
PI  Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX  WPI; 1995-178887/23.
XX
XX  New arrays of oligo:nucleotide probes - used for comparing known
PT  sequences with variants for detection of mutation(s) and sequencing.
XX
XX  Claim 87; Page 154; 223pp; English.
XX
XX  An array of oligonucleotide probes immobilised on a solid support (a
CC  chip) comprises a set of probes chosen from sequences AAQ88353-Q88360.
CC  Each probe comprises a segment of at least 3 nucleotides exactly
CC  complementary to a subsequence of the CFTR gene, the segment including at
CC  least one interrogation position complementary to a corresp. nucleotide
CC  in the CFTR gene. The array also comprises three more probe sets which
CC  each have sequences identical to the first set except at the
CC  interrogation position. A target sequence can be analysed by determining
CC  the extent of hybridisation at particular probes in the array
XX
XX  Sequence 10 BP; 4 A; 1 C; 2 G; 2 T; 0 U; 1 Other;
SQ

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11  TCATCCTT 18
      |||||
Db      9  TCATCCTT 2

RESULT 723
AAT29354
ID  AAT29354 standard; DNA; 10 BP.
XX
XX  AAT29354;
AC
XX
XX  25-MAR-2003 (revised)
DT  28-JUN-1996 (first entry)
XX
XX  5'-primer for mammalian G-protein coupled receptor coding sequences.
DE
XX  5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
KW  characterisation; biological samples; PCR amplification; indexing;
KW  identification; cloning; analysis; genes; genome mapping;
KW  disease diagnosis; ss.
XX
XX  Synthetic.
OS
XX  WO9531574-A1.
PN

```



```

XX 23-NOV-1995.
XX PD
XX XX
XX 12-MAY-1995; 95WO-US006032.
XX PF
XX 16-MAY-1994; 94US-00242887.
XX PR
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX PA
XX Lopeznieto CE, Nigam SK;
XX PI
XX WPI; 1996-010958/01.
XX DR
XX Characterisation of nucleotide sequences using primer pairs - by PCR
XX PT amplification and indexing of amplification prods. w.r.t. primers used
XX PT for genome mapping and disease diagnosis.
XX FS
XX Claim 46; Page 55; 72pp; English.
XX CC
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived
XX CC from them, which target mammalian G-protein coupled receptor coding
XX CC sequences, together comprise a PCR primer kit. The kit is used in a new
XX CC method for the characterisation of nucleic acid sequences obtd. from
XX CC mammalian biological samples, which comprises PCR amplification and
XX CC indexing of the prods. w.r.t the primer pair that hybridised to its
XX CC delineating subsequences. The method may be used in the identification,
XX CC cloning and analysis of genes, e.g. in genome mapping, and disease
XX CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)
XX SQ
XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 11 TCATCCT 17
Db 1 TCATCCT 7

```

RESULT 724

```

AAZ77697
ID AAZ77697 standard; DNA; 10 BP.
AC
AC AAZ77697;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:125.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX OS
XX Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX PR
XX 19-JUN-1998; 98US-0089844P.
XX PR
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089878P.
XX PR
XX 19-JUN-1998; 98US-0089991P.
XX PR
XX 19-JUN-1998; 98US-0089992P.
XX PR
XX 19-JUN-1998; 98US-0089993P.
XX PR
XX 19-JUN-1998; 98US-0089994P.
XX PR
XX 19-JUN-1998; 98US-0089997P.
XX PR
XX 19-JUN-1998; 98US-0089999P.
XX PR

```

```

PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090003P.
PR 19-JUN-1998; 98US-00900036P.
PR 19-JUN-1998; 98US-00900039P.
PR 19-JUN-1998; 98US-00900040P.
PR 19-JUN-1998; 98US-00900041P.
PR 19-JUN-1998; 98US-00900042P.
PR 19-JUN-1998; 98US-00900043P.
PR 19-JUN-1998; 98US-00900044P.
PR 19-JUN-1998; 98US-00900045P.
PR 19-JUN-1998; 98US-00900047P.
PR 19-JUN-1998; 98US-00900048P.
PR 19-JUN-1998; 98US-00900072P.
PR 19-JUN-1998; 98US-00900076P.
PR 19-JUN-1998; 98US-00900077P.
PR 19-JUN-1998; 98US-00900078P.
PR 19-JUN-1998; 98US-00900079P.
PR 19-JUN-1998; 98US-00900080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX PI
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 67; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX CC expression) tags used to identify mRNA transcripts encoding or
XX CC immunostimulatory cofactor proteins which are preferentially or
XX CC differentially expressed in monocyte-derived dendritic cells compared
XX CC with monocytes. Some of the transcripts correspond to known genes or ESTs
XX CC (expressed sequence tags) which were previously unknown to be
XX CC preferentially or differentially expressed in dendritic cells, while
XX CC other transcripts correspond to novel genes. Antigen-presenting cell
XX CC (APC)-associated costimulatory factors play an important role in the
XX CC activation of the cytotoxic immune response, particularly against tumour
XX CC cells. Tumour antigen presentation via the MHC (major histocompatibility
XX CC complex) and subsequent recognition by T-cell receptors is alone
XX CC insufficient to activate a robust cytotoxic immune response that can lyse
XX CC the tumour cells, immunostimulatory cofactors also being required for
XX CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX CC sequences identified using the SAGE tags have several potential uses.
XX CC They may be used in vaccines to induce an immune response, particularly
XX CC against a tumour antigen; to modulate the genotype of an APC; to screen
XX CC for agents that modulate expression of differentially expressed genes in
XX CC an APC; and as hybridisation probes/amplification primers for the
XX CC diagnosis, prognosis and monitoring of diseases related to abnormal
XX CC expression of these genes. Detection of the dendritic cell differentially
XX CC expressed genes, or of their encoded proteins, can be used to identify
XX CC cells as belonging to the monocyte lineage. Cells containing these genes
XX CC can be used in active immunotherapy (or to stimulate production of a
XX CC population of antigen-specific effector cells) and vectors containing
XX CC them are used in gene therapy. Co-administration of tumour antigens and
XX CC APC-associated costimulatory factors ensures adequate antigen
XX CC presentation to endogenous APCs and upregulates the APCs for the
XX CC presentation of co-stimulatory signals, migration to T cell-rich sites,
XX CC secretion of T cell growth factors and secretion of chemokines for
XX CC recruitment of immune effector cells
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 12 CATCCTT 18

```

```

Db      |||||
        3 CATCCTT 9

RESULT 725
AAZ79520/c
ID      AAZ79520 standard; DNA; 10 BP.
XX
AC      AAZ79520;
XX
DT      10-APR-2000 (first entry)
XX
DE      Human dendritic cell SAGE tag, SEQ ID NO:1948.
XX
XX      SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW      APC; monocyte-derived dendritic cell; differential gene expression;
KW      immunostimulatory cofactor; costimulatory factor; CTL;
KW      cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS      Homo sapiens.
XX
PN      WO9965924-A2.
XX
XX      23-DEC-1999.
XX
XX      18-JUN-1999; 99WO-US013800.
XX
PR      19-JUN-1998; 98US-0089833P.
PR      19-JUN-1998; 98US-0089844P.
PR      19-JUN-1998; 98US-0089853P.
PR      19-JUN-1998; 98US-0089878P.
PR      19-JUN-1998; 98US-008991P.
PR      19-JUN-1998; 98US-008992P.
PR      19-JUN-1998; 98US-008993P.
PR      19-JUN-1998; 98US-008994P.
PR      19-JUN-1998; 98US-008997P.
PR      19-JUN-1998; 98US-008999P.
PR      19-JUN-1998; 98US-009000P.
PR      19-JUN-1998; 98US-009003P.
PR      19-JUN-1998; 98US-0090036P.
PR      19-JUN-1998; 98US-0090039P.
PR      19-JUN-1998; 98US-0090040P.
PR      19-JUN-1998; 98US-0090041P.
PR      19-JUN-1998; 98US-0090042P.
PR      19-JUN-1998; 98US-0090043P.
PR      19-JUN-1998; 98US-0090044P.
PR      19-JUN-1998; 98US-0090045P.
PR      19-JUN-1998; 98US-0090047P.
PR      19-JUN-1998; 98US-0090048P.
PR      19-JUN-1998; 98US-0090072P.
PR      19-JUN-1998; 98US-0090076P.
PR      19-JUN-1998; 98US-0090077P.
PR      19-JUN-1998; 98US-0090078P.
PR      19-JUN-1998; 98US-0090079P.
PR      19-JUN-1998; 98US-0090080P.
PR      08-DEC-1998; 98US-0111715P.
XX
XX      (GENZ ) GENZYME CORP.
PA      (ROBE/) ROBERTS B L.
PA      (SHAN/) SHANKARA S.
XX
XX      Roberts BL, Shankara S;
XX
XX      WPI; 2000-106077/09.
XX
XX      Isolated polynucleotides differentially expressed in antigen-presenting
XX      cells, useful in gene vaccines against cancer.
XX
XX      Claim 1; Page 120; 130pp; English.
XX
XX      Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
XX      expression) tags used to identify mRNA transcripts encoding
XX      immunostimulatory cofactor proteins which are preferentially or

```

differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 Db 10 CATCCTT 4
 |||||

RESULT 726
 AAZ77689/c
 ID AAZ77689 standard; DNA; 10 BP.
 XX
 AC AAZ77689;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:117.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 XX
 XX 23-DEC-1999.
 XX
 XX 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-008991P.
 PR 19-JUN-1998; 98US-008992P.
 PR 19-JUN-1998; 98US-008993P.
 PR 19-JUN-1998; 98US-008994P.
 PR 19-JUN-1998; 98US-008997P.

PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.

(GENZ) GENZYME CORP.
 (ROBE/) ROBERTS B L.
 (SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 67; 130pp; English.

Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CGACTTC 12
 Db |||||
 7 CGACTTC 1

RESULT 727

AAZ78497/C
 ID AAZ78497 standard; DNA; 10 BP.

XX AC
 XX AAZ78497;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:925.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089991P.

XX PR 19-JUN-1998; 98US-0089992P.

XX PR 19-JUN-1998; 98US-0089993P.

XX PR 19-JUN-1998; 98US-0089994P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0089999P.

XX PR 19-JUN-1998; 98US-0090000P.

XX PR 19-JUN-1998; 98US-0090035P.

XX PR 19-JUN-1998; 98US-0090036P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PR 19-JUN-1998; 98US-0090042P.

XX PR 19-JUN-1998; 98US-0090043P.

XX PR 19-JUN-1998; 98US-0090044P.

XX PR 19-JUN-1998; 98US-0090045P.

XX PR 19-JUN-1998; 98US-0090047P.

XX PR 19-JUN-1998; 98US-0090048P.

XX PR 19-JUN-1998; 98US-0090072P.

XX PR 19-JUN-1998; 98US-0090076P.

XX PR 19-JUN-1998; 98US-0090077P.

XX PR 19-JUN-1998; 98US-0090078P.

XX PR 19-JUN-1998; 98US-0090079P.

XX PR 19-JUN-1998; 98US-0090080P.

XX 08-DEC-1998; 98US-0111715P.

(GENZ) GENZYME CORP.

(ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 92; 130pp; English.

Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding

CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 XX Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 Db 7 CATCCTT 1

RESULT 728

AAZ78928/C
 ID AAZ78928 standard; DNA; 10 BP.

XX AC AAZ78928;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:1356.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN W09965924-A2.

XX FD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089991P.

XX PR 19-JUN-1998; 98US-0089992P.

XX PR 19-JUN-1998; 98US-0089993P.

XX PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.

PT Isolated polynucleotides differentially expressed in antigen-presenting
 cells, useful in gene vaccines against cancer.

PS Claim 1; Page 104; 130pp; English.

XX Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 XX Sequence 10 BP; 4 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATC 15
| | | | |
Db 10 CTTTCATC 4

RESULT 729
AAZ85072
ID AAZ85072 standard; DNA; 10 BP.
XX
AC AAZ85072;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4306.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX
Claim 1; Page 174; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

RESULT 730
AAZ84663/c
ID AAZ84663 standard; DNA; 10 BP.
XX
AC AAZ84663;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3897.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX
Claim 1; Page 162; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

```

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GACTTCA 13
   |||||
Db 8 GACTTCA 2

RESULT 731
ID AAZ82467 standard; DNA; 10 BP.
XX
AC AAZ82467;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1701.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
FA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 104; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GACTTCA 13
   |||||
Db 8 GACTTCA 2

RESULT 732
ID AAZ83044 standard; DNA; 10 BP.
XX
AC AAZ83044;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2278.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
FA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 120; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
```

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7

Db 4 GTGAGCG 10

RESULT 733

AAZ86171/c
 ID AAZ86171 standard; DNA; 10 BP.

XX AAZ86171;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5405.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 202; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17

Db 10 TCATCCT 4

RESULT 734

AAZ82672/c
 ID AAZ82672 standard; DNA; 10 BP.

XX AAZ82672;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #1906.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
 XX treatment of cancer.

XX Claim 1; Page 110; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
|||||||
Db 7 TCATCCT 1

RESULT 735
AAZ82301/C
ID AAZ82301 standard; DNA; 10 BP.

XX AC AAZ82301;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #1535.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX FN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX PS Claim 1; Page 99; 219pp; English.

XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences).

CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
|||||||
Db 7 TTCATCC 1

RESULT 736
AAZ83912/C
ID AAZ83912 standard; DNA; 10 BP.

XX AC AAZ83912;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #3146.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.

XX OS Homo sapiens.

XX FN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.

XX PS Claim 1; Page 143; 219pp; English.

XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
 |||||
 Db 9 GTGAGCG 3

RESULT 737
 AAZ84299/C
 ID AAZ84299 standard; DNA; 10 BP.

XX AC AAZ84299;

XX AC AAZ84299;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #3533.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and

XX treatment of cancer.

XX Claim 1; Page 153; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

XX that are preferentially transcribed in the metastatic breast tumour

XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX

SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12

|||||

Db 7 CGACTTC 1

RESULT 738

AAZ85672/C

ID AAZ85672 standard; DNA; 10 BP.

XX AC AAZ85672;

XX AC AAZ85672;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4906.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

XX (ROBE/) ROBERTS B L.

XX (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and

XX treatment of cancer.

XX Claim 1; Page 189; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

XX that are preferentially transcribed in the metastatic breast tumour

XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

XX to AAZ86677 represent tags corresponding to distinct transcripts that are

XX preferentially transcribed in the primary or non-metastatic breast tumour

XX tissue (i.e. are downregulated in metastatic breast tumour cells). These

XX transcripts can be used for diagnosis, prognosis, monitoring and

XX treatment of breast cancer, particularly where metastatic. Diagnosis is

XX by standard immunoassays or hybridisation/amplification reactions.

CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 Db 8 CATCCTT 2
 |||||

RESULT 739

AAZ81332
 ID AAZ81332 standard; DNA; 10 BP.

XX AC AAZ81332;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #566.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX Claim 1; Page 73; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

XX SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGACTT 11
 Db 1 GCGACTT 7
 |||||

RESULT 740

AAZ85381

ID AAZ85381 standard; DNA; 10 BP.

XX AC AAZ85381;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #4615.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX Claim 1; Page 182; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour

CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
 |||||
 Db 1 GACTTCA 7

RESULT 741
 AAZ82094/C
 ID AAZ82094 standard; DNA; 10 BP.

AC AAZ82094;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1328.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and

XX treatment of cancer.

XX Claim 1; Page 94; 219pp; English.

CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17

|||||

Db 7 TCATCCT 1

RESULT 742

AAZ83333/C

ID AAZ83333 standard; DNA; 10 BP.

AC AAZ83333;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #2567.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

XX non-metastatic breast cancer cells, useful for diagnosis, prevention and

XX treatment of cancer.

XX Claim 1; Page 128; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 9 CTTTCATC 15
 Db 10 CTTTCATC 4
 |||||

RESULT 743
 AAZ84131/C
 ID AAZ84131 standard; DNA; 10 BP.

AC AAZ84131;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #3365.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.

XX Claim 1; Page 149; 219pp; English.
 PS
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 12 CATCCTT 18
 Db 7 CATCCTT 1
 |||||

RESULT 744

AAZ85948

ID AAZ85948 standard; DNA; 10 BP.

XX AAZ85948;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5182.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 PS Claim 1; Page 196; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTGAGCG 7
 Db 2 GTGAGCG 8
 |||||
 |||||
 RESULT 745
 AA286466
 ID AA286466 standard; DNA; 10 BP.
 XX
 AC AA286466;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5700.
 XX
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 FI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 PS Claim 1; Page 209; 219pp; English.
 XX
 CC AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 CATCCTT 18
 Db 1 CATCCTT 7
 |||||
 |||||
 RESULT 746
 AA282152/C
 ID AA282152 standard; DNA; 10 BP.
 XX
 AC AA282152;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #1386.
 XX
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 FI Roberts BL, Shankara S;
 XX

```

XX WPI; 2000-106079/09.
DR
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 95; 219pp; English.
PS
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
Db 8 GACTTCA 2
|||||

RESULT 747
AAZ85841/C
ID AAZ85841 standard; DNA; 10 BP.
XX AC
XX AAZ85841;
XX AC
XX
XX 07-APR-2000 (first entry)
XX AC
XX
XX Metastatic breast tumour cell downregulated transcript tag #5075.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX (ROBE/) ROBERTS B L.
XX
XX (SHAN/) SHANKARA S.
XX

```

```

XX Roberts BL, Shankara S;
PI
XX
XX WPI; 2000-106079/09.
DR
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 193; 219pp; English.
PS
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 3 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCAT 14
Db 10 ACTTCAT 4
|||||

RESULT 748
AAZ74109/C
ID AAC74109 standard; cDNA; 10 BP.
XX AC
XX AAC74109;
XX AC
XX
XX 02-FEB-2001 (first entry)
XX
XX Human dendritic cell and monocyte expressed gene oligonucleotide #196.
DE
XX Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200060074-A1.
XX
XX 12-OCT-2000.
XX
XX 30-MAR-2000; 2000WO-JP002019.
XX
XX 01-APR-1999; 99JP-00095481.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Hashimoto S, Matsushima K, Suzuki T;
XX
XX WPI; 2000-619172/59.
XX

```

PT Groups of genes expressed in human dendritic cells at a greater or lesser
 PT extent than in monocytes for investigation and diagnosis of autoimmune
 PT disease and tumors.

PS Claim 10; Page 13; 95pp; Japanese.

XX
 CC The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterized in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases

XX Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12

Db 7 CGACTTC 1

RESULT 749

AAA56456/C

ID AAA56456 standard; DNA; 10 BP.

XX AC AAA56456;

XX 07-SEP-2000 (first entry)

XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:350.

XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
 KW granulocyte-macrophage colony-stimulating factor; characterisation;
 KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
 KW disease onset mechanism; genetic disease; drug development; ss.

XX Homo sapiens.

XX WO200024892-A1.

XX 04-MAY-2000.

XX 28-OCT-1999; 99WO-JP005982.

XX 28-OCT-1998; 98JP-00307532.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Hashimoto S, Matsushima K, Suzuki T;

XX WPI; 2000-350734/30.

XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.

XX Claim 25; Page 109; 138pp; Japanese.

XX The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody

CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
 CC specifically claimed oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages

XX Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18

Db 9 CATCCTT 3

RESULT 750

AAA15242

ID AAA15242 standard; DNA; 10 BP.

XX AC AAA15242;

XX 04-SEP-2000 (first entry)

XX Primer MR7 for modified differential display of tumour antigens.

XX Epitope; tumour specific epitope; antigen; vaccine; tumour regression;
 KW cancer; infection; primer; ss.

XX Synthetic.

XX WO200028016-A1.

XX 18-MAY-2000.

XX 10-NOV-1998; 98WO-US024029.

XX 10-NOV-1998; 98WO-US024029.

XX (UYRP) UNIV ROCHESTER.

XX Zauderer M;

XX WPI; 2000-376533/32.

XX Novel method of identifying target epitopes or antigens specific for
 PT human tumors, cancers and infected cells involving screening expression
 PT library products of a cell expressing the target epitope.

XX Disclosure; Page 68; 132pp; English.

XX AAA15239-50 represent arbitrary primers which are used for modified
 CC differential display of tumour antigens, in the method of the invention.
 CC The specification describes a method for identifying a target epitope.
 CC The method comprises screening the products of an expression library from
 CC a cell expressing the target epitope with cytotoxic T cells generated
 CC against the cell to identify DNA clones expressing the target epitope.
 CC The method may also comprise providing a cytotoxic T cell specific for a
 CC gene product differentially expressed by a cell and measuring the cross-
 CC reactivity of the cytotoxic T cell. The methods are useful for
 CC identifying tumour specific target epitopes and antigens which are useful
 CC in immunogenic compositions or vaccines to induce the regression of
 CC tumors, cancers or infections in mammals. The genes expressed in a panel
 CC of tumour cells that are derived from single immortalised, non-

CC tumourigenic cell line are used to generate HLA restricted cytotoxic T
 CC cells which are evaluated for activity against tumour cells. The method
 CC is useful to identify potential antigens expressed not only by the
 CC pathogen but also by the host cells whose gene expression is altered as a
 CC result of infection. The differential gene expression strategies can be
 CC applied to identify immunogenic molecules of cells infected with virus,
 CC fungus or mycobacterium

SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
 |||||
 Db 4 GACTTCA 10

RESULT 751

AAF77152
 ID AAF77152 standard; DNA; 10 BP.

XX AC AAF77152;

XX DT 22-MAY-2001 (first entry)

XX DE R-structure wing sequence #11.

XX KW Resonating; R-structure; tertiary structure; anti-viral; ss.

XX OS Ebola virus.

XX PN US6194155-B1.

XX PD 27-FEB-2001.

XX PF 05-MAY-1999; 99US-00305408.

XX PR 05-MAY-1999; 99US-00305408.

XX PA (COHE/) COHEN J.

XX PI Cohen J;

XX PX WPI; 2001-234428/24.

XX Computerized method for identifying and locating resonating, self-
 PT hybridizing nucleic acid elements comprises employing a memory device,
 PT which has computer program instructions for creating data structures and
 PT operator modules.

XX Example 1; Col 14-16; 21pp; English.

XX The present invention relates to identifying resonating, self-hybridizing
 CC molecular genetic nucleotide structures (R-structures) in a nucleic acid
 CC sequence, employing a memory device. The method is also useful for
 CC identifying viral nucleic acid sequences that form tertiary structures.
 CC The ability to identify such structures or sequences may lead to faster
 CC development of anti-viral therapies

SQ Sequence 10 BP; 3 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
 |||||
 Db 4 CTTTCATC 10

RESULT 752

AAF77162
 ID AAF77162 standard; DNA; 10 BP.

XX AC AAF77162;

XX DT 22-MAY-2001 (first entry)

XX DE R-structure 5899.

XX KW Resonating; R-structure; tertiary structure; anti-viral; ss.

XX OS Ebola virus.

XX PN US6194155-B1.

XX PD 27-FEB-2001.

XX PF 05-MAY-1999; 99US-00305408.

XX PR 05-MAY-1999; 99US-00305408.

XX PA (COHE/) COHEN J.

XX PI Cohen J;

XX PX WPI; 2001-234428/24.

XX Computerized method for identifying and locating resonating, self-
 PT hybridizing nucleic acid elements comprises employing a memory device,
 PT which has computer program instructions for creating data structures and
 PT operator modules.

XX Example 1; Col 17; 21pp; English.

XX The present invention relates to identifying resonating, self-hybridizing
 CC molecular genetic nucleotide structures (R-structures) in a nucleic acid
 CC sequence, employing a memory device. The method is also useful for
 CC identifying viral nucleic acid sequences that form tertiary structures.
 CC The ability to identify such structures or sequences may lead to faster
 CC development of anti-viral therapies

XX SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
 |||||
 Db 4 CTTTCATC 10

RESULT 753

AAF77153/C
 ID AAF77153 standard; DNA; 10 BP.

XX AC AAF77153;

XX DT 22-MAY-2001 (first entry)

XX DE R-structure wing sequence #12.

XX KW Resonating; R-structure; tertiary structure; anti-viral; ss.

XX OS Ebola virus.

XX PN US6194155-B1.

XX PD 27-FEB-2001.

XX PF 05-MAY-1999; 99US-00305408.

XX PR 05-MAY-1999; 99US-00305408.


```
XX FA (COHE/) COHEN J.
XX PI Cohen J;
XX DR WPI; 2001-234428/24.
XX PT Computerized method for identifying and locating resonating, self-
XX PT hybridizing nucleic acid elements comprises employing a memory device,
XX PT which has computer program instructions for creating data structures and
XX PT operator modules.
XX PS Example 1; Col 14-16; 21pp; English.
XX CC The present invention relates to identifying resonating, self-hybridizing
XX CC molecular genetic nucleotide structures (R-structures) in a nucleic acid
XX CC sequence, employing a memory device. The method is also useful for
XX CC identifying viral nucleic acid sequences that form tertiary structures.
XX CC The ability to identify such structures or sequences may lead to faster
XX CC development of anti-viral therapies
XX SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTCATC 15
Db 7 CTCATC 1

RESULT 754
AAH63972
ID AAH63972 standard; cDNA; 10 BP.
AC AAH63972;
XX 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 812.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velulescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX Claim 13; Page 57; 94pp; English.
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 7 TCATCCT 1

RESULT 756
AAH63197
ID AAH63197 standard; cDNA; 10 BP.
XX
```

```
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTCATC 15
Db 3 CTCATC 9

RESULT 755
AAH63664/c
ID AAH63664 standard; cDNA; 10 BP.
XX AAH63664;
XX 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 504.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
XX WO200138577-A2.
XX 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
XX 24-NOV-1999; 99US-00448480.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velulescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX Claim 13; Page 50; 94pp; English.
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 7 TCATCCT 1

RESULT 756
AAH63197
ID AAH63197 standard; cDNA; 10 BP.
XX
```


CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcripts described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
 |||||
 Db 3 CTTTCATC 9

RESULT 759

AAH63634/C
 ID AAH63634 standard; cDNA; 10 BP.

XX AC
 XX AAH63634;

XX 20-SEP-2001 (first entry)

XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 474.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.

XX Claim 13; Page 49; 94pp; English.

XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcripts described in the exemplification of the invention

XX Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGA 8
 |||||
 Db 9 TGAGCGA 3

RESULT 760

AAS57323/C

ID AAS57323 standard; DNA; 10 BP.

XX

AC AAS57323;

XX 16-JAN-2002 (first entry)

XX Human CHRN2 allele specific oligonucleotide PCR primer terminus #48.

XX Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;
 KW CHRN2; memory disorder; Alzheimer's disease; epilepsy; learning;
 KW chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;

XX ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss;
 KW allele specific oligonucleotide; ASO; PCR primer.

XX Homo sapiens.

XX WO200174833-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010666.

XX 03-APR-2000; 2000US-0194155P.

XX 13-JUL-2000; 2000US-0217952P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Kliem SE, Koshy B, Lee HH, Sanchis A;

XX WPI; 2001-626374/72.

XX Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an
 PT individual involves determining for two copies of the gene, the identity
 PT of nucleotide pair at polymorphic sites selected from PSI-24.

XX Claim 17; Page 15; 82pp; English.

XX The invention relates to genotyping/haplotyping the cholinergic receptor,
 CC nicotinic, beta-polypeptide 2 (neuronal) (CHRN2) gene of an individual,
 CC comprising determining for the two copies of the CHRN2 gene present in
 CC the individual, the identity of the nucleotide pair at one or more
 CC polymorphic sites selected from PSI-24. Also include are oligonucleotides
 CC for performing the method and the nucleotide sequence of the polymorphic
 CC variants of CHRN2. The method is useful for detecting novel CHRN2
 CC polymorphisms and for determining if an individual has a haplotype or
 CC haplotype pairs defined in the specification and to validate CHRN2 as a
 CC candidate agent for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity (e.g. a memory disorder, Alzheimer's
 CC disease, epilepsy, a learning disorder, schizophrenia, attention
 CC deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal
 CC frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials of
 CC candidate drugs for treating a specific condition or disease predicted to
 CC be associated with CHRN2 activity. The method is useful to screen for
 CC compounds targeting CHRN2 to treat a specific condition or disease
 CC associated with CHRN2 activity. The polymorphic nucleic acids are useful
 CC in studying the expression and function of CHRN2, and in expressing
 CC CHRN2 protein for use in screening for candidate drugs to treat diseases
 CC related to CHRN2 activity and are useful for therapeutic purposes. The
 CC CHRN2 gene is located on chromosome 1q21. The present sequence is an
 CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for
 CC performing the method of the invention

XX Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 |||||
 Db 10 CATCCTT 4

RESULT 761

AAH32725/c
ID AAH32725 standard; cDNA; 10 BP.
XX
AC AAH32725;
XX
DT 13-AUG-2001 (first entry)
XX
XX LPS activated human monocyte expression gene cDNA tag SEQ:98.
DE
XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
XX JP2001069993-A.
PN
XX 21-MAR-2001.
PD
XX 28-APR-2000; 2000JP-00131079.
XX
XX 08-JUL-1999; 99JP-00195103.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2001-304369/32.
DR
XX LPS activated human monocyte expression gene group.
PT
XX Claim 10; Page 24; 52pp; Japanese.
PS
XX The present invention describes a lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the high-ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the cDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3', nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role. AAH32628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH32944 represents an LPS activated human monocyte expression gene cDNA sequence encoding AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7 GACTTCA 13
DB 9 GACTTCA 3
XX
RESULT 762
AAH32733/c
ID AAH32733 standard; cDNA; 10 BP.
XX
AC AAH32733;
XX
DT 13-AUG-2001 (first entry)
XX
XX LPS activated human monocyte expression gene cDNA tag SEQ:106.
DE
XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
XX JP2001069993-A.
PN
XX 21-MAR-2001.
PD
XX

28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2001-304369/32.
DR
XX LPS activated human monocyte expression gene group.
PT
XX Claim 10; Page 25; 52pp; Japanese.
PS
XX The present invention describes a lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the high-ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the cDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3', nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role. AAH32628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH32944 represents an LPS activated human monocyte expression gene cDNA sequence encoding AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 CGACTTC 12
DB 7 CGACTTC 1
XX
RESULT 763
AAF36541/c
ID AAF36541 standard; DNA; 10 BP.
XX
AC AAF36541;
XX
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3280.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
PN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US016223.
PP
XX 16-JUN-1999; 99US-00335032.
PR
XX (UVOJO) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
PI
XX WPI; 2001-061874/07.
DR
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 117; 419pp; English.
XX

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
 Db 7 CTTTCATC 1

RESULT 764

AAAF41808/C

ID AAF41808 standard; DNA; 10 BP.

XX AAF41808;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8547.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
 XX serial analysis of gene expression; antifungal; tag; identification;
 XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 305; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 Db 8 CATCCTT 2

RESULT 765

AAAF35626/C

ID AAF35626 standard; DNA; 10 BP.

XX AAF35626;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2365.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
 XX serial analysis of gene expression; antifungal; tag; identification;
 XX linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 84; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 10 CTTTCATC 4
|||||

RESULT 766

AAF36462
ID AAF36462 standard; DNA; 10 BP.

XX AC AAF36462;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3201.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.

XX PS Example; Page 114; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 1 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9
|||||

RESULT 767

AAF38906/C
ID AAF38906 standard; DNA; 10 BP.

XX AC AAF38906;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5645.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX XX

```
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Veiculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 201; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 CATCCTT 18
Db 7 CATCCTT 1
| | | | |
RESULTS
AAAF36183/c
ID AAF36183 standard; DNA; 10 BP.
XX
XX AAF36183;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2922.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation, cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX
XX WO200077214-A2.
PN
XX
XX 21-DEC-2000.
FD
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
```

```
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Veiculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 104; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCAT 14
Db 10 ACTTCAT 4
| | | | |
RESULTS
AAAF40128/c
ID AAF40128 standard; DNA; 10 BP.
XX
XX AAF40128;
AC
XX
XX 23-MAR-2001 (first entry)
DT
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6867.
DE
XX
XX Yeast; Saccharomyces cerevisiae; characterisation, cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX
XX WO200077214-A2.
PN
XX
XX 21-DEC-2000.
FD
XX
XX 14-JUN-2000; 2000WO-US016223.
PF
```

```

PD 21-DEC-2000.
PP
PF
PX 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 245; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 6 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
    Query Match      38.9%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 3.5e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 ACTTCAT 14
Db 7 ACTTCAT 1

RESULT 770
AAF40706
ID AAF40706 standard; DNA; 10 BP.
XX
XX AAF40706;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7445.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.

```

```

XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX PF 16-JUN-1999; 99US-00335032.
XX
XX PR 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 265; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
    Query Match      38.9%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 3.5e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 ACTTCAT 14
Db 4 ACTTCAT 10

RESULT 771
AAF34367
ID AAF34367 standard; DNA; 10 BP.
XX
XX AAF34367;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1106.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX

```


KW linker; PCR primer; ds.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 39; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
 SQ Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 TTTCATCC 16
 |||||
 Db 3 TTTCATCC 9
 RESULT 772
 AAF36277/C
 ID AAF36277 standard; DNA; 10 BP.
 XX AAF36277;
 XX AAF36277;
 XX 23-MAR-2001 (first entry)
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3016.
 XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 107; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 CATCCTT 18
 |||||
 Db 9 CATCCTT 3
 RESULT 773
 AAF37614/C
 ID AAF37614 standard; DNA; 10 BP.
 XX AAF37614;
 XX AAF37614;
 XX 23-MAR-2001 (first entry)
 DT

```

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4353.
XX XX
XX DT
XX XX
XX XX
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX OS WO200077214-A2.
XX PN
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Example; Page 155; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 CATCCTT 18
Db |||||
10 CATCCTT 4
RESULT 774
AAF40734
ID AAF40734 standard; DNA; 10 BP.
XX

```

```

AC AAF40734;
XX XX
XX DT 23-MAR-2001 (first entry)
XX XX
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7473.
XX XX
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX OS WO200077214-A2.
XX PN
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Example; Page 266; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 CATCCTT 18
Db |||||
1 CATCCTT 7
RESULT 775

```

```
AAAF42712
ID  AAFA42712 standard; DNA; 10 BP.
XX
AC  AAFA42712;
XX
DT  23-MAR-2001 (first entry)
XX
DE  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10851.
XX
KW  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
OS  Saccharomyces cerevisiae.
XX
PN  WO200077214-A2.
XX
PD  21-DEC-2000.
XX
PP  14-JUN-2000; 2000WO-US016223.
XX
PR  16-JUN-1999; 99US-00335032.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Velculescu V, Vogelstein B, Kinzler K;
XX
DR  WPI; 2001-061874/07.
XX
PT  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
PS  Example; Page 337; 419pp; English.
XX
CC  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
SQ  Sequence 10 BP; 2 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8 ACTTCAT 14
Db  3 ACTTCAT 9
```

```

Qy      6 CGACTTC 12
      |||||
Db      9 CGACTTC 3

RESULT 777
AAF42504/C
ID  AAF42504 standard; DNA; 10 BP.
XX
AC  AAF42504;
XX
XX  23-MAR-2001 (first entry)
XX
XX  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10643.
XX
XX  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
XX  Saccharomyces cerevisiae.
XX
XX  WO200077214-A2.
XX
XX  21-DEC-2000.
XX
XX  14-JUN-2000; 2000WO-US016223.
XX
XX  16-JUN-1999; 99US-00335032.
XX
XX  (UYJO ) UNIV JOHNS HOPKINS.
XX
XX  Velulescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
XX  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
XX  Example; Page 330; 419pp; English.
XX
XX  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
SQ  Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
      38.9%; Score 7; DB 1; Length 10;
Query Match

```

```

Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GACTTCA 13
      |||||
Db      10 GACTTCA 4

RESULT 778
AAF42922
ID  AAF42922 standard; DNA; 10 BP.
XX
AC  AAF42922;
XX
XX  23-MAR-2001 (first entry)
XX
XX  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11061.
XX
XX  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
XX  Saccharomyces cerevisiae.
XX
XX  WO200077214-A2.
XX
XX  21-DEC-2000.
XX
XX  14-JUN-2000; 2000WO-US016223.
XX
XX  16-JUN-1999; 99US-00335032.
XX
XX  (UYJO ) UNIV JOHNS HOPKINS.
XX
XX  Velulescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
XX  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
XX  Example; Page 345; 419pp; English.
XX
XX  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
XX

```

SQ Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
 |||||
 Db 4 CTTTCATC 10

RESULT 779
 AAF35273/c
 ID AAF35273 standard; DNA; 10 BP.
 XX AC AAF35273;
 XX DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2012.
 XX DT
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 71; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
 |||||
 Db 8 TCATCCT 2

RESULT 780
 AAF43489/c
 ID AAF43489 standard; DNA; 10 BP.
 XX AC AAF43489;
 XX DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11628.
 XX DT
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 365; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.

CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 CTTTCATC 15
|||||||
Db 10 CTTTCATC 4

RESULT 781
AAF35108/C
ID AAF35108 standard; DNA; 10 BP.

XX AAF35108;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1847.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 66; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GCGACTT 11
|||||||
Db 9 GCGACTT 3

RESULT 782
AAF35646/C

ID AAF35646 standard; DNA; 10 BP.

XX AAF35646;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2385.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 85; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 CATCTTT 18
 Db 8 CATCTTT 2

RESULT 783
 AAF36303/c
 ID AAF36303 standard; DNA; 10 BP.

XX AAF36303;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3042.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 108; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCAT 14
 Db 7 ACTTCAT 1

RESULT 784

AAF38071/c

ID AAF38071 standard; DNA; 10 BP.

XX AAF38071;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4810.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 171; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression

varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
|||||||
Db 8 AGCGACT 2

RESULT 785

AAF39675
ID AAF39675 standard; DNA; 10 BP.

XX AAF39675;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6414.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 229; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
|||||||
Db 1 AGCGACT 7

RESULT 786

AAF42156/c
ID AAF42156 standard; DNA; 10 BP.

XX AAF42156;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8895.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 317; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTATC 15
| | | | |
Db 7 CTTATC 1

RESULT 787
AAF38429/C
ID AAF38429 standard; DNA; 10 BP.
AC AAF38429;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5168.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UWJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 184; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGACTT 11
| | | | |
Db 10 GCGACTT 4

RESULT 788
AAF43238/C
ID AAF43238 standard; DNA; 10 BP.
XX
XX AAF43238;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11377.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UWJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX

PS Example; Page 356; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTATCC 16

Db |||||

8 TTATCC 2

RESULT 789

AAF36982

ID AAF36982 standard; DNA; 10 BP.

XX AAF36982;

AC AAF36982;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3721.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX WO200077214-A2.

FN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

PA Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

PS Example; Page 132; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

SQ Query Match 38.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTCATC 15

Db |||||

4 CTCATC 10

RESULT 790

AAF35394/C

ID AAF35394 standard; DNA; 10 BP.

XX AAF35394;

AC AAF35394;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2133.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX WO200077214-A2.

FN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

PA Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

```

DR WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 76; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence: 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 CTTTCATC 15
Db 8 CTTTCATC 2
RESULT 791
AAF37498/c
ID AAF37498 standard; DNA; 10 BP.
AC AAF37498;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4237.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.

```

```

XX Veiculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX Example; Page 151; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence: 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
SQ Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCATCCT 17
Db 10 TCATCCT 4
RESULT 792
AAF38878
ID AAF38878 standard; DNA; 10 BP.
XX AAF38878;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5617.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.

```

```

PR 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 200; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
Db 2 AGCGACT 8
|||||
2 AGCGACT 8

RESULT 793
AAF42917/C
ID AAF42917 standard; DNA; 10 BP.
XX
XX AAF42917;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11056.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX

```

```

XX 14-JUN-2000; 2000WO-US016223.
XX PF
XX 16-JUN-1999; 99US-00335032.
XX PR
XX (UYJO ) UNIV JOHNS HOPKINS.
XX PA
XX Velculescu V, Vogelstein B, Kinzler K;
XX PI
XX WPI; 2001-061874/07.
XX PT
XX DR
XX DR
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 344; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
XX
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGA 8
Db 7 TGAGCGA 1
|||||
7 TGAGCGA 1

RESULT 794
AAF40129/C
ID AAF40129 standard; DNA; 10 BP.
XX
XX AAF40129;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6868.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX OS
XX OS

```

```

PN WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 245; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 8 ACTTCAT 14
XX Db 7 ACTTCAT 1
XX
XX RESULT 795
XX AAF33628/c
XX ID AAF33628 standard; DNA; 10 BP.
XX
XX AC AAF33628;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:367.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Claim 1; Page 388; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 38.9%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 AGCGACT 10
XX Db 8 AGCGACT 2
XX
XX RESULT 796
XX AAF34498/c
XX ID AAF34498 standard; DNA; 10 BP.
XX
XX AC AAF34498;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1237.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

```

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 44; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CGACTTC 12
|||||||
Db 7 CGACTTC 1
RESULT 797
AAF35237/c
ID AAF35237 standard; DNA; 10 BP.
XX AAF35237;
AC AAF35237;
XX 23-MAR-2001 (first entry)
DT XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1976.
XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 70; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCATCCT 17
|||||||
Db 7 TCATCCT 1
RESULT 798
AAF36405
ID AAF36405 standard; DNA; 10 BP.
XX AAF36405;
AC AAF36405;

```

XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3144.
XX DT
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX FN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX FS Example; Page 112; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 CATCCTT 18
Db 2 CATCCTT 8

```

RESULT 799
AAF39465

```

ID AAF39465 standard; DNA; 10 BP.
XX AC AAF39465;
XX DT
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6204.
XX DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX FN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX FS Example; Page 221; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCAT 14
Db 1 ACTTCAT 7

```

```
RESULT 800
AAF33629/C
ID AAF33629 standard; DNA; 10 BP.
XX AC AAF33629;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:368.
XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Claim 1; Page 388; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
Oy 4 AGCGACT 10
```

```
|||||
8 AGCGACT 2

RESULT 801
AAF41221/C
ID AAF41221 standard; DNA; 10 BP.
XX AC AAF41221;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7960.
XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX PS Example; Page 284; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
```


Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 TCATCCT 17
| | | | |
Db 10 TCATCCT 4

RESULT 802
AAS95353/C
ID AAS95353 standard; DNA; 10 BP.
XX
AC AAS95353;
XX
XX 14-FEB-2002 (first entry)
XX
DE Human Histamine H2 receptor ASO primer extension PCR primer #13.
XX
XX Human; histamine H2 receptor; H2; ss; PCR primer; polymorphic variant;
KW haplotyping; genotyping; acid-peptic disorder; mammary cancer;
KW gastric carcinoma; allele specific oligonucleotide; ASO;
KW primer extension.
XX
XX Homo sapiens.
OS
XX WO200179220-A2.
XX
XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US011941.
XX
XX 12-APR-2000; 2000US-0196406P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX PA
XX Chew A, Choi JY, Koshy B;
PI
XX WPI; 2002-055249/07.
DR
XX
XX New human histamine H2 receptor (HRH2) isogene polymorphic variants,
PT useful in expressing HRH2 protein for use in screening for candidate
PT drugs to treat diseases related to HRH2 activity.
XX
XX Claim 17; Page 14; 62pp; English.

The invention relates to an isolated polynucleotide comprising a
polymorphic variant of a reference sequence for human Histamine H2
receptor (HRH2) gene, its fragment or complement, and the polymorphic
variant contains an HRH2 isogene defined by a haplotype listed in the
specification. Also disclosed are methods for haplotyping and genotyping
the HRH2 gene of an individual, a method for predicting a haplotype pair
for the HRH2 gene of an individual, identifying an association between a
trait and at least one haplotype or haplotype pair of HRH2 gene, allele
specific oligonucleotides (ASO) for performing the haplotyping/
genotyping, a recombinant nonhuman organisms transformed or transfected
with the polymorphic variant, the protein expressed by the polymorphic
variant, an antibody raised against the protein and screening for drugs
targeting the polypeptide by contacting HRH2 polymorphic variant with a
candidate agent and assaying for binding activity. The polymorphisms are
useful for studying the biological function of HRH2 gene, as well as in
identifying drugs targeting this protein for the treatment of disorder
related to its abnormal expression or function. The polymorphic variants
may be used in screening for compounds targeting CALM1 to treat a
specific condition or disease predicted to be associated with HRH2
activity, in studying the effect of the variation on the biological
activity of HRH2 as well as on the binding affinity of candidate drugs
targeting HRH2 for the treatment of acid-peptic disorders of the
gastrointestinal tract and also possibly human mammary cancer and gastric
carcinoma. The polymorphism and haplotype data can also be used for
validating whether HRH2 is a suitable drug target for drugs to treat acid
-peptic disorders of the gastrointestinal tract, screening of such drugs
and reducing bias in clinical trials of such drugs. The present sequence
is the 3' terminus of an ASO primer extension PCR primer used to detect
the polymorphisms of the invention

XX SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 ACTTCAT 14
| | | | |
Db 10 ACTTCAT 4

RESULT 803
AAD25096/C
ID AAD25096 standard; DNA; 10 BP.
XX
AC AAD25096;
XX
XX 12-MAR-2002 (first entry)
DT
DE Primer #23 used to detect human OSM gene polymorphism.
XX
XX Human; oncostatin M; OSM gene; haplotyping; genotyping; cancer; primer;
KW lung inflammation; polymorphism; rheumatoid arthritis; ss.
XX
XX Homo sapiens.
OS
XX WO200187907-A2.
XX
XX 22-NOV-2001.
PD
XX 17-MAY-2001; 2001WO-US016157.
PF
XX 17-MAY-2000; 2000US-0204868P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Duda AE, Kazemi A, Koshy B;
PI
XX WPI; 2002-055680/07.
DR
XX New isolated human oncostatin M polynucleotide, useful for therapeutic
PT purposes, for studying the expression and function of the polynucleotide
PT and for expressing oncostatin protein.
XX
XX Claim 18; Page 14; 71pp; English.

The invention relates to genetic variants of human oncostatin M (OSM)
gene. The invention also relates to compositions and methods for
haplotyping and/or genotyping OSM gene in an individual. Polynucleotides
of the invention are useful in studying the expression and function of
OSM, and in expressing OSM protein for use in screening candidate drugs
to treat diseases related to OSM activity. They are also useful for
therapeutic purposes. Methods of the invention are useful for determining
whether an individual has a haplotype or haplotype pairs. The method is
also useful for improving the efficacy and reliability of several steps
in the discovery and development of drugs for treating diseases
associated with OSM activity, e.g. cancer, diseases involving lung
inflammation and rheumatoid arthritis. The present sequence is a primer
used for detecting human OSM gene polymorphisms

XX SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 CATCCTT 18
| | | | |
Db 10 CATCCTT 4

RESULT 804

```

AAD25317
ID  AAD25317 standard; DNA; 10 BP.
AC  AAD25317;
XX
DT  12-MAR-2002 (first entry)
XX
DE  Human HSD3B1 gene polymorphism detecting primer #22.
XX
KW  Human; steroid biosynthesis disorder; congenital adrenal hyperplasia;
KW  hydroxy-delta-5-steroid dehydrogenase 3 beta- steroid delta-isomerase 1;
KW  HSD3B1; cytostatic; antisense gene therapy; drug screening; primer; ss.
XX
OS  Homo sapiens.
XX
FN  WO200179552-A1.
XX
PD  25-OCT-2001.
XX
PF  12-APR-2001; 2001WO-US011945.
XX
PR  12-APR-2000; 2000US-0196324P.
XX
PA  (GENA-) GENAISSANCE PHARM INC.
XX
PI  Chew A, Choi JY, Koshy B;
XX
DR  WPI; 2002-066373/09.
XX
PT  New genetic variants of human hydroxy-delta-5-steroid dehydrogenase, 3
PT  beta- and steroid delta-isomerase 1 gene for expressing protein for use
PT  in screening for drugs to treat steroid biosynthesis disorders.
XX
PS  Claim 18; Page 15; 77pp; English.
XX
SQ  The invention relates to an isolated polynucleotide which is a
CC  polymorphic variant of human hydroxy-delta-5-steroid dehydrogenase, 3beta
CC  - and steroid delta-isomerase 1 (HSD3B1) gene. HSD3B1 polypeptide is
CC  useful for screening drugs which are used for treating diseases related
CC  to HSD3B1 activity. HSD3B1 DNA is used for treating disorders related to
CC  steroid biosynthesis such as congenital adrenal hyperplasia. A
CC  polymorphic variant of HSD3B1 is used for studying the effect of
CC  variation on the biological activity of HSD3B1, on the binding affinity
CC  of candidate drugs targeting HSD3B1 for the treatment of disorders
CC  related to steroid biosynthesis and in assays to measure the binding
CC  affinities of one or more candidate drugs targeting the HSD3B1 protein.
CC  A recombinant human transgenic animal is used for studying expression of
CC  HSD3B1 isogenes in vivo, for screening and testing for drugs against
CC  HSD3B1 protein and for testing the efficacy of therapeutic agents and
CC  compounds for disorders related to steroid biosynthesis in a biological
CC  system. HSD3B1 antibody is used for detecting HSD3B1 protein isoforms in
CC  biological samples, frozen tissue sections, cells which have been fixed
CC  or unfixed and prepared on slides, for use in immunohistochemical,
CC  immunocytochemical and immunofluorescence techniques. The present
CC  sequence is a primer used for detecting human HSD3B1 gene polymorphism
XX
SQ  Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
Db 2 GACTTCA 8
|||||

RESULT 805
ABL01185/c
ID  ABL01185 standard; DNA; 10 BP.
XX
AC  ABL01185;
XX

12-MAR-2002 (first entry)
Human AKR1B1 gene polymorphism detection primer SEQ ID NO:82.
Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
Homo sapiens.
WO200179223-A2.
25-OCT-2001.
12-APR-2001; 2001WO-US011944.
12-APR-2000; 2000US-0196315P.
(GENA-) GENAISSANCE PHARM INC.
Choi JY, Nandabalan K, Rounds E, Sanchis A;
WPI; 2002-075056/10.
Novel polymorphic variants of aldo-keto reductase family 1, member b1
gene useful in studying expression and function of the protein, useful
for screening drugs to treat diseases e.g. diabetes.
Claim 18; Page 15; 103pp; English.
The present invention describes an isolated polynucleotide (I) comprising
a sequence which is a polymorphic variant (PV) of a reference sequence
for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
fragment, having the 22214 base pair sequence given in ABL01105. AKR1B1
has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
used in the treatment of diabetes. The human AKR1B1 gene is located on
chromosome 7q35. ABL01107 to ABL01129 represent allele-specific
oligonucleotide (ASO) probes used in the detection of polymorphisms in
the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
ABL01221 represent preferred primers used in the detection of
polymorphisms in the human AKR1B1 gene
Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 7 CATCCTT 1
|||||

RESULT 806
ABL42892/c
ID  ABL42892 standard; cDNA; 10 BP.
XX
AC  ABL42892;
XX
DT  12-APR-2002 (first entry)
XX
DE  Human maturation/activation dendritic cell expression gene tag #266.
XX
KW  Human; maturation/activation dendritic cell expression gene; tag;
KW  maturation; activation; dendritic cell; ss.
XX
OS  Homo sapiens.
XX
FN  JP2001327293-A.
XX
PD  27-NOV-2001.
XX

```

PF 22-MAY-2000; 2000JP-00150562.
XX
PR 22-MAY-2000; 2000JP-00150562.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-127070/17.
XX
PT Human maturation/activation dendritic cell expression gene group.
XX
PS Claim 19; Page 16; 41pp; Japanese.
XX
CC The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. ABL42627 to ABL42926 represent specifically claimed human maturation/activation DC expression gene tags from the present invention

XX
SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TGAGCGA 8
Db 9 TGAGCGA 3

RESULT 807
ABL42786/C
ID ABL42786 standard; cDNA; 10 BP.
XX
AC ABL42786;
XX
DT 12-APR-2002 (first entry)
XX
DE Human maturation/activation dendritic cell expression gene tag #160.
XX
KW Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
OS Homo sapiens.
XX
FN JP2001327293-A.
XX
PD 27-NOV-2001.
XX
FF 22-MAY-2000; 2000JP-00150562.
XX
PR 22-MAY-2000; 2000JP-00150562.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-127070/17.
XX
PT Human maturation/activation dendritic cell expression gene group.
XX
PS Claim 10; Page 13; 41pp; Japanese.
XX
CC The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human

CC DC. ABL42627 to ABL42926 represent specifically claimed human maturation/activation DC expression gene tags from the present invention
CC
SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GACTTCA 13
Db 9 GACTTCA 3

RESULT 808
ABK81441/C
ID ABK81441 standard; DNA; 10 BP.
XX
AC ABK81441;
XX
DT 13-AUG-2002 (first entry)
XX
DE SCYA20 primer extension oligonucleotide #3.
XX
KW Small inducible cytokine subfamily A (Cys-Cys) member 20; SCYA20; polymorphism; haplotype; psoriasis; gene expression;
KW primer extension oligonucleotide; ss.
XX
OS Homo sapiens.
XX
FN WO200232927-A2.
XX
PD 25-APR-2002.
XX
PF 19-OCT-2001; 2001WO-US046093.
XX
PR 19-OCT-2000; 2000US-0241725P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PI Bieglecki KM, Chew A, Russo DP, Sausker EA;
XX
DR WPI; 2002-435525/46.
XX
PT New genetic variants comprising haplotypes of the small inducible cytokine subfamily A, member 20 (SCYA20) gene, useful in improving the efficiency drug screening protocols for compounds (e.g. antipsoriatic drug) targeting SCYA20.
XX
PS Claim 16; Page 13; 62pp; English.
XX
CC The invention describes an isolated polynucleotide, which comprises genes and haplotypes of the small inducible cytokine subfamily A (Cys-Cys) member 20 (SCYA20) gene. The polynucleotide comprises polymorphic sites referred to as PSI-9 to designate the order in which they are located in the gene. The polymorphisms and haplotypes of SCYA20 gene are useful for validating whether SCYA20 is a suitable target for drugs to treat psoriasis and disorders associated with its abnormal expression or function, screening for such drugs and reducing bias in clinical trials of such drugs. Haplotype information would be useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, early phase clinical trials. The methods are useful in screening for compounds targeting SCYA20 to treat a specific condition or disease predicted to be associated with SCYA20 activity, e.g. psoriasis. This sequence represents a primer extension oligonucleotide used to identify polymorphisms in the SCYA20 gene
XX
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX AC ABN80655;
 XX PD 19-JUL-2002 (first entry)
 XX DT
 XX DE Human P450(cytochrome) oxidoreductase ASO primer extension oligo #43.
 XX KW Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
 XX KW single nucleotide polymorphism; flavoprotein; enzyme;
 XX KW primer extension oligonucleotide; ss.
 XX OS Homo sapiens.
 XX PN WO200226768-A2.
 XX PD 04-APR-2002.
 XX PF 01-OCT-2001; 2001WO-US030877.
 XX PR 29-SEP-2000; 2000US-0236449P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;
 XX DR WPI; 2002-394236/42.
 XX KW New genetic variants comprising haplotypes of the P450 (cytochrome)
 XX PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
 XX PT screening protocols for compounds targeting POR.
 XX PS Claim 16; Page 15; 14lpp; English.
 XX CC The present invention provides the protein, gene and cDNA sequences of
 XX CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
 XX CC polymorphisms (SNPs) identified therein. The sequences can be used to
 XX CC haplotype the POR gene of an individual, and to establish whether POR is
 XX CC a suitable target for drugs to treat cancer and disorders associated with
 XX CC impaired protein synthesis in cells. The present sequence is an allele
 XX CC specific primer extension oligonucleotide for the coding sequences of the
 XX CC invention
 XX SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GTGAGCG 7
 Db 8 GTGAGCG 2
 RESULT 812
 ABK87758
 ID ABK87758 standard; DNA; 10 BP.
 XX AC
 XX AC ABK87758;
 XX DT 24-SEP-2002 (first entry)
 XX DE
 XX DE Mouse receptor-activity-modifying protein, RAMP2, homology arm #2.
 XX KW Mouse; ds; RAMP2; receptor-activity-modifying protein; cardiant;
 XX KW hypotensive; hepatotropic; transgenic; liver function disorder;
 XX KW muscle metabolism disorder; heart failure; mitral stenosis;
 XX KW acute myocardial infarction; hypertension; chronic hepatitis;
 XX KW acute hepatitis; hepatomegaly; hepatic steatosis; biliary atresia;
 XX KW gallstone; drug-induced hepatotoxicity; chemical-induced hepatotoxicity;
 XX KW homologous recombination; homology arm.
 XX OS Mus musculus.
 XX OS

PN EPI212941-A2.
 XX PD 12-JUN-2002.
 XX PF 27-NOV-2001; 2001EP-00309928.
 XX PR 30-NOV-2000; 2000US-0250965P.
 XX PA (PFIZ) PFIZER PROD INC.
 XX PI Mcneish JD, Soeller WC, Thompson JF;
 XX DR WPI; 2002-530574/57.
 XX KW Genetically-modified non-human mammal where the genetic modification
 XX PT results in a disrupted RAMP1, RAMP2 or RAMP3 gene, such that agents can
 XX PT be identified which modulate the activity.
 XX PS Example 1; Fig 3; 29pp; English.
 XX CC The invention relates to a genetically-modified non-human mammal where
 XX CC the genetic modification results in a disrupted RAMP1 or RAMP3 (receptor-
 XX CC activity-modifying protein) gene. Also included are a genetically-
 XX CC modified non-human mammal where the mammal is heterozygous for a genetic
 XX CC modification which results in a disrupted RAMP2 gene and results in
 XX CC expression of an exogenous reporter gene under the control of regulatory
 XX CC sequences of the RAMP2 gene, a membrane preparation derived from the
 XX CC genetically-modified animal cell treating a disorder associated with
 XX CC liver function and/or muscle metabolism in a mammal where the method
 XX CC comprises administering an agent that modulates RAMP1 activity and
 XX CC identifying an agent that modulates RAMP1, RAMP2 or RAMP3 protein or gene
 XX CC activity. An agent which increases RAMP1 activity is used in the
 XX CC manufacture of a medicament for the treatment of a mammal with a disorder
 XX CC associated with liver function and/or a disorder associated with muscle
 XX CC metabolism. Disorders treated include heart failure, mitral stenosis,
 XX CC acute myocardial infarction, hypertension, chronic or acute hepatitis,
 XX CC hepatomegaly, hepatic steatosis, biliary atresia, gallstones, or
 XX CC chemical or drug-induced hepatotoxicity. The invention provides a means
 XX CC of understanding the complex role of RAMP in metabolism. The present
 XX CC sequence is the homology arm flanking a fragment of the RAMP2 gene used
 XX CC in an experiment to disrupt the RAMP 2 gene by homologous recombination
 XX SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 CATCCTT 18
 Db 1 CATCCTT 7
 RESULT 813
 ABV84329
 ID ABV84329 standard; cDNA; 10 BP.
 XX AC
 XX AC ABV84329;
 XX DT 12-DEC-2002 (first entry)
 XX DE
 XX DE Human phosphatidic acid phosphatase type 2b-like EST SAGE tag #139.
 XX KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 XX KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 XX KW expression pattern; differential expression; EST; expressed sequence tag;
 XX KW ss.
 XX OS Homo sapiens.
 XX PN JP2002209591-A.
 XX PD 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.
 PF XX
 PR 19-JAN-2001; 2001JP-00012328.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA XX
 PS WPI; 2002-631294/68.
 DR XX
 XX Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 PF XX
 PS Claim 10; Page 13; 139pp; Japanese.
 XX The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly
 CC expressed genes out of those genes which are underexpressed in chronic
 CC hepatitis C liver tissue compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 3 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 CATCCTT 18
 Db |||||
 3 CATCCTT 9
 RESULT 814
 ID AAS95616/c
 AC AAS95616 standard; DNA; 10 BP.
 XX AAS95616;
 XX
 DT 14-FEB-2002 (first entry)
 XX Apolipoprotein C-IV allele-specific oligonucleotide #37.
 DE Apolipoprotein C-IV; APOC4; human; antilipaeamic; haplotyping;
 KW hypertriglyceridaemia; allele-specific oligonucleotide; ASO; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200177127-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 10-APR-2001; 2001WO-US011715.
 PF
 XX 11-APR-2000; 2000US-0195825P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (LEE H.) LEE H H.
 FA
 XX Choi JY, Klie SE, Koshy B;
 PI

XX WPI; 2002-041284/05.
 DR
 XX New haplotypes of human apolipoprotein C-IV gene, useful to diagnose and
 PT treat diseases associated with its activity such as hypertriglyceridemia.
 PF
 XX Claim 18; Page 14; 64pp; English.
 PS
 XX The invention relates to haplotyping the apolipoprotein C-IV (APOC4) gene
 CC of an individual, comprising determining if the individual has one of the
 CC APOC4 haplotypes or haplotype pairs fully defined in the specification.
 CC Haplotyping the APOC4 gene of an individual, comprises determining the
 CC identity of the nucleotide at two or more polymorphic sites in one copy
 CC of the gene. The method also comprises identifying an association between
 CC a trait and a haplotype or haplotype pair of the APOC4 gene, comprising
 CC comparing the frequency of the haplotype/pair in a population exhibiting
 CC the trait with that of a reference population. A higher frequency in the
 CC trait population indicates the trait is associated with the haplotype.
 CC The polymorphisms and screened compounds are useful for developing
 CC treatment for diseases associated with APOC4 activity such as
 CC hypertriglyceridaemia. AAS95580-AAS95634 represent human apolipoprotein C
 CC -IV allele-specific oligonucleotides of the invention
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 GAGCGAC 9
 Db |||||
 9 GAGCGAC 3
 RESULT 815
 ID ABL45894/c
 AC ABL45894 standard; DNA; 10 BP.
 XX ABL45894;
 XX
 DT 26-APR-2002 (first entry)
 XX Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 88.
 DE Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;
 KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
 KW cytosstatic; antiinflammatory; gene therapy; SNP;
 KW single nucleotide polymorphism; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200206446-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 17-JUL-2001; 2001WO-US022523.
 PF
 XX 17-JUL-2000; 2000US-0218727P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA Klie SE, Koshy B;
 XX
 XX WPI; 2002-171804/22.
 DR
 XX New genetic variants of endothelial differentiation, G-protein coupled
 PT receptor-6 gene for studying expression, function of the gene and
 PF expressing EDG6 protein for use in screening drugs to treat cancer,
 PT inflammation.
 XX
 XX Claim 18; Page 14; 111pp; English.
 PS
 XX The present invention provides the gene, protein and cDNA sequences of
 CC

CC the human endothelial differentiation, G-protein coupled receptor 6
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
CC within the sequences. The sequences can be used in the identification of
CC the haplotype of an individual, and in the treatment of cancer,
CC angiogenesis and inflammation. The present sequence is an allele specific
CC primer extension oligonucleotide for the EDG6 gene, which is found on
CC chromosome 19p13.3
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
|||||||
Db 9 CTTTCATC 3

RESULT 816

ABL45906
ID ABL45906 standard; DNA; 10 BP.

XX
AC ABL45906;

XX
DT 26-APR-2002 (first entry)

XX Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 100.
XX Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;
XX haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
XX cytostatic; antiinflammatory; gene therapy; SNP;
XX single nucleotide polymorphism; primer; ss.

OS Homo sapiens.

XX
FN WO200206446-A2.

XX
PD 24-JAN-2002.

XX
PF 17-JUL-2001; 2001WO-US022523.

XX
PR 17-JUL-2000; 2000US-0218727P.

XX
PA (GENA-) GENAISSANCE PHARM INC.

XX
PI Kliem SE, Koshy B;

XX
DR WPI; 2002-171804/22.

XX New genetic variants of endothelial differentiation, G-protein coupled
XX receptor-6 gene for studying expression, function of the gene and
XX expressing EDG6 protein for use in screening drugs to treat cancer,
XX inflammation.

XX
PS Claim 18; Page 14; 111pp; English.

XX The present invention provides the gene, protein and cDNA sequences of
XX the human endothelial differentiation, G-protein coupled receptor 6
XX (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
XX within the sequences. The sequences can be used in the identification of
XX the haplotype of an individual, and in the treatment of cancer,
XX angiogenesis and inflammation. The present sequence is an allele specific
XX primer extension oligonucleotide for the EDG6 gene, which is found on
XX chromosome 19p13.3

XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACCGA 8

Db
3 TGACCGA 9
|||||||

RESULT 817

AAL47237
ID AAL47237 standard; DNA; 10 BP.

XX
AC AAL47237;

XX
DT 22-AUG-2002 (first entry)

XX Allergic disease examination method related PCR primer SEQ ID NO: 5.
XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX atopic dermatitis; human; PCR; primer; ss.

OS Unidentified.

XX
FN WO200233122-A1.

XX
PD 25-APR-2002.

XX
PF 11-OCT-2001; 2001WO-JP008937.

XX
PR 13-OCT-2000; 2000JP-00314093.

XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA) EISAI CO LTD.

XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX Takahashi E;

XX
DR WPI; 2002-372313/40.

XX Method for examining allergic diseases by differential display of
XX intersectin 2 gene showing different expression particularly significant
XX increase in eosinophils in patients.

XX
PS Disclosure; Page 54; 90pp; Japanese.

XX The present invention relates to a method for examining allergic diseases
XX with intersectin 2 gene or a gene with equivalent function of intersectin
XX 2 as an indicator gene, which comprises determining the expression level
XX of the gene in the eosinophils in a patient, and comparing the expression
XX level with that in the eosinophils of a healthy individual. The method is
XX for examining allergic diseases, particularly atopic dermatitis, which is
XX also applicable in screening candidate compounds for remedies. The
XX present sequence is a PCR primer described in the exemplification of the
XX invention

XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGACCGA 8

Db 4 TGACCGA 10

RESULT 818

ABL91888
ID ABL91888 standard; DNA; 10 BP.

XX
AC ABL91888;

XX
DT 11-JUL-2002 (first entry)

XX Human LIPG gene primer extension oligonucleotide 27.

XX

KW Human; ss; primer; extension oligonucleotide;
KW single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
KW drug screening; atherosclerosis; cardiovascular disorder;
KW LIPG haplotyping; LIPG genotyping.
XX
OS Homo sapiens.
XX
PN WO200216397-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US026639.
XX
XX 25-AUG-2000; 2000US-0227825P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Duda A, Kazemi A, Kliem SE, Messer C;
XX
XX WPI; 2002-292055/33.
XX
XX Novel genetic variants of Lipase, Endothelial isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX
XX Claim 18; Page 14; 134pp; English.
XX
XX The invention comprises the DNA and amino acid sequence of the human
CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
CC LIPG coding sequence and protein are useful for screening drugs that can
CC be used to treat atherosclerosis and other cardiovascular disorders. The
CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
CC gene of an individual. The DNA sequences ABL91862 - ABL91901 represent
CC LIPG gene primer extension oligonucleotides
XX
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGA 8
Db 2 TGAGCGA 8

RESULT 819
ABL57223
ID ABL57223 standard; DNA; 10 BP.
XX
XX ABL57223;
AC ABL57223;
XX
XX 05-AUG-2002 (first entry)
XX
XX Primer extension oligonucleotide for FY gene polymorphism detection.
XX
XX Duffy; blood group; FY; human; receptor; haplotyping; genotyping;
KW transgenic animal; malaria; inflammation; antimalarial; protozoacide;
KW antiinflammatory; single nucleotide polymorphism; SNP; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200230950-A2.
XX
XX 18-APR-2002.
XX
XX Primer extension oligonucleotide for FY gene polymorphism detection.
XX
XX Duffy; blood group; FY; human; receptor; haplotyping; genotyping;
KW transgenic animal; malaria; inflammation; antimalarial; protozoacide;
KW antiinflammatory; single nucleotide polymorphism; SNP; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200230950-A2.
XX
XX 18-APR-2002.
XX
XX 15-OCT-2001; 2001WO-US042725.
XX
XX 13-OCT-2000; 2000US-0240275P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Choi JY, Koshiy B;
XX
XX WPI; 2002-426264/45.
XX
XX Novel genetic variants of Duffy Blood group (FY) gene useful for
PT screening drugs to treat diseases e.g. malaria and inflammatory
PT disorders.
XX
XX Claim 17; Page 15; 98pp; English.
XX
XX The present sequence is a portion of an allele-specific oligonucleotide

PI Chew A, Choi JY, Koshiy B;
XX
XX WPI; 2002-426264/45.
XX
XX Novel genetic variants of Duffy Blood group (FY) gene useful for
PT screening drugs to treat diseases e.g. malaria and inflammatory
PT disorders.
XX
XX Claim 17; Page 15; 98pp; English.
XX
XX The present sequence is a portion of an allele-specific oligonucleotide
CC primer designed to detect a polymorphism in the human Duffy blood group
CC (FY) gene (see ABL57150) by primer extension. Preferred primers for use
CC in primer extension terminate in a nucleotide sequence selected from the
CC group given in ABL57199-230, including the present sequence. The
CC extension sequence of each primer is located immediately adjacent to the
CC polymorphic site to be detected. The invention provides novel genetic
CC variants of the FY gene, and discloses various genotypes, haplotypes and
CC haplotype pairs that exist in the general United States population.
CC Compositions and methods for haplotyping and/or genotyping the FY gene in
CC an individual are also disclosed. The polymorphism and haplotype data are
CC useful for validating FY as a candidate target for treating a condition
CC or disease associated with FY activity, such as malaria and inflammatory
CC disorders
XX
SQ Sequence 10 BP; 1 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 4 CTTTCATC 10

RESULT 820
ABL57229/C
ID ABL57229 standard; DNA; 10 BP.
XX
XX ABL57229;
AC ABL57229;
XX
XX 05-AUG-2002 (first entry)
XX
XX Primer extension oligonucleotide for FY gene polymorphism detection.
XX
XX Duffy; blood group; FY; human; receptor; haplotyping; genotyping;
KW transgenic animal; malaria; inflammation; antimalarial; protozoacide;
KW antiinflammatory; single nucleotide polymorphism; SNP; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200230950-A2.
XX
XX 18-APR-2002.
XX
XX 15-OCT-2001; 2001WO-US042725.
XX
XX 13-OCT-2000; 2000US-0240275P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Choi JY, Koshiy B;
XX
XX WPI; 2002-426264/45.
XX
XX Novel genetic variants of Duffy Blood group (FY) gene useful for
PT screening drugs to treat diseases e.g. malaria and inflammatory
PT disorders.
XX
XX Claim 17; Page 15; 98pp; English.
XX
XX The present sequence is a portion of an allele-specific oligonucleotide

CC primer designed to detect a polymorphism in the human Duffy blood group
 CC (FY) gene (see ABL57150) by primer extension. Preferred primers for use
 CC in primer extension terminate in a nucleotide sequence selected from the
 CC group given in ABL57199-230, including the present sequence. The
 CC extension sequence of each primer is located immediately adjacent to the
 CC polymorphic site to be detected. The invention provides novel genetic
 CC variants of the FY gene, and discloses various genotypes, haplotypes and
 CC haplotype pairs that exist in the general United States population.
 CC Compositions and methods for haplotyping and/or genotyping the FY gene in
 CC an individual are also disclosed. The polymorphism and haplotype data are
 CC useful for validating FY as a candidate target for treating a condition
 CC or disease associated with FY activity, such as malaria and inflammatory
 CC disorders

SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
 |||||
 Db 8 CATCCTT 2

RESULT 821
 AAD31785
 ID AAD31785 standard; DNA; 10 BP.

AC AAD31785;

DT 18-JUN-2002 (first entry)

MR 7 arbitrary primer used for modified differential display.

Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
 vaccine; immune response; cytostatic; primer; ss.

Unidentified.

US2002018785-A1.

14-FEB-2002.

02-APR-2001; 2001US-00822250.

22-SEP-1997; 97US-00935377.

(UYRP) UNIV ROCHESTER.

Zauderer M;

WPI; 2002-239252/29.

Representational Difference Analysis method for identification of
 antigens recognized by cytotoxic T cells and specific for human tumors,
 comprises improved selection of genes encoding target antigens.

Example 4; Page 19; 54pp; English.

The present invention relates to novel methods for the identification of
 antigens recognised by cytotoxic T cells (CTLs) and specific for human
 tumours, cancers and infected cells. The method involves screening the
 products of an expression library generated from DNA/RNA of a cell
 expressing a target epitope with cytotoxic T cells generated against the
 cell to identify DNA clones expressing target epitope or providing
 cytotoxic T cells specific for a gene product differentially expressed by
 a cell and measuring the cross-reactivity of the cytotoxic T cells for
 cells expressing a target epitope in which the target epitope is
 identified as a gene product inducing cytotoxic T cells. The method is
 useful for identifying a target epitope or antigen specific for a tumour
 cell. The target epitope is also useful for identifying target antigens
 in other target cells against which it is desirable to induce cell-

CC mediated immunity. The antigen identified by the method is useful in
 CC immunogenic compositions and vaccine preparations to induce the
 CC regression of tumours, cancers and infections in mammals. The invention
 CC also relates to vaccinia viral vectors which are useful for treating
 CC tumour-bearing mammals, including humans to generate immune response
 CC against the tumour cells. They are also useful for immunising or
 CC vaccinating tumour-free subjects to prevent tumour formation. The present
 CC DNA sequence is an arbitrary primer which is used for modified
 CC differential display of genes encoding potential tumour immunogens. This
 CC primer is used in the exemplification of the invention

SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
 |||||
 Db 4 GACTTCA 10

RESULT 822

ABK96529
 ID ABK96529 standard; DNA; 10 BP.

AC ABK96529;

DT 24-SEP-2002 (first entry)

Human PLAU gene, primer extension primer 3' terminus #2.

Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer;
 cytostatic; serine protease; thrombolytic disorder; isogene; PCR;
 pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP;
 single nucleotide polymorphism; thrombolytic; gene therapy;
 primer extension.

Homo sapiens.

WO200240503-A2.

23-MAY-2002.

14-NOV-2001; 2001WO-US044001.

17-NOV-2000; 2000US-0249703P.

(GENA-) GENAISSANCE PHARM INC.

Anastasio AE, Bentivegna SC, Koshy B;

WPI; 2002-519370/55.

Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
 useful for improving efficiency and reliability in drug development for
 treating thrombolytic disorders and cancer.

Claim 16; Page 14; 92pp; English.

The invention relates to a polynucleotide comprising a first nucleotide
 sequence (NSI) comprising a PLAU (plasminogen activator, urokinase, a
 serine protease) isogene selected from isogenes 1-9 and 11-20 given in
 the specification, where each isogene comprises the regions of the PLAU
 gene or cDNA and is further defined by the corresponding sequence of
 polymorphisms (defining single nucleotide polymorphisms, SNP). Also
 included are methods of haplotyping/genotyping (and predicting the
 haplotype/genotype of the PLAU gene of an individual, identifying an
 association between a trait and at least one haplotype or haplotype pair
 of the PLAU gene, an isolated oligonucleotide for detecting a
 polymorphism in the PLAU gene, a recombinant non-human organism
 transformed or transfected with the gene or cDNA, fragments of the
 polynucleotides of at least 10 base pairs encompassing a polymorphic

CC site, an isolated polymorphic variant PLAU protein or fragment, an
 CC isolated monoclonal antibody specific for PLAU, a computer system for
 CC storing and analysing polymorphism data for the PLAU gene and a genome
 CC anthology for the PLAU gene. PLAU is useful in screening for drugs
 CC targeting PLAU that are useful for treating thrombolytic disorders and
 CC cancers. The methods are useful for improving the efficiency and
 CC reliability of the discovery and development of drugs for treating
 CC diseases associated with PLAU activity, in validating PLAU as a drug
 CC target and in the design of clinical trials for treating a specific
 CC condition of disease associated with PLAU activity. The antibody is
 CC useful in diagnostic, prognostic and therapeutic methods. PLAU
 CC polynucleotides are useful in studying the expression and function of
 CC PLAU, and in expressing PLAU protein for use in screening for candidate
 CC drugs to treat diseases related to PLAU activity. The gene for PLAU is
 CC located on chromosome 10q24-qter. The present sequence is the 3' terminus
 CC of an allele specific primer used to amplify PLAU polynucleotides with a
 CC specific polymorphism using the technique of primer extension

XX SQ Sequence 10 BP; 3 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCATC 15
 Db 1 CTTCATC 7
 |||||

RESULT 823
 ACC78757/c
 ID ACC78757 standard; DNA; 10 BP.
 XX AC ACC78757;
 XX DT 02-SEP-2003 (first entry)
 XX DE Normal estrogen responsive cells derived SAGE tag.
 XX KW ERE; reporter construct; estrogen response element; cytostatic; rat;
 XX KW gene therapy; breast cancer; SAGE; ds.
 XX OS Homo sapiens.
 XX PN WO2003042364-A2.
 XX XX 22-MAY-2003.
 XX PF 08-NOV-2002; 2002WO-US035901.
 XX PR 09-NOV-2001; 2001US-0338136P.
 XX FA (DAND) DANA FARBER CANCER INST INC.
 XX PI Polyak K, Pankaj S;
 XX WPI; 2003-449570/42.
 XX PT New reporter construct for identifying and isolating estrogen-responsive
 XX PT cells comprises an estrogen response segment, a promoter segment and a
 XX PT nucleotide sequence that encodes a reporter polypeptide.
 XX PS Example 4; Page 31; 51pp; English.

XX The invention relates to a reporter construct comprising: (a) an estrogen
 CC response segment having 5 or more estrogen response elements (ERE); (b) a
 CC promoter segment having at least one promoter nucleic acid sequence; and
 CC (c) a nucleotide sequence that encodes a reporter polypeptide, where the
 CC nucleotide sequence is operably linked to the promoter segment and the
 CC estrogen response segment. The reporter construct and vector are useful
 CC in identifying and isolating estrogen-responsive cells. The methods are
 CC useful in inhibiting the proliferation or survival of estrogen-responsive
 CC breast cancer cells or in enhancing the proliferation or survival of

CC estrogen-receptor non-expressing, estrogen-non-responsive cells.
 CC Sequences ACC78740-75 represent SAGE tags for transcripts specifically or
 CC most abundantly expressed in normal estrogen responsive cells

XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 38.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
 Db 7 TCATCCT 1
 |||||

RESULT 824
 ADE14179
 ID ADE14179 standard; DNA; 10 BP.
 XX AC ADE14179;
 XX DT 29-JAN-2004 (first entry)
 XX DE Optineurin promoter motif, repeat element or regulatory region #288.
 XX KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 XX KW SNP; glaucoma; progressive ocular hypertensive disorder;
 XX KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX OS Homo sapiens.
 XX PN US2003190617-A1.
 XX PD 09-OCT-2003.
 XX PF 06-MAR-2002; 2002US-00091281.
 XX PR 06-MAR-2002; 2002US-00091281.
 XX PA (SIEE/) SI E.
 XX PA (RAYM/) RAYMOND V.
 XX PA (MORI/) MORISSETTE J.
 XX PI Raymond V, Morissette J, Si E;
 XX WPI; 2003-864168/80.
 XX PT New nucleic acid sequences of the optineurin gene are useful to detect
 XX PT polymorphisms particularly single nucleotide polymorphisms in the
 XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 XX PT disorders.
 XX PS Claim 11; SEQ ID NO 290; 159pp; English.

XX The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid

CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCAT 14
| | | | |
Db 4 ACTTCAT 10

RESULT 825
ADE14178
ID ADE14178 standard; DNA; 10 BP.
XX AC ADE14178;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #287.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
OS
XX
XX US2003190617-A1.
XX
XX 09-OCT-2003.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (STEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
XX Raymond V. Morissette J, Si E;
XX
XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX
XX Claim 11; SEQ ID NO 289; 159pp; English.

CC The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing
CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin

CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 ACTTCAT 14
| | | | |
Db 4 ACTTCAT 10

RESULT 826
ADE48067
ID ADE48067 standard; DNA; 10 BP.
XX AC ADE48067;
XX
DT 29-JAN-2004 (first entry)
XX
DE Primer #12 of the invention.
XX
KW hairpin type polyamide; cancer; primer; ss.
XX
XX Synthetic.
OS
XX WO2003076412-A1.
XX
XX 18-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-JP002423.
XX
XX 08-MAR-2002; 2002JP-00063608.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Sugiyama H, Bando T, Saito I;
XX WPI; 2003-767409/72.
XX
XX New hairpin type polyamide used for treating cancer contains pyrrole and
XX imidazole units and alkylation site.
XX
XX Disclosure; SEQ ID NO 12; 46pp; Japanese.

CC The present invention relates to a new hairpin type polyamide that
CC contains N-methyl-pyrrole and N-methyl imidazole polyamide terminals and
CC an alkylation site linked through a vinyl linker. The method is used for
CC suppressing gene expression and treating cancer. The present sequence
CC represents a primer of the invention.
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GACTTCA 13
| | | | |
Db 4 GACTTCA 10

Search completed: September 9, 2004, 11:27:18
Job time : 3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:28:56 ; Search time 0.001 Seconds
(without alignments)
109.332 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18

Sequence: 1 gtgagcacttcattcctt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 292 seqs, 3037 residues

Total number of hits satisfying chosen parameters: 584

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 292 summaries

Database : rni32.seq *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|--------------------|-------|-------------|--------|----|--------------------|
| 1 | 18 | 100.0 | 18 | 1 | US-09-256-465-32 |
| 2 | 13 | 72.2 | 18 | 1 | US-09-256-465-33 |
| 3 | 12.4 | 68.9 | 15 | 1 | US-08-182-968A-434 |
| 4 | 12.4 | 68.9 | 15 | 1 | US-08-774-306A-434 |
| 5 | 12.4 | 68.9 | 15 | 1 | US-09-064-156A-434 |
| 6 | 10.8 | 60.0 | 15 | 1 | US-09-081-646-434 |
| 7 | 10 | 55.6 | 14 | 1 | US-08-233-030-22 |
| 8 | 10 | 55.6 | 15 | 1 | US-08-182-968A-435 |
| 9 | 10 | 55.6 | 15 | 1 | US-08-774-306A-435 |
| 10 | 10 | 55.6 | 15 | 1 | US-09-064-156A-435 |
| 11 | 9.8 | 54.4 | 15 | 1 | US-08-182-968A-261 |
| 12 | 9.8 | 54.4 | 15 | 1 | US-08-774-306A-261 |
| 13 | 9.8 | 54.4 | 15 | 1 | US-09-064-156A-261 |
| 14 | 9.8 | 54.4 | 15 | 1 | US-09-081-646-599 |
| 15 | 9 | 50.0 | 10 | 1 | US-08-522-384-29 |
| 16 | 9 | 50.0 | 10 | 1 | US-08-522-384-51 |
| 17 | 9 | 50.0 | 10 | 1 | US-08-522-384-52 |
| 18 | 8.8 | 48.9 | 12 | 1 | US-08-874-825-79 |
| 19 | 8.8 | 48.9 | 12 | 1 | US-08-663-824-79 |
| 20 | 8.8 | 48.9 | 12 | 1 | US-09-231-303-79 |
| 21 | 8.4 | 46.7 | 10 | 1 | US-08-522-384-65 |
| 22 | 8.4 | 46.7 | 11 | 1 | US-08-478-470-4 |
| 23 | 8.4 | 46.7 | 11 | 1 | US-08-478-470-5 |
| 24 | 8.4 | 46.7 | 11 | 1 | US-08-478-470-6 |
| 25 | 8.4 | 46.7 | 11 | 1 | US-08-214-599-4 |
| 26 | 8.4 | 46.7 | 11 | 1 | US-08-214-599-5 |
| 27 | 8.4 | 46.7 | 11 | 1 | US-08-214-599-6 |
| 28 | 8.4 | 46.7 | 11 | 1 | US-08-473-015-4 |
| 29 | 8.4 | 46.7 | 11 | 1 | US-08-473-015-5 |
| 30 | 8.4 | 46.7 | 11 | 1 | US-08-473-015-6 |
| 31 | 8.4 | 46.7 | 11 | 1 | US-08-603-566-2 |
| 32 | 8.4 | 46.7 | 11 | 1 | US-08-465-368-4 |
| 33 | 8.4 | 46.7 | 11 | 1 | US-08-465-368-5 |
| 34 | 8.4 | 46.7 | 11 | 1 | US-08-465-368-6 |
| 35 | 8.4 | 46.7 | 11 | 1 | US-08-663-918-10 |
| 36 | 8.4 | 46.7 | 11 | 1 | US-08-477-306-4 |
| 37 | 8.4 | 46.7 | 11 | 1 | US-08-477-306-5 |
| 38 | 8.4 | 46.7 | 11 | 1 | US-08-477-306-6 |
| 39 | 8.4 | 46.7 | 11 | 1 | US-08-771-789-10 |
| 40 | 8.4 | 46.7 | 11 | 1 | US-08-173-489C-289 |
| 41 | 8.4 | 46.7 | 11 | 1 | US-08-700-448-4 |
| 42 | 8.4 | 46.7 | 11 | 1 | US-08-700-448-5 |
| 43 | 8.4 | 46.7 | 11 | 1 | US-08-700-448-6 |
| 44 | 8.4 | 46.7 | 11 | 1 | US-08-923-386A-4 |
| 45 | 8.4 | 46.7 | 11 | 1 | US-08-923-386A-5 |
| 46 | 8.4 | 46.7 | 11 | 1 | US-08-923-386A-6 |
| 47 | 8.4 | 46.7 | 12 | 1 | US-08-413-813-34 |
| 48 | 8.4 | 46.7 | 12 | 1 | US-08-344-820-11 |
| 49 | 8.4 | 46.7 | 12 | 1 | US-08-344-820-14 |
| 50 | 8.4 | 46.7 | 12 | 1 | US-08-547-214-27 |
| 51 | 8.4 | 46.7 | 12 | 1 | US-08-467-346-34 |
| 52 | 8.4 | 46.7 | 12 | 1 | US-08-663-823B-27 |
| 53 | 8.4 | 46.7 | 12 | 1 | US-08-874-825-84 |
| 54 | 8.4 | 46.7 | 12 | 1 | US-08-874-825-99 |
| 55 | 8.4 | 46.7 | 12 | 1 | US-08-663-824-84 |
| 56 | 8.4 | 46.7 | 12 | 1 | US-08-663-824-99 |
| 57 | 8.4 | 46.7 | 12 | 1 | US-08-942-406-27 |
| 58 | 8.4 | 46.7 | 12 | 1 | US-09-322-617-27 |
| 59 | 8.4 | 46.7 | 12 | 1 | US-09-203-231B-31 |
| 60 | 8.4 | 46.7 | 12 | 1 | US-09-231-303-84 |
| 61 | 8.4 | 46.7 | 12 | 1 | US-09-231-303-99 |
| 62 | 8.4 | 46.7 | 12 | 1 | US-09-751-561-27 |
| 63 | 8.4 | 46.7 | 12 | 1 | US-09-724-385-27 |
| 64 | 8.4 | 46.7 | 12 | 1 | US-09-757-528-27 |
| 65 | 8 | 44.4 | 10 | 1 | US-08-522-384-91 |
| 66 | 8 | 44.4 | 10 | 1 | US-09-240-639-29 |
| 67 | 7.8 | 43.3 | 11 | 1 | US-08-068-945A-35 |
| 68 | 7.8 | 43.3 | 11 | 1 | US-08-442-806-35 |
| 69 | 7.8 | 43.3 | 12 | 1 | US-07-967-893-33 |
| 70 | 7.8 | 43.3 | 12 | 1 | US-08-195-072-31 |
| 71 | 7.8 | 43.3 | 12 | 1 | US-08-195-735-31 |
| 72 | 7.8 | 43.3 | 12 | 1 | US-08-195-747-31 |
| 73 | 7.8 | 43.3 | 12 | 1 | US-08-446-884-31 |
| 74 | 7.8 | 43.3 | 12 | 1 | US-08-195-073-31 |
| 75 | 7.8 | 43.3 | 12 | 1 | US-08-198-175-31 |
| 76 | 7.8 | 43.3 | 12 | 1 | US-08-443-153-31 |
| 77 | 7.8 | 43.3 | 12 | 1 | US-08-547-214-10 |
| 78 | 7.8 | 43.3 | 12 | 1 | US-08-663-823B-10 |
| 79 | 7.8 | 43.3 | 12 | 1 | US-08-874-825-96 |
| 80 | 7.8 | 43.3 | 12 | 1 | US-08-663-824-96 |
| 81 | 7.8 | 43.3 | 12 | 1 | US-08-442-807-31 |
| 82 | 7.8 | 43.3 | 12 | 1 | US-08-942-406-10 |
| 83 | 7.8 | 43.3 | 12 | 1 | US-09-322-617-10 |
| 84 | 7.8 | 43.3 | 12 | 1 | US-08-192-946-13 |
| 85 | 7.8 | 43.3 | 12 | 1 | US-09-281-418-100 |
| 86 | 7.8 | 43.3 | 12 | 1 | US-09-203-231B-14 |
| 87 | 7.8 | 43.3 | 12 | 1 | US-09-231-303-96 |
| 88 | 7.8 | 43.3 | 12 | 1 | US-09-751-561-10 |
| 89 | 7.8 | 43.3 | 12 | 1 | US-09-724-385-10 |
| 90 | 7.8 | 43.3 | 12 | 1 | US-09-757-528-10 |
| 91 | 7.8 | 43.3 | 12 | 1 | US-09-844-493-13 |
| 92 | 7.8 | 43.3 | 12 | 1 | US-09-844-265-13 |
| 93 | 7.8 | 43.3 | 12 | 1 | US-08-874-601-138 |
| 94 | 7.4 | 41.1 | 9 | 1 | US-08-605-163-4 |
| 95 | 7.4 | 41.1 | 10 | 1 | US-09-985-799-12 |
| 96 | 7.4 | 41.1 | 10 | 1 | US-07-860-445-17 |
| 97 | 7.4 | 41.1 | 10 | 1 | US-08-665-511-17 |
| 98 | 7.4 | 41.1 | 10 | 1 | US-08-594-031-12 |
| 99 | 7.4 | 41.1 | 10 | 1 | US-08-173-489C-303 |
| 100 | 7.4 | 41.1 | 10 | 1 | US-08-477-396A-14 |
| 101 | 7.4 | 41.1 | 10 | 1 | US-08-780-835B-5 |
| 102 | 7.4 | 41.1 | 10 | 1 | US-08-780-835B-6 |
| 103 | 7.4 | 41.1 | 10 | 1 | US-08-265-484B-3 |
| 104 | 7.4 | 41.1 | 10 | 1 | US-08-388-353-185 |
| 105 | 7.4 | 41.1 | 10 | 1 | US-08-388-353-186 |
| 106 | 7.4 | 41.1 | 10 | 1 | US-08-488-551B-185 |
| Sequence 6, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 4, Appli | | | | | |
| Sequence 5, Appli | | | | | |
| Sequence 6, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 289, App | | | | | |
| Sequence 4, Appli | | | | | |
| Sequence 5, Appli | | | | | |
| Sequence 6, Appli | | | | | |
| Sequence 4, Appli | | | | | |
| Sequence 5, Appli | | | | | |
| Sequence 6, Appli | | | | | |
| Sequence 11, Appli | | | | | |
| Sequence 14, Appli | | | | | |
| Sequence 27, Appli | | | | | |
| Sequence 34, Appli | | | | | |
| Sequence 27, Appli | | | | | |
| Sequence 84, Appli | | | | | |
| Sequence 99, Appli | | | | | |
| Sequence 99, Appli | | | | | |
| Sequence 27, Appli | | | | | |
| Sequence 31, Appli | | | | | |
| Sequence 91, Appli | | | | | |
| Sequence 29, Appli | | | | | |
| Sequence 35, Appli | | | | | |
| Sequence 33, Appli | | | | | |
| Sequence 31, Appli | | | | | |
| Sequence 31, Appli | | | | | |
| Sequence 31, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 13, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 14, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 13, Appli | | | | | |
| Sequence 10, Appli | | | | | |
| Sequence 17, Appli | | | | | |
| Sequence 12, Appli | | | | | |
| Sequence 17, Appli | | | | | |
| Sequence 303, App | | | | | |
| Sequence 14, Appli | | | | | |
| Sequence 5, Appli | | | | | |
| Sequence 6, Appli | | | | | |
| Sequence 3, Appli | | | | | |
| Sequence 185, App | | | | | |
| Sequence 186, App | | | | | |
| Sequence 185, App | | | | | |

| | | | | | | | | | | | | | |
|-------|-----|------|----|---|--------------------|-------------------|-------|-----|------|----|---|--------------------|--------------------|
| c 107 | 7.4 | 41.1 | 10 | 1 | US-08-488-551B-186 | Sequence 186, App | 180 | 7 | 38.9 | 10 | 1 | US-09-508-753B-209 | Sequence 209, App |
| c 108 | 7.4 | 41.1 | 10 | 1 | US-09-033-743-17 | Sequence 17, Appl | 181 | 7 | 38.9 | 10 | 1 | US-09-508-753B-299 | Sequence 299, App |
| c 109 | 7.4 | 41.1 | 10 | 1 | US-08-765-257A-3 | Sequence 30, Appl | 182 | 7 | 38.9 | 10 | 1 | US-10-032-307-41 | Sequence 41, Appl |
| c 110 | 7.4 | 41.1 | 10 | 1 | US-08-522-384-50 | Sequence 50, Appl | c 183 | 6.8 | 37.8 | 10 | 1 | US-08-078-662A-12 | Sequence 12, Appl |
| c 111 | 7.4 | 41.1 | 10 | 1 | US-08-522-384-53 | Sequence 53, Appl | c 184 | 6.8 | 37.8 | 10 | 1 | US-08-335-565A-17 | Sequence 17, Appl |
| c 112 | 7.4 | 41.1 | 10 | 1 | US-08-522-384-64 | Sequence 64, Appl | c 185 | 6.8 | 37.8 | 10 | 1 | US-08-440-787A-83 | Sequence 83, Appl |
| c 113 | 7.4 | 41.1 | 10 | 1 | US-08-522-384-75 | Sequence 75, Appl | c 186 | 6.8 | 37.8 | 10 | 1 | US-08-545-253A-15 | Sequence 15, Appl |
| c 114 | 7.4 | 41.1 | 10 | 1 | US-09-303-268-5 | Sequence 5, Appl | c 187 | 6.8 | 37.8 | 10 | 1 | US-08-780-835B-3 | Sequence 3, Appl |
| c 115 | 7.4 | 41.1 | 10 | 1 | US-09-303-268-6 | Sequence 6, Appl | c 188 | 6.8 | 37.8 | 10 | 1 | US-08-481-658B-23 | Sequence 23, Appl |
| c 116 | 7.4 | 41.1 | 10 | 1 | US-08-991-789A-103 | Sequence 103, App | c 189 | 6.8 | 37.8 | 10 | 1 | US-08-053-451B-156 | Sequence 156, App |
| c 117 | 7.4 | 41.1 | 10 | 1 | US-09-116-049-7 | Sequence 7, Appl | c 190 | 6.8 | 37.8 | 10 | 1 | US-08-477-504A-23 | Sequence 23, Appl |
| c 118 | 7.4 | 41.1 | 10 | 1 | US-09-116-049-8 | Sequence 8, Appl | c 191 | 6.8 | 37.8 | 10 | 1 | US-08-486-756A-23 | Sequence 23, Appl |
| c 119 | 7.4 | 41.1 | 10 | 1 | US-09-062-451-103 | Sequence 103, App | c 192 | 6.8 | 37.8 | 10 | 1 | US-08-485-862B-23 | Sequence 23, Appl |
| c 120 | 7.4 | 41.1 | 10 | 1 | US-09-598-326-103 | Sequence 103, App | c 193 | 6.8 | 37.8 | 10 | 1 | US-08-388-353-189 | Sequence 189, App |
| c 121 | 7.4 | 41.1 | 10 | 1 | US-08-370-838-48 | Sequence 48, Appl | c 194 | 6.8 | 37.8 | 10 | 1 | US-08-388-353-261 | Sequence 261, App |
| c 122 | 7.4 | 41.1 | 10 | 1 | US-09-428-236-6 | Sequence 6, Appl | c 195 | 6.8 | 37.8 | 10 | 1 | US-08-388-353-455 | Sequence 455, App |
| c 123 | 7.4 | 41.1 | 10 | 1 | US-09-508-753B-63 | Sequence 63, App | c 196 | 6.8 | 37.8 | 10 | 1 | US-08-488-551B-189 | Sequence 189, App |
| c 124 | 7.4 | 41.1 | 10 | 1 | US-09-508-753B-387 | Sequence 387, App | c 197 | 6.8 | 37.8 | 10 | 1 | US-08-488-551B-261 | Sequence 261, App |
| c 125 | 7.4 | 41.1 | 10 | 1 | US-09-508-753B-389 | Sequence 389, App | c 198 | 6.8 | 37.8 | 10 | 1 | US-08-488-551B-455 | Sequence 455, App |
| c 126 | 7.4 | 41.1 | 10 | 1 | US-09-884-363-7 | Sequence 7, Appl | c 199 | 6.8 | 37.8 | 10 | 1 | US-08-787-739-23 | Sequence 23, Appl |
| c 127 | 7.4 | 41.1 | 10 | 1 | US-08-884-363-8 | Sequence 8, Appl | c 200 | 6.8 | 37.8 | 10 | 1 | US-08-787-739-24 | Sequence 24, Appl |
| c 128 | 7.4 | 41.1 | 10 | 1 | US-09-289-198-103 | Sequence 103, App | c 201 | 6.8 | 37.8 | 10 | 1 | US-08-719-337-15 | Sequence 15, Appl |
| c 129 | 7.4 | 41.1 | 10 | 1 | US-09-429-755-103 | Sequence 103, App | c 202 | 6.8 | 37.8 | 10 | 1 | US-08-487-077A-23 | Sequence 23, Appl |
| c 130 | 7.4 | 41.1 | 11 | 1 | US-08-180-195-20 | Sequence 20, Appl | c 203 | 6.8 | 37.8 | 10 | 1 | US-08-485-863A-23 | Sequence 23, Appl |
| c 131 | 7.4 | 41.1 | 11 | 1 | US-07-860-445-22 | Sequence 22, Appl | c 204 | 6.8 | 37.8 | 10 | 1 | US-09-063-450-30 | Sequence 30, Appl |
| c 132 | 7.4 | 41.1 | 11 | 1 | US-08-171-389-619 | Sequence 619, App | c 205 | 6.8 | 37.8 | 10 | 1 | US-08-522-384-77 | Sequence 77, Appl |
| c 133 | 7.4 | 41.1 | 11 | 1 | US-08-344-695-24 | Sequence 24, Appl | c 206 | 6.8 | 37.8 | 10 | 1 | US-08-564-100-8 | Sequence 8, Appl |
| c 134 | 7.4 | 41.1 | 11 | 1 | US-08-344-695-25 | Sequence 25, Appl | c 207 | 6.8 | 37.8 | 10 | 1 | US-09-303-268-3 | Sequence 3, Appl |
| c 135 | 7.4 | 41.1 | 11 | 1 | US-08-344-695-26 | Sequence 26, Appl | c 208 | 6.8 | 37.8 | 10 | 1 | US-08-485-049D-23 | Sequence 23, Appl |
| c 136 | 7.4 | 41.1 | 11 | 1 | US-08-344-695-27 | Sequence 27, Appl | c 209 | 6.8 | 37.8 | 10 | 1 | US-09-116-049-5 | Sequence 5, Appl |
| c 137 | 7.4 | 41.1 | 11 | 1 | US-08-344-695-29 | Sequence 29, Appl | c 210 | 6.8 | 37.8 | 10 | 1 | US-09-178-115-23 | Sequence 23, Appl |
| c 138 | 7.4 | 41.1 | 11 | 1 | US-07-996-783-19 | Sequence 19, Appl | c 211 | 6.8 | 37.8 | 10 | 1 | US-09-178-115-24 | Sequence 24, Appl |
| c 139 | 7.4 | 41.1 | 11 | 1 | US-08-484-499-19 | Sequence 19, Appl | c 212 | 6.8 | 37.8 | 10 | 1 | US-08-177-776-23 | Sequence 23, Appl |
| c 140 | 7.4 | 41.1 | 11 | 1 | US-08-665-511-22 | Sequence 22, Appl | c 213 | 6.8 | 37.8 | 10 | 1 | US-09-177-776-24 | Sequence 24, Appl |
| c 141 | 7.4 | 41.1 | 11 | 1 | US-08-123-936-619 | Sequence 619, App | c 214 | 6.8 | 37.8 | 10 | 1 | US-09-140-084-15 | Sequence 15, Appl |
| c 142 | 7.4 | 41.1 | 11 | 1 | US-08-475-221B-19 | Sequence 19, Appl | c 215 | 6.8 | 37.8 | 10 | 1 | US-08-618-834C-46 | Sequence 46, Appl |
| c 143 | 7.4 | 41.1 | 11 | 1 | US-08-476-876-19 | Sequence 19, Appl | c 216 | 6.8 | 37.8 | 10 | 1 | US-09-498-608A-11 | Sequence 11, Appl |
| c 144 | 7.4 | 41.1 | 11 | 1 | US-08-477-329-20 | Sequence 20, Appl | c 217 | 6.8 | 37.8 | 10 | 1 | US-09-724-297-15 | Sequence 15, Appl |
| c 145 | 7.4 | 41.1 | 11 | 1 | US-08-475-458-20 | Sequence 20, Appl | c 218 | 6.8 | 37.8 | 10 | 1 | US-09-154-750A-33 | Sequence 33, Appl |
| c 146 | 7.4 | 41.1 | 11 | 1 | US-08-173-489C-290 | Sequence 290, App | c 219 | 6.8 | 37.8 | 10 | 1 | US-09-508-753B-77 | Sequence 77, Appl |
| c 147 | 7.4 | 41.1 | 11 | 1 | US-08-475-228A-619 | Sequence 619, App | c 220 | 6.8 | 37.8 | 10 | 1 | US-09-508-753B-154 | Sequence 154, App |
| c 148 | 7.4 | 41.1 | 11 | 1 | US-08-482-080A-619 | Sequence 619, App | c 221 | 6.8 | 37.8 | 10 | 1 | US-09-508-753B-247 | Sequence 247, App |
| c 149 | 7.4 | 41.1 | 11 | 1 | US-08-980-400-20 | Sequence 20, Appl | c 222 | 6.8 | 37.8 | 10 | 1 | US-09-508-753B-282 | Sequence 282, App |
| c 150 | 7.4 | 41.1 | 11 | 1 | US-09-033-743-22 | Sequence 22, Appl | c 223 | 6.8 | 37.8 | 10 | 1 | US-09-508-753B-411 | Sequence 411, App |
| c 151 | 7.4 | 41.1 | 11 | 1 | US-08-136-523-26 | Sequence 26, Appl | c 224 | 6.8 | 37.8 | 10 | 1 | US-08-894-454-132 | Sequence 132, App |
| c 152 | 7.4 | 41.1 | 11 | 1 | US-08-083-945C-8 | Sequence 8, Appl | c 225 | 6.8 | 37.8 | 10 | 1 | US-09-769-482-30 | Sequence 30, Appl |
| c 153 | 7.4 | 41.1 | 11 | 1 | US-09-583-459A-20 | Sequence 20, Appl | c 226 | 6.8 | 37.8 | 10 | 1 | US-09-884-363-5 | Sequence 5, Appl |
| c 154 | 7.4 | 41.1 | 11 | 1 | US-09-583-210-20 | Sequence 20, Appl | c 227 | 6.8 | 37.8 | 10 | 1 | US-09-989-789-1268 | Sequence 1268, Ap |
| c 155 | 7.4 | 41.1 | 11 | 1 | US-09-583-449A-20 | Sequence 20, Appl | c 228 | 6.8 | 37.8 | 10 | 1 | US-09-989-789-1630 | Sequence 1630, Ap |
| c 156 | 7.4 | 41.1 | 11 | 1 | US-09-435-059-20 | Sequence 20, Appl | c 229 | 6.8 | 37.8 | 10 | 1 | US-09-989-789-1631 | Sequence 1631, Ap |
| c 157 | 7.4 | 41.1 | 11 | 1 | US-09-334-947-619 | Sequence 619, App | c 230 | 6.8 | 37.8 | 10 | 1 | 5175268-10 | Patent No. 5175268 |
| c 158 | 7.4 | 41.1 | 11 | 1 | US-09-249-155A-4 | Sequence 4, Appl | c 231 | 6.4 | 35.6 | 8 | 1 | US-08-232-144-9 | Sequence 9, Appl |
| c 159 | 7.4 | 41.1 | 11 | 1 | US-09-249-155A-163 | Sequence 163, App | c 232 | 6.4 | 35.6 | 8 | 1 | US-08-509-858-3 | Sequence 3, Appl |
| c 160 | 7.4 | 41.1 | 11 | 1 | US-09-249-155A-267 | Sequence 267, App | c 233 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-42 | Sequence 42, Appl |
| c 161 | 7.4 | 41.1 | 11 | 1 | US-09-249-155A-317 | Sequence 317, App | c 234 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-95 | Sequence 95, Appl |
| c 162 | 7.4 | 41.1 | 11 | 1 | PCT-US93-12388-619 | Sequence 619, App | c 235 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-146 | Sequence 146, App |
| c 163 | 7.4 | 41.1 | 11 | 1 | PCT-US94-07107A-8 | Sequence 8, Appl | c 236 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-152 | Sequence 152, App |
| c 164 | 7.4 | 41.1 | 11 | 1 | US-08-859-954-85 | Sequence 85, Appl | c 237 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-155 | Sequence 155, App |
| c 165 | 7.4 | 38.9 | 8 | 1 | US-08-859-954-111 | Sequence 111, App | c 238 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-197 | Sequence 197, App |
| c 166 | 7.4 | 38.9 | 8 | 1 | US-08-859-954-365 | Sequence 365, App | c 239 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-213 | Sequence 213, App |
| c 167 | 7.4 | 38.9 | 9 | 1 | US-09-432-020B-14 | Sequence 14, Appl | c 240 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-217 | Sequence 217, App |
| c 168 | 7.4 | 38.9 | 9 | 1 | US-09-163-485-23 | Sequence 23, Appl | c 241 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-247 | Sequence 247, App |
| c 169 | 7.4 | 38.9 | 9 | 1 | US-09-133-242-38 | Sequence 38, Appl | c 242 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-446 | Sequence 446, App |
| c 170 | 7.4 | 38.9 | 9 | 1 | US-09-989-789-2472 | Sequence 2472, Ap | c 243 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-539 | Sequence 539, App |
| c 171 | 7.4 | 38.9 | 9 | 1 | US-09-989-789-2477 | Sequence 2477, Ap | c 244 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-543 | Sequence 543, App |
| c 172 | 7.4 | 38.9 | 10 | 1 | US-08-441-887A-306 | Sequence 306, App | c 245 | 6.4 | 35.6 | 8 | 1 | US-08-859-954-544 | Sequence 544, App |
| c 173 | 7.4 | 38.9 | 10 | 1 | US-08-522-384-116 | Sequence 116, App | c 246 | 6.4 | 35.6 | 8 | 1 | US-09-041-675-26 | Sequence 26, Appl |
| c 174 | 7.4 | 38.9 | 10 | 1 | US-09-305-408-21 | Sequence 21, App | c 247 | 6.4 | 35.6 | 8 | 1 | US-09-256-340-6 | Sequence 6, Appl |
| c 175 | 7.4 | 38.9 | 10 | 1 | US-09-305-408-22 | Sequence 22, App | c 248 | 6.4 | 35.6 | 8 | 1 | US-09-256-340-7 | Sequence 7, Appl |
| c 176 | 7.4 | 38.9 | 10 | 1 | US-09-305-408-31 | Sequence 31, App | c 249 | 6.4 | 35.6 | 8 | 1 | US-09-813-378-6 | Sequence 6, Appl |
| c 177 | 7.4 | 38.9 | 10 | 1 | US-08-927-165A-32 | Sequence 32, App | c 250 | 6.4 | 35.6 | 8 | 1 | US-09-813-378-7 | Sequence 7, Appl |
| c 178 | 7.4 | 38.9 | 10 | 1 | US-09-508-753B-34 | Sequence 34, Appl | c 251 | 6.4 | 35.6 | 8 | 1 | US-09-232-000B-27 | Sequence 27, Appl |
| c 179 | 7.4 | 38.9 | 10 | 1 | US-09-508-753B-132 | Sequence 132, App | c 252 | 6.4 | 35.6 | 8 | 1 | US-09-232-000B-30 | Sequence 30, Appl |

```
253 6.4 35.6 8 1 US-09-232-000B-40 Sequence 40, Appl
254 6.4 35.6 8 1 US-10-010-717-6 Sequence 6, Appl
255 6.4 35.6 8 1 US-10-010-717-7 Sequence 7, Appl
256 6.4 35.6 9 1 US-09-194-842A-13 Sequence 13, Appl
257 6.4 35.6 9 1 US-09-194-842A-24 Sequence 24, Appl
258 6.4 35.6 9 1 US-09-194-842A-27 Sequence 27, Appl
259 6.4 35.6 9 1 US-09-989-789-2014 Sequence 2014, Ap
260 6.4 35.6 9 1 US-09-989-789-2167 Sequence 2167, Ap
261 6.4 35.6 9 1 US-09-989-789-2236 Sequence 2236, Ap
262 6.2 34.4 9 1 PCT-US91-03680-53 Sequence 53, Appl
263 6.2 33.3 8 1 US-08-436-145-6 Sequence 6, Appl
264 6.2 33.3 8 1 US-08-480-173A-27 Sequence 27, Appl
265 6.2 33.3 8 1 US-08-859-954-60 Sequence 60, Appl
266 6.2 33.3 8 1 US-08-859-954-168 Sequence 168, App
267 6.2 33.3 8 1 US-08-859-954-184 Sequence 184, App
268 6.2 33.3 8 1 US-08-859-954-245 Sequence 245, App
269 6.2 33.3 8 1 US-08-859-954-246 Sequence 246, App
270 6.2 33.3 8 1 US-08-859-954-277 Sequence 277, App
271 6.2 33.3 8 1 US-08-859-954-346 Sequence 346, App
272 6.2 33.3 8 1 US-08-859-954-549 Sequence 549, App
273 6.2 33.3 8 1 US-08-859-954-561 Sequence 561, App
274 6.2 33.3 8 1 US-08-484-408A-27 Sequence 27, Appl
275 6.2 33.3 9 1 US-08-097-349-11 Sequence 11, Appl
276 6.2 33.3 9 1 US-08-586-329-10 Sequence 10, Appl
277 6.2 33.3 9 1 US-08-503-671-11 Sequence 11, Appl
278 6.2 33.3 9 1 US-08-318-947A-12 Sequence 12, Appl
279 6.2 33.3 9 1 US-08-605-163-19 Sequence 19, Appl
280 6.2 33.3 9 1 US-08-795-303-12 Sequence 12, Appl
281 6.2 33.3 9 1 US-08-383-630-18 Sequence 18, Appl
282 6.2 33.3 9 1 US-09-194-842A-12 Sequence 12, Appl
283 6.2 33.3 9 1 US-09-989-789-455 Sequence 455, App
284 6.2 33.3 9 1 US-09-989-789-456 Sequence 456, App
285 6.2 33.3 9 1 US-09-989-789-577 Sequence 577, App
286 6.2 33.3 9 1 US-09-989-789-2103 Sequence 2103, Ap
287 6.2 33.3 9 1 US-09-989-789-2231 Sequence 2231, Ap
288 6.2 33.3 9 1 US-09-989-789-2232 Sequence 2232, Ap
289 6.2 33.3 9 1 US-09-989-789-2246 Sequence 2246, Ap
290 6.2 33.3 9 1 US-09-989-789-2498 Sequence 2498, Ap
291 6.2 33.3 9 1 PCT-US91-03680-43 Sequence 43, Appl
292 6.2 33.3 9 1 5256568-5 Patent No. 5256568
```

ALIGNMENTS

```
RESULT 1
US-09-256-465-32
; Sequence 32, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-32
```

```
Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCCTT 18
   |||||
Db 1 GTGAGCGACTTCCTT 18
```

```
RESULT 2
US-09-256-465-33
; Sequence 33, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-33

Query Match 72.2%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
   |||||
Db 6 GTGAGCGACTTCA 18

RESULT 3
US-08-182-968A-434/c
; Sequence 434, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 434:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
US-08-182-968A-434
Query Match 68.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.4;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
Db 14 GTGAGCGACTTTAT 1

RESULT 4
US-08-774-306A-434/c
; Sequence 434, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774.306A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 434:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-434

Query Match 68.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.4;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
Db 14 GTGAGCGACTTTAT 1

RESULT 5
US-09-064-156A-434/c
; Sequence 434, Application US/09064156A
; Patent No. 6132966
```

```
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 434:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-434

Query Match 68.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.4;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
Db 14 GTGAGCGACTTTAT 1

RESULT 6
US-09-081-646-434/c
; Sequence 434, Application US/09081646
; Patent No. 6331152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: Fast-SEQ for Windows Version 3.0
```


; SEQ ID NO 434
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-434

Query Match 60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. NO. 19;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
| | | | | | | | | | | | | | | |
Db 15 GTGAGCGTCATCAT 2

RESULT 7
US-08-233-030-22/c
; Sequence 22, Application US/08233030
; Patent No. 5639655
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TREATMENT OF PROMYELOCYTIC
; LEUKEMIA
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,030
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,910
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-233-030-22

Query Match 55.6%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. NO. 27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
| | | | | | | | | | | | | | | |
Db 10 ACTTCATCCT 1

RESULT 8
US-08-182-968A-435/c
; Sequence 435, Application US/08182968A

; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; INHIBITING HEPATITIS C
; VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-435

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
| | | | | | | | | | | |
Db 10 GTGAGCGACT 1

RESULT 9
US-08-774-306A-435/c
; Sequence 435, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; INHIBITING HEPATITIS C
; VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-435

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
|||
Db 10 GTGAGCGACT 1

RESULT 10
US-09-064-156A-435/c
; Sequence 435, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-435

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
|||
Db 10 GTGAGCGACT 1

RESULT 11
US-08-182-968A-261
; Sequence 261, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-261

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13

Db 1 3 GUGAUCGACUGCA 15

RESULT 12

US-08-774-306A-261
; Sequence 261, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-261

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
Db 3 GUGAUCGACUGCA 15

RESULT 13
US-08-774-306A-261
; Sequence 261, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 261:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-261

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
Db 3 GUGAUCGACUGCA 15

RESULT 14
US-09-081-646-599/c
; Sequence 599, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 599
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-599

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 32;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
|||||
Db 14 TGAGAGACTGCAT 2

RESULT 15

US-08-522-384-29
; Sequence 29, Application US/08522384
; Patent No. 6110667

; GENERAL INFORMATION:

; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-29

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 2 CTTTCATCCT 10

RESULT 16

US-08-522-384-51
; Sequence 51, Application US/08522384
; Patent No. 6110667

; GENERAL INFORMATION:

; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-51

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 1 CTTTCATCCT 9

RESULT 17

US-08-522-384-52
; Sequence 52, Application US/08522384
; Patent No. 6110667

; GENERAL INFORMATION:

; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-52

Query Match 50.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 1 CTTTCATCCT 9

RESULT 18

US-08-874-825-79/c
; Sequence 79, Application US/08874825
; Patent No. 6057101

; GENERAL INFORMATION:

; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Meijia
; APPLICANT: Knight, James
; APPLICANT: Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,824
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-874-825-79

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCA 13
| | | | | | | |
Db 12 TCAGCGACTGCA 1

RESULT 19

US-08-663-824-79/c
; Sequence 79, Application US/08663824
; Patent No. 6083693
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
; FILE REFERENCE: 7934-006
; CURRENT APPLICATION NUMBER: US/08/663,824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-79

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCA 13
| | | | | | | |
Db 12 TCAGCGACTGCA 1

RESULT 20

US-09-231-303-79/c
; Sequence 79, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-79

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCA 13
| | | | | | | |
Db 12 TCAGCGACTGCA 1

RESULT 21

US-08-522-384-65
; Sequence 65, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-65

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
| | | | | | | |
Db 1 GCCTTCATCC 10

RESULT 22

US-08-478-470-4
; Sequence 4, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYAZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3'-P5, PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE
; TITLE OF INVENTION: RESISTANCE PROPERTIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; ADDRESSEE: Huddleson & Tatum
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
US-08-478-470-4

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||
Db 1 CTTCTTCCTT 10

RESULT 23
US-08-478-470-5
; Sequence 5, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYAZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3'-P5' PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE
; TITLE OF INVENTION: RESISTANCE PROPERTIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
US-08-478-470-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||
Db 1 CTTCTTCCTT 10

RESULT 24
US-08-478-470-6
; Sequence 6, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYAZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3'-P5' PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE
; TITLE OF INVENTION: RESISTANCE PROPERTIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /note= "where the intersubunit
; bonds are "np"
US-08-478-470-6

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||
Db 1 CTTCTTCCTT 10

RESULT 25
US-08-214-599-4
; Sequence 4, Application US/08214599
; Patent No. 5599922

```
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
; US-08-214-599-4
;
; Query Match 46.7%; Score 8.4; DB 1; Length 11;
; Best Local Similarity 90.0%; Pred. No. 46;
; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 9 CTTTCATCCTT 18
; Db 1 CTTCTTCCTT 10
;
; RESULT 26
; US-08-214-599-5
; Sequence 5, Application US/08214599
; Patent No. 5599922
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
; US-08-214-599-5
;
; Query Match 46.7%; Score 8.4; DB 1; Length 11;
; Best Local Similarity 90.0%; Pred. No. 46;
; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 9 CTTTCATCCTT 18
; Db 1 CTTCTTCCTT 10
;
; RESULT 27
; US-08-214-599-6
; Sequence 6, Application US/08214599
; Patent No. 5599922
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
```

;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 2
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..11
;; OTHER INFORMATION: /note= "where the intersubunit
;; OTHER INFORMATION: bonds are "np"
US-08-214-599-6

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 1 CTTCTTCCTT 10

RESULT 28
US-08-473-015-4
; Sequence 4, Application US/08473015
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
US-08-473-015-4

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 1 CTTCTTCCTT 10

RESULT 29
US-08-473-015-5
; Sequence 5, Application US/08473015
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
US-08-473-015-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 1 CTTCTTCCTT 10

RESULT 30
US-08-473-015-6
; Sequence 6, Application US/08473015
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,015
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
US-08-473-015-4


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473.015
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,599
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 5525-0012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 2
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..11
OTHER INFORMATION: /note="where the intersubunit
US-08-473-015-6
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCATCCTT 10

RESULT 31
US-08-603-566-2
Sequence 2, Application US/08603566
Patent No. 5684143
GENERAL INFORMATION:
APPLICANT: Sergei Gryaznov, Ronald G. Schultz
TITLE OF INVENTION: Oligo-2'-fluoronucleotide N3'->P5' Phosphoramidates
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Macintosh PowerBook 5300cs
OPERATING SYSTEM: Macintosh OS 7.52
SOFTWARE: Microsoft Word 5.1

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603.566
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: LYNX-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-603-566-2
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CUUCUCCUU 10

RESULT 32
US-08-465-368-4
Sequence 4, Application US/08465368
Patent No. 5726297
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei
APPLICANT: Schultz, Ronald G.
APPLICANT: Chen, Jer-kang
TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.368
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,505
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 5525-0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
US-08-465-368-4

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 33
US-08-465-368-5
; Sequence 5, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,368
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,505
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
US-08-465-368-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 34
US-08-465-368-6
; Sequence 6, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,368
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,505
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /note= "where the intersubunit
; OTHER INFORMATION: bonds are "np."
US-08-465-368-6

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 1 CTTCTTCCTT 10

RESULT 35
US-08-663-918-10
; Sequence 10, Application US/08663918

```
; Patent No. 5824793
; GENERAL INFORMATION:
; APPLICANT: Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeff
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide N3 (symbol 174 \f "Sy
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,918
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: LYNX-035/01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-663-918-10

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CUUCUCCUU 10

RESULT 36
US-08-477-306-4
; Sequence 4, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-ps'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid

; Patent No. 5824793
; GENERAL INFORMATION:
; APPLICANT: Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeff
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide N3 (symbol 174 \f "Sy
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,918
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: LYNX-035/01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-663-918-10

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CUUCUCCUU 10

RESULT 37
US-08-477-306-5
; Sequence 5, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-ps'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
US-08-477-306-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 1 CTTTCATCCTT 10

RESULT 38

US-08-477-306-6
Sequence 6, Application US/08477306
Patent No. 5837835
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei
TITLE OF INVENTION: Oligonucleotide N3'-P5'
TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
TITLE OF INVENTION: Properties
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,306
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,599
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 5525-0012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 2

FEATURE:
NAME/KEY: misc feature
LOCATION: 1..11
OTHER INFORMATION: /note="where the intersubunit
OTHER INFORMATION: bonds are "np"
US-08-477-306-6

Query Match 46.7%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
||| |||||
Db 1 CTTTCATCCTT 10

RESULT 39

US-08-771-789-10
Sequence 10, Application US/08771789
Patent No. 5859233
GENERAL INFORMATION:
APPLICANT: Bernard Hirschbein
APPLICANT: Karen Fearon
APPLICANT: Sergei Gryaznov
APPLICANT: Sarah McCurdy
APPLICANT: Jeffery Nelson
APPLICANT: Ronald G. Schultz
TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide
TITLE OF INVENTION: N3 {symbol 174 \f "Symbol" \s 12}}P5 Phosphoramidates
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: Microsoft Word for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,789
FILING DATE: 20-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,918
FILING DATE: 14-JUN-1996
APPLICATION NUMBER: 08/603,566
FILING DATE: 21-FEB-96
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: LYNX-035/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-771-789-10
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||:| :||:
Db 1 CUUCUCCUU 10

RESULT 40

US-08-173-489C-289/C
Sequence 289, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.

APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 16S rRNA gene from Clostridium
DESCRIPTION: pasteurianum (Accession # M23930) nucleotides
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Clostridium pasteurianum
PUBLICATION INFORMATION:
AUTHORS: Weisburg, W G, Tully, J G, Rose, D L,
AUTHORS: Petzel, J P, Oyaizu, H, Yang, D, Mandelco,
AUTHORS: L, Sechrest, J, Lawrence, T G, Van Etten, J,
AUTHORS: Maniloff, J, Woese, C R.
TITLE: A phylogenetic analysis of
JOURNAL: Journal of Bacteriology
VOLUME: 171
PAGES: 6455-6467
DATE: 1989
RELEVANT RESIDUES IN SEQ ID NO: 289 :FROM 1 TO 11
US-08-173-489C-289

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 11 CTTTCCTCCTT 2

RESULT 41

US-08-700-448-4
Sequence 4, Application US/08700448
Patent No. 5965720
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei et al.
TITLE OF INVENTION: Oligonucleotide N3'-ps'

TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,448
FILING DATE: 01/10/97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent M. Powers
REGISTRATION NUMBER: 36,246
REFERENCE/DOCKET NUMBER: 5525-0012.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 2
US-08-700-448-4
Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTTTCATCCTT 18
Db 1 CTTTCCTCCTT 10
RESULT 42
US-08-700-448-5
Sequence 5, Application US/08700448
Patent No. 5965720
GENERAL INFORMATION:
APPLICANT: Gryaznov, Sergei et al.
TITLE OF INVENTION: Oligonucleotide N3'-ps'
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,448
FILING DATE: 01/10/97

```
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent M. Powers
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 5525-0012.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 2
US-08-700-448-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 43
US-08-700-448-6
; Sequence 6, Application US/08700448
; Patent No. 5965720
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei et al.
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,448
; FILING DATE: 01/10/97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent M. Powers
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 5525-0012.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 3
US-08-923-386A-4

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 44
US-08-923-386A-4
; Sequence 4, Application US/08923386A
; Patent No. 6169170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Oligonucleotide 4, Fig. 3
US-08-923-386A-4

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTCTTCCTT 10

RESULT 45
```

US-08-923-386A-5
; Sequence 5, Application US/08923386A
; Patent No. 6169170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923.386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: RNA Oligonucleotide 5, Fig. 3
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /note="where the intersubunit
; OTHER INFORMATION: bonds are "np"
; US-08-923-386A-5

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCATCCTT 10

RESULT 46
US-08-923-386A-6
; Sequence 6, Application US/08923386A
; Patent No. 6169170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923.386A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 80852YX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923.386A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 5525-0012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA Oligonucleotide 6, Fig. 3
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..11
OTHER INFORMATION: /note="where the intersubunit
OTHER INFORMATION: bonds are "np"
US-08-923-386A-6

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTTCATCCTT 10

RESULT 47
US-08-413-813-34/c
; Sequence 34, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413.813
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 80852YX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR

```
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-34

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 12 CTTTCATCCTT 3

RESULT 48
US-08-344-820-11
; Sequence 11, Application US/08344820
; Patent No. 5717085
; GENERAL INFORMATION:
; APPLICANT: LYTTLE, MATTHEW H.
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: CODON AMIDITES AND METHOD OF USING THEM
; TITLE OF INVENTION: TO PRODUCE OLIGONUCLEOTIDES AND MUTAGENESIS LIBRARIES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: DROST, PATRICIA M.
; REGISTRATION NUMBER: 29,790
; REFERENCE/DOCKET NUMBER: 2550-0023.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-344-820-11

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 3 CATCATCCTT 12

RESULT 49
US-08-344-820-14
; Sequence 14, Application US/08344820
; Patent No. 5717085
; GENERAL INFORMATION:
; APPLICANT: LYTTLE, MATTHEW H.
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: CODON AMIDITES AND METHOD OF USING THEM
; TITLE OF INVENTION: TO PRODUCE OLIGONUCLEOTIDES AND MUTAGENESIS LIBRARIES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: DROST, PATRICIA M.
; REGISTRATION NUMBER: 29,790
; REFERENCE/DOCKET NUMBER: 2550-0023.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-344-820-14

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 3 CATCATCCTT 12

RESULT 50
US-08-547-214-27/c
; Sequence 27, Application US/08547214
; Patent No. 5871697
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 24-OCT-1995
```


CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-790-9090
TELEFAX: (212)-869-8864
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-547-214-27

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 51
US-08-467-346-34/c
Sequence 34, Application US/08467346
Patent No. 5872105
GENERAL INFORMATION:
APPLICANT: Kool, Eric T.
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,346
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,813
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZYX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-346-34

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 12 CTTTCATCCTT 3

RESULT 52
US-08-663-823B-27/c
Sequence 27, Application US/08663823B
Patent No. 5972693
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
TITLE OF INVENTION: WITHOUT SEQUENCING
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,823B
FILING DATE: 14-June-1996
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-663-823B-27

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 53
US-08-874-825-84
Sequence 84, Application US/08874825
Patent No. 6057101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Yang, Meijia
APPLICANT: Knight, James
APPLICANT: Kalbfleisch, Theodore
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

```
;
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-874-825-84

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 54
US-08-874-825-99
; Sequence 99, Application US/08874825
; Patent No. 6057101
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Meijia
; APPLICANT: Knight, James
; APPLICANT: Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-874-825-99

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 55
US-08-663-824-84
; Sequence 84, Application US/08663824
; Patent No. 6083693
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
; FILE REFERENCE: 7934-006
; CURRENT APPLICATION NUMBER: US/08/663,824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
; US-08-663-824-84

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 2 GCGCTTCAT 11

RESULT 56
US-08-663-824-99
; Sequence 99, Application US/08663824
; Patent No. 6083693
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
; FILE REFERENCE: 7934-006
```

```
; CURRENT APPLICATION NUMBER: US/08/663,824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-99

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
    ||| |||||
Db 2 GCGCTTCAT 11

RESULT 57
US-08-942-406-27/c
; Sequence 27, Application US/08942406
; Patent No. 6141657
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,406
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-942-406-27

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
    ||| |||||
Db 10 GTGAGCGACT 1

RESULT 58
US-09-322-617-27/c
; Sequence 27, Application US/09322617
; Patent No. 6231812
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; Deem, Michael
; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,617
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-322-617-27

Query Match          46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
    ||| |||||
Db 10 GTGAGCGACT 1

RESULT 59
US-09-203-231B-31/c
; Sequence 31, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; Nallur, Girish N
; Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; DIFFERENTIAL GENE EXPRESSION
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
```

; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-31

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACT 10
||| |||||
Db 10 GTCAGCGGACT 1

RESULT 60
US-09-231-303-84
; Sequence 84, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-84

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTTCAT 14
||| |||||
Db 2 GCGTTCAT 11

RESULT 61
US-09-231-303-99
; Sequence 99, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 99
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-99

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTTCAT 14
||| |||||
Db 2 GCGGTTTCAT 11

RESULT 62
US-09-751-561-27/c
; Sequence 27, Application US/09751561
; Patent No. 6418382
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-751-561-27

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACT 10
||| |||||
Db 10 GTCAGCGGACT 1

RESULT 63

US-09-724-385-27/c
; Sequence 27, Application US/09724385
; Patent No. 6432361
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; ; Deem, Michael
; ; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,385
; FILING DATE: 28-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/322,617
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-724-385-27

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 64

US-09-757-528-27/c
; Sequence 27, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; ; Deem, Michael
; ; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,528
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-757-528-27

Query Match 46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
||| |||||
Db 10 GTCAGCGACT 1

RESULT 65

US-08-522-384-91
; Sequence 91, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-91

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCAATCC 16
||| |||||
Db 3 CTTCAATCC 10

RESULT 66

US-09-240-639-29/c

; Sequence 29, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 29
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-240-639-29

Query Match 44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 10 TCATCCTT 3

RESULT 67
US-08-068-945A-35/c
; Sequence 35, Application US/08068945A
; Patent No. 5616483
; GENERAL INFORMATION:
; APPLICANT: Bjursell, Gunnar
; APPLICANT: Carlsson, Peter
; APPLICANT: Enerback, Sven
; APPLICANT: Hansson, Lennart
; APPLICANT: Lidberg, Ulf
; APPLICANT: Nilsson, Jeanette
; APPLICANT: Tornell, Jan
; TITLE OF INVENTION: New DNA Sequences
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,945A
; FILING DATE: 27-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201809-2
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201826-6
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202088-2
; FILING DATE: 03-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300902-5
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-052

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-068-945A-35

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 62;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
Db 11 ACTTCCTTCTT 1

RESULT 68
US-08-442-806-35/c
; Sequence 35, Application US/08442806
; Patent No. 5716817
; GENERAL INFORMATION:
; APPLICANT: Bjursell, Gunnar
; APPLICANT: Carlsson, Peter
; APPLICANT: Enerback, Sven
; APPLICANT: Hansson, Lennart
; APPLICANT: Lidberg, Ulf
; APPLICANT: Nilsson, Jeanette
; APPLICANT: Tornell, Jan
; TITLE OF INVENTION: Genomic DNA Sequences
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,945
; FILING DATE: 27-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201809-2
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201826-6
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202088-2
; FILING DATE: 03-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300902-5
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-052
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-442-806-35

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 62;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCTT 18
|||||
Db 11 ACTTCCTCTT 1

RESULT 69
US-07-967-693-33/c
Sequence 33, Application US/07967693
Patent No. 5494814
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/967,693
FILING DATE: 19921027
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 coop ul

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-967-693-33

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
|||||
Db 11 TGAAGGACTTC 1

RESULT 70
US-08-195-072-31/c
Sequence 31, Application US/08195072
Patent No. 5543508
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,072
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 coop ul

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-072-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
|||||
Db 11 TGAAGGACTTC 1

RESULT 71
US-08-195-735-31/c
Sequence 31, Application US/08195735
Patent No. 5574143
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,735
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40313-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-195-735-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAAGGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 72
US-08-195-747-31/c
; Sequence 31, Application US/08195747
; Patent No. 5589580
; GENERAL INFORMATION:
; APPLICANT: James P. Haseloff
; APPLICANT: Wayne L. Gerlach
; APPLICANT: Philip A. Jennings
; APPLICANT: Fiona H. Cameron
; TITLE OF INVENTION: RIBOZYMES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,747
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40313-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-195-747-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAAGGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 73
US-08-446-884-31/c
; Sequence 31, Application US/08446884
; Patent No. 5707835
; GENERAL INFORMATION:
; APPLICANT: James P. Haseloff
; APPLICANT: Wayne L. Gerlach
; APPLICANT: Philip A. Jennings
; APPLICANT: Fiona H. Cameron
; TITLE OF INVENTION: RIBOZYMES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Durham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,884
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40313-BX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-446-884-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAAGGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 74
US-08-195-073-31/c
; Sequence 31, Application US/08195073
; Patent No. 5747335
; GENERAL INFORMATION:
; APPLICANT: James P. Haseloff
; APPLICANT: Wayne L. Gerlach
```


APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,073
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-C
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-073-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 75
US-08-198-175-31/c
Sequence 31, Application US/08198175
Patent No. 5766942
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,175
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-F
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-198-175-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGGACTTC 12
Db 11 TGAAGGACTTC 1

RESULT 76
US-08-443-153-31/c
Sequence 31, Application US/08443153
Patent No. 5840874
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,153
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-BY
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-443-153-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      2 TGAGCGACTTC 12
      ||| |||||
Db      11 TGAAGGACTTC 1

RESULT 77
US-08-547-214-10
; Sequence 10, Application US/08547214
; Patent No. 5871697
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample without
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/547,214
; FILING DATE: 24-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-547-214-10

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGCGACTTCAT 14
      ||| |||||
Db      1 AGTGGCTTCAT 11

RESULT 78
US-08-663-823B-10
; Sequence 10, Application US/08663823B
; Patent No. 5972693
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
; TITLE OF INVENTION: CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
```

```
; ADDRESSEE: Pennie and Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,823B
; FILING DATE: 14-June-1996
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-663-823B-10

Query Match      43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 AGCGACTTCAT 14
      ||| |||||
Db      1 AGTGGCTTCAT 11

RESULT 79
US-08-874-825-96
; Sequence 96, Application US/08874825
; Patent No. 6057101
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Yang, Meijia
; APPLICANT: Knight, James
; APPLICANT: Kalbfleisch, Theodore
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,825
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,824
```

```

; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-874-825-96

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
   ||| |||||
Db 1 AGCTGCTTCAT 11

RESULT 80
US-08-824-96
; Sequence 96, Application US/08663824
; Patent No. 6083693
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
; FILE REFERENCE: 7934-006
; CURRENT APPLICATION NUMBER: US/08/663.824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 96
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-824-96

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
   ||| |||||
Db 1 AGCTGCTTCAT 11

RESULT 81
US-08-442-807-31/c
; Sequence 31, Application US/08442807
; Patent No. 6127114
; GENERAL INFORMATION:
; APPLICANT: James P. Haseloff
; APPLICANT: Wayne L. Gerlach
; APPLICANT: Philip A. Jennings
; APPLICANT: Fiona H. Cameron
; TITLE OF INVENTION: RIBOZYMES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
```

```

; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442.807
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40313-BZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-442-807-31

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
   ||| |||||
Db 11 TGAAGGACTTC 11

RESULT 82
US-08-942-406-10
; Sequence 10, Application US/08942406
; Patent No. 6141657
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942.406
; FILING DATE: 01-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
```


; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 100
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-100

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
||| ||| |||
Db 12 GACTTCGCCT 2

RESULT 86
US-09-231B-14
; Sequence 14, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-14

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| ||| |||
Db 1 AGTGGCTTCAT 11

RESULT 87
US-09-231-303-96
; Sequence 96, Application US/09231303
; Patent No. 6395478
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; EARLIER FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 12

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-96

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| ||| |||
Db 1 AGTGGCTTCAT 11

RESULT 88
US-09-751-561-10
; Sequence 10, Application US/09751561
; Patent No. 6418382
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-751-561-10

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| ||| |||
Db 1 AGTGGCTTCAT 11

RESULT 89

US-09-724-385-10
; Sequence 10, Application US/09724385
; Patent No. 6432361
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; ; Deem, Michael
; ; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,385
; FILING DATE: 28-No. 6432361-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/322,617
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: 66441 PENNIE
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-724-385-10
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11
RESULT 90
US-09-757-528-10
; Sequence 10, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; ; Deem, Michael
; ; Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,528
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: 66441 PENNIE
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-757-528-10
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 0;
Qy 4 AGCGACTTCAT 14
Db 1 AGTGGCTTCAT 11
RESULT 91
US-09-844-493-13
; Sequence 13, Application US/09844493
; Patent No. 6511808
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: Li, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: METHODS FOR DESIGNING EXOGENOUS REGULATORY MOLECULES
; FILE REFERENCE: 8325-0016
; CURRENT APPLICATION NUMBER: US/09/844,493
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,605
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible
; OTHER INFORMATION: end
US-09-844-493-13
Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| |||
Db 1 GATCGAATTCA 11

RESULT 92

US-09-844-265-13
; Sequence 13, Application US/09844265
; Patent No. 6610489
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: Li, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: PHARMACOGENOMICS AND IDENTIFICATION OF DRUG TARGETS BY
; TITLE OF INVENTION: RECONSTRUCTION OF SIGNAL TRANSDUCTION PATHWAYS BASED ON
; TITLE OF INVENTION: SEQUENCES OF ACCESSIBLE REGIONS
; FILE REFERENCE: 8325-0017
; CURRENT APPLICATION NUMBER: US/09/844,265
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,608
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible
; OTHER INFORMATION: end
US-09-844-265-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| |||
Db 1 GATCGAATTCA 11

RESULT 93

US-09-874-601-138/c
; Sequence 138, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 138

; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-138

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCCT 17
||| |||
Db 11 GAATCATCCT 1

RESULT 94

US-08-605-163-4
; Sequence 4, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Applications to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-605-163-4

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||
Db 1 CTTTCATCCT 9

```
RESULT 95
US-09-985-799-12/c
; Sequence 12, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/985,799
; FILING DATE: 06-NOV-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-985-799-12
;
; Query Match 41.1%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 67;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
Db 9 GACTTGATC 1

RESULT 96
US-07-860-445-17
; Sequence 17, Application US/07860445
; Patent No. 5573905
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5573905th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/860,445
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/860445
; FILING DATE: 30-MAR-1992
; ATTORNEY/AGENT INFORMATION:
```

```
;
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5573905th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/860,445
; FILING DATE: 19920330
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSP5023P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-07-860-445-17
;
; Query Match 41.1%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 67;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
Db 1 AGTACTTC 9

RESULT 97
US-08-665-511-17
; Sequence 17, Application US/08665511
; Patent No. 5723598
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5723598th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,511
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/860445
; FILING DATE: 30-MAR-1992
; ATTORNEY/AGENT INFORMATION:
```


NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: T5R5023P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-665-511-17

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
||| |||||
Db 1 AGCTACTTC 9

RESULT 98
US-08-594-031-12/c
Sequence 12, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 08146-0110
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-12

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GACTTCATC 15
||| |||||
Db 9 GACTTGATC 1

RESULT 99
US-08-173-489C-303/C
Sequence 303, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 303:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 16S rRNA gene from Chlamydia psittaci
DESCRIPTION: (Accession # M13769) nucleotides 1181 to 1190
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Chlamydia psittaci
PUBLICATION INFORMATION:
AUTHORS: Weisburg, W G, Hatch, T P, Woese, C R.
TITLE: Eubacterial Origin of
TITLE: Chlamydiae
JOURNAL: Journal of Bacteriology
VOLUME: 167
PAGES: 570-574
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 303 :FROM 1 TO 10
US-08-173-489C-303

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 9 CTTCTCCT 17
Db 9 CTTCTCCT 1

RESULT 100
US-08-477-396A-14
; Sequence 14, Application US/08477396A
; Patent No. 5872235
; GENERAL INFORMATION:
; APPLICANT: Chen, Lan Bo
; APPLICANT: Bao, Shideng
; APPLICANT: Liu, Yuan
; TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
; TITLE OF INVENTION: ISOLATING SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477.396A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,488
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US 08/448,388
; FILING DATE: 28-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12502
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-333BX
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-477-396A-14

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGGACT 10
Db 1 TGAGTACT 9

RESULT 101
US-08-780-835B-5/c
; Sequence 5, Application US/08780835B
; Patent No. 5922688
; GENERAL INFORMATION:

```

```

; APPLICANT: Hung, Mien-Chie
; APPLICANT: King, Xiangming
; TITLE OF INVENTION: PE3 is a Tumor Suppressor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,835B
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSC500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-835B-5

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACTTCCTCC 2

RESULT 102
US-08-780-835B-6/c
; Sequence 6, Application US/08780835B
; Patent No. 5922688
; GENERAL INFORMATION:
; APPLICANT: Hung, Mien-Chie
; APPLICANT: King, Xiangming
; TITLE OF INVENTION: PE3 is a Tumor Suppressor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,835B
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSC500

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-780-835B-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
 Db 9 TTTCCTCCTT 1

RESULT 103

US-08-265-484B-3
 Sequence 3, Application US/08265484B
 Patent No. 5998193

GENERAL INFORMATION:
 APPLICANT: Keese, Paul
 APPLICANT: Stapper, Marianne
 APPLICANT: Perriman, Rhonda
 TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
 TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
 TITLE OF INVENTION: Ribozymes and Compositions Thereof
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/265,484B
 FILING DATE: 24-JUN-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 45284
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other Nucleic Acid
 US-08-265-484B-3

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 77.8%; Pred. No. 67;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
 Db 2 GUGAGCGGC 10

RESULT 104

US-08-388-353-185/c
 Sequence 185, Application US/08388353
 Patent No. 6010895

GENERAL INFORMATION:
 APPLICANT: Deacon, Nicholas J.
 APPLICANT: Learmont, Jennifer C.
 APPLICANT: McPhee, Dale A.
 APPLICANT: Crowe, Suzanne
 APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/388,353
 FILING DATE: 14-FEB-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: DiGiglio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 9606
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 185:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-388-353-185

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
 Db 10 CTTTCCTCCT 2

RESULT 105

US-08-388-353-186/c
 Sequence 186, Application US/08388353
 Patent No. 6010895

GENERAL INFORMATION:
 APPLICANT: Deacon, Nicholas J.
 APPLICANT: Learmont, Jennifer C.
 APPLICANT: McPhee, Dale A.
 APPLICANT: Crowe, Suzanne
 APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-186

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTCTCCT 17
Db 9 CTTCTCCT 1

RESULT 106
US-08-488-551B-185/c
Sequence 185, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-185

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTCTCCT 17
Db 10 CTTCTCCT 2

RESULT 107
US-08-488-551B-186/c
Sequence 186, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-186

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCT 17
 |||||
 Db 9 CTTTCCTCT 1

RESULT 108

US-09-033-743-17
 ; Sequence 17, Application US/09033743
 ; Patent No. 6060596
 ; GENERAL INFORMATION:
 ; APPLICANT: Lerner, Richard
 ; APPLICANT: Janda, Kim
 ; APPLICANT: Brenner, Sydney
 ; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 No. 6060596th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/033,743
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/665,511
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSP023P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-09-033-743-17

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 AGCGACTTC 12
 |||||
 Db 1 AGCTACTTC 9

RESULT 109

US-08-765-257A-3
 ; Sequence 3, Application US/08765257A
 ; Patent No. 6107078
 ; GENERAL INFORMATION:
 ; APPLICANT: Keese, Paul
 ; APPLICANT: Stapper, Marianne

; APPLICANT: Perriman, Rhonda
 ; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
 ; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
 ; TITLE OF INVENTION: and Compositions Thereof
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH, 1.44MB
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/765,257A
 ; FILING DATE: June 24, 1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 45284
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 977 9550
 ; TELEFAX: 212 977 9809

; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Other Nucleic Acid
 ; US-08-765-257A-3

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 77.8%; Pred. No. 67;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTGAGCGAC 9
 |:|||||
 Db 2 GUGAGCGGC 10

RESULT 110

US-08-522-384-50
 ; Sequence 50, Application US/08522384
 ; Patent No. 6110667
 ; GENERAL INFORMATION:
 ; APPLICANT: LOPEZ-NIETO, CARLOS E
 ; APPLICANT: NIGAM, SANJAY KUMAR
 ; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
 ; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
 ; FILE REFERENCE: 2458-4029
 ; CURRENT APPLICATION NUMBER: US/08/522,384
 ; CURRENT FILING DATE: 1996-11-15
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 50
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Primer
 ; US-08-522-384-50

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 67;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 CTTTCATCT 17

```

; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-75

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GACTTCATC 15
Db      2 GCCTTCATC 10

RESULT 114
US-09-303-268-5/c
; Sequence 5, Application US/09303268
; Patent No. 6172212
; GENERAL INFORMATION:
; APPLICANT: Hung, Mien-Chie
;           King, Xiangming
; TITLE OF INVENTION: PEAS3 is a Tumor Suppressor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,268
; FILING DATE: 30-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,835
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSC500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-303-268-5

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 ACTTCATCC 16

```

```

; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-53

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCT 17
Db      1 CTTTCATCT 9

RESULT 112
US-08-522-384-64
; Sequence 64, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-64

Query Match          41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GACTTCATC 15
Db      1 GCCTTCATC 9

RESULT 113
US-08-522-384-75
; Sequence 75, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR

```

Db 10 ACTTCCTCC 2

RESULT 115

US-09-303-268-6/C
; Sequence 6, Application US/09303268
; Patent No. 6172212
; GENERAL INFORMATION:
; APPLICANT: Hung, Mien-Chie
; ; Xing, Xiangming
; TITLE OF INVENTION: PEA3 is a Tumor Suppressor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,268
; FILING DATE: 30-Apr-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,835
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSC500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-303-268-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
Db 9 TTTCCTCCTT 1

RESULT 116

US-08-991-789A-103
; Sequence 103, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; ; Smith, John M.
; ; Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; ; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington

COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-991-789A-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCAACCT 9

RESULT 117

US-09-116-049-7/c
; Sequence 7, Application US/09116049A
; Patent No. 6248351
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/116,049A
; CURRENT FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-116-049-7

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACTTCCTCC 2

RESULT 118

US-09-116-049-8/c
; Sequence 8, Application US/09116049A
; Patent No. 6248351
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582

```
; CURRENT APPLICATION NUMBER: US/09/116.049A
; CURRENT FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-116-049-8

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCTCCTT 18
Db      9 TTCTCCTT 1

RESULT 119
US-09-062-451-103
; Sequence 103, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-062-451-103

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCCTT 17
Db      1 CTTTCCTT 9

RESULT 120
US-09-062-451-103
; Sequence 103, Application US/09598326
; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 247
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-598-326-103

Query Match      41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCCTT 17
Db      1 CTTTCCTT 9

RESULT 121
US-09-370-838-48
; Sequence 48, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
```


US-09-370-838-48

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCTT 17
|||||
Db 1 CTTCAACCT 9

RESULT 122

US-09-428-236-6/c

; Sequence 6, Application US/09428236

; Patent No. 6472153

; GENERAL INFORMATION:

; APPLICANT: Dempcy, Robert, O.

; APPLICANT: Afonina, Irina A.

; APPLICANT: Vermeulen, Nicolaas M.

; TITLE OF INVENTION: HYBRIDIZATION-TRIGGERED FLUORESCENT

; FILE REFERENCE: 344692000600

; CURRENT APPLICATION NUMBER: US/09/428,236

; CURRENT FILING DATE: 1999-10-26

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic construct.

US-09-428-236-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
|||||
Db 9 AGCAACTTC 1

RESULT 123

US-09-508-753B-63/c

; Sequence 63, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI

; APPLICANT: Yuko SHIBATA

; APPLICANT: Hiroko FUNAKI

; APPLICANT: Eiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 63

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-63

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 10 GACTTCACC 2

RESULT 124

US-09-508-753B-387

; Sequence 387, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI

; APPLICANT: Yuko SHIBATA

; APPLICANT: Hiroko FUNAKI

; APPLICANT: Eiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 387

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-387

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
|||||
Db 2 AGCGATTTC 10

RESULT 125

US-09-508-753B-389/c

; Sequence 389, Application US/09508753B

; Patent No. 6544736

; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI

; APPLICANT: Yuko SHIBATA

; APPLICANT: Hiroko FUNAKI

; APPLICANT: Eiji OHARA

; APPLICANT: Masanori WATAHIKI

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; FILE REFERENCE: 00162/HG

; CURRENT APPLICATION NUMBER: US/09/508,753B

; CURRENT FILING DATE: 2000-06-16

; PRIOR FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 389

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-508-753B-389

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
|||||
Db 9 AGCGATTTC 1

```
RESULT 126
US-09-884-363-7/c
; Sequence 7, Application US/09884363
; Patent No. 6582725
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-884-363-7

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 10 ACTTCCTCC 2

RESULT 127
US-09-884-363-8/c
; Sequence 8, Application US/09884363
; Patent No. 6582725
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-884-363-8

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
Db 9 TTTCCTCCTT 1

RESULT 128
US-09-289-198-103
; Sequence 103, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; CURRENT FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-289-198-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCACTCT 17
Db 1 CTTCACTCT 9

RESULT 129
US-09-429-755-103
; Sequence 103, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-429-755-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCACTCT 17
Db 1 CTTCACTCT 9

RESULT 130
US-08-180-195-20/c
```

; Sequence 20, Application US/08180195
; Patent No. 5567584
; GENERAL INFORMATION:
; APPLICANT: Sledziwski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,195
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,510
; FILING DATE:
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
; US-08-180-195-20
; Query Match 41.1%; Score 7.4; DB 1; Length 11;
; Best Local Similarity 88.9%; Pred. No. 75;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TGACGGACT 10
Db 11 TGAGCGTCT 3
RESULT 131
US-07-860-445-22
; Sequence 22, Application US/07860445
; Patent No. 5573905
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES

; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5573905th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/860,445
; FILING DATE: 19920330
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: T5R5023P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-07-860-445-22
; Query Match 41.1%; Score 7.4; DB 1; Length 11;
; Best Local Similarity 88.9%; Pred. No. 75;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 AGCGACTTC 12
Db 1 AGCTACTTC 9
RESULT 132
US-08-171-389-619
; Sequence 619, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/171,389
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-08-171-389-619

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
||| |||||
Db 1 TTCCTCCTT 9

RESULT 133
US-08-344-695-24/c
; Sequence 24, Application US/08344695
; Patent No. 5614398
; GENERAL INFORMATION:
; APPLICANT: O'BROCHTA, DAVID
; APPLICANT: WARREN, WILLIAM
; APPLICANT: ATKINSON, PETER
; TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; STREET: Arlington
; CITY: Virginia
; STATE: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,695
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2747-058-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-344-695-25

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
||| |||||
Db 2 TTCATCCTT 10

; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-344-695-24

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
||| |||||
Db 10 TTCATCCTT 2

RESULT 134
US-08-344-695-25
; Sequence 25, Application US/08344695
; Patent No. 5614398
; GENERAL INFORMATION:
; APPLICANT: O'BROCHTA, DAVID
; APPLICANT: WARREN, WILLIAM
; APPLICANT: ATKINSON, PETER
; TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; STREET: Arlington
; CITY: Virginia
; STATE: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,695
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2747-058-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-344-695-25

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
||| |||||
Db 2 TTCATCCTT 10

RESULT 135
US-08-344-695-26/c
; Sequence 26, Application US/08344695
; Patent No. 5614398
; GENERAL INFORMATION:
; APPLICANT: O'BROCHTA, DAVID
; APPLICANT: WARREN, WILLIAM
; APPLICANT: ATKINSON, PETER
; TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,695
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 536
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30, 073
; REFERENCE/DOCKET NUMBER: 2747-058-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; US-08-344-695-26

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 10 TTATCCCTT 18
| | | | | | |
Db 10 TTATCCCTT 2

RESULT 136
US-08-344-695-27
; Sequence 27, Application US/08344695
; Patent No. 5614398
; GENERAL INFORMATION:
; APPLICANT: O'BROCHTA, DAVID
; APPLICANT: WARREN, WILLIAM
; APPLICANT: ATKINSON, PETER
; TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,695
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 536
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30, 073
; REFERENCE/DOCKET NUMBER: 2747-058-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; US-08-344-695-27

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 10 TTATCCCTT 18
| | | | | | |
Db 10 TTATCCCTT 2

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIFICATION: 536
NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30, 073
REFERENCE/DOCKET NUMBER: 2747-058-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-344-695-27

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 10 TTATCCCTT 18
| | | | | | |
Db 2 TTATCCCTT 10

RESULT 137
US-08-344-695-29
; Sequence 29, Application US/08344695
; Patent No. 5614398
; GENERAL INFORMATION:
; APPLICANT: O'BROCHTA, DAVID
; APPLICANT: WARREN, WILLIAM
; APPLICANT: ATKINSON, PETER
; TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,695
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 536
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30, 073
; REFERENCE/DOCKET NUMBER: 2747-058-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid

```

; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-344-695-29

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 2 TTCATCCTT 10

RESULT 138
US-07-996-783-19
; Sequence 19, Application US/07996783
; Patent No. 5693463
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; TITLE OF INVENTION: SEQUENCE-DIRECTED DNA-BINDING MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter J. Dehlinger
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/996,783
; FILING DATE: 19921223
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0075.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-08-484-499-19

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

RESULT 140
US-08-665-511-22
; Sequence 22, Application US/08665511
; Patent No. 5723598
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5723598th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/665,511
 FILING DATE: 18-JUN-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/860445
 FILING DATE: 30-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: T5R5023P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-665-511-22

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. NO. 75;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
 |||||
 Db 1 AGTACTTC 9

RESULT 141

US-08-123-936-619
 ; Sequence 619, Application US/08123936
 ; Patent No. 5726014
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Cynthia A.
 ; APPLICANT: Cantor, Charles R.
 ; APPLICANT: Andrews, Beth M.
 ; APPLICANT: Turin, Lisa M.
 ; TITLE OF INVENTION: Screening Assay for the Detection of
 ; TITLE OF INVENTION: DNA-Binding Molecules
 ; NUMBER OF SEQUENCES: 640
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genelabs Technologies, Inc.
 ; STREET: 505 Penobscot Drive
 ; CITY: Redwood City
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94063
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 23-DEC-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/996,783
 ; FILING DATE: 27-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
 ; TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 619:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: a sample distamycin target sequence
 US-08-123-936-619

Query Match 41.1%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. NO. 75;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
 |||||
 Db 1 TTCCTCCTT 9

RESULT 142

US-08-475-221B-19
 ; Sequence 19, Application US/08475221B
 ; Patent No. 5738990
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Cynthia A.
 ; APPLICANT: Fry, Kirk E.
 ; APPLICANT: Cantor, Charles R.
 ; APPLICANT: Andrews, Beth M.
 ; TITLE OF INVENTION: Sequence-Directed DNA-Binding Molecules
 ; TITLE OF INVENTION: Compositions and Methods
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Ave., Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,221B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/996,783
 ; FILING DATE: 23-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/723,618
 ; FILING DATE: 27-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stratford, Carol A.
 ; REGISTRATION NUMBER: 34,444
 ; REFERENCE/DOCKET NUMBER: 4600-0075.34
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-324-0880
 ; TELEFAX: 415-324-0960
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: a sample distamycin target sequence

US-08-475-221B-19

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
||| |||||
Db 1 TTTCCTCCTT 9

RESULT 143

US-08-476-876-19
; Sequence 19, Application US/08476876
; Patent No. 5744131
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A
; APPLICANT: Fry, Kirk E
; APPLICANT: Cantor, Charles R
; APPLICANT: Andrews, Beth M
; TITLE OF INVENTION: Sequence-Directed DNA-Binding Molecules
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,876
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0075.33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-08-476-876-19

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
||| |||||
Db 1 TTTCCTCCTT 9

RESULT 144

US-08-477-329-20/c
; Sequence 20, Application US/08477329
; Patent No. 5750375
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z

APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,329
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
US-08-477-329-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGTCT 3

RESULT 145

US-08-475-458-20/c
; Sequence 20, Application US/08475458
; Patent No. 5843725
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:


```
; APPLICATION NUMBER: US/08/475,458
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446DS
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
US-08-475-458-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGICT 3

RESULT 146
US-08-173-489C-290
; Sequence 290, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 bases
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from C.
; DESCRIPTION: pasteurianum 16s region in Seq ID No. 5861244289
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; TELECOMMUNICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 290 :FROM 1 TO 11
US-08-173-489C-290

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
|||||
Db 2 TTCTCTCCTT 10

RESULT 147
US-08-475-228A-619
; Sequence 619, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-08-475-228A-619

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
| | | | |
Db 1 TTCCTCCTT 9

RESULT 148
US-08-482-080A-619
; Sequence 619, Application US/08482080A
; Patent No. 6010849
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.080A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,389
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-08-482-080A-619

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
| | | | |
Db 1 TTCCTCCTT 9

RESULT 149
US-08-980-400-20/c
; Sequence 20, Application US/08980400
; Patent No. 6018026
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,400
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,329
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
US-08-980-400-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
| | | | |
Db 11 TGAGCGTCT 3

RESULT 150

US-09-033-743-22
; Sequence 22, Application US/09033743
; Patent No. 6060596
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 6060596th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/665,511
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR5023P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-033-743-22

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
Db 1 AGCTACTTC 9

RESULT 151
US-09-196-523-26
; Sequence 26, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 11

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-26

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 2 GTAAGCGAC 10

RESULT 152
US-08-083-945C-8/c
; Sequence 8, Application US/08083945C
; Patent No. 6274134
; GENERAL INFORMATION:
; APPLICANT: Beckner, Marie E.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Krutzsch, Henry C.
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,945C
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-083-945C-8

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCTCCT 17
Db 9 CTTCTCCT 1

RESULT 153
US-09-583-459A-20/c
; Sequence 20, Application US/09583459A

; Patent No. 6291212
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583.459A
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
; US-09-583-459A-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
| | | | | | |
Db 11 TGAGCGTCT 3

RESULT 154
US-09-583-210-20/c
; Sequence 20, Application US/09583210
; Patent No. 6291646
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS

; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,210
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
; US-09-583-210-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
| | | | | | |
Db 11 TGAGCGTCT 3

RESULT 155
US-09-583-449A-20/c
; Sequence 20, Application US/09583449A
; Patent No. 6300099
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,449A
FILING DATE: 30-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,510
FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: ZC1893
US-09-583-449A-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGTCT 3

RESULT 156
US-09-435-059-20/c
Sequence 20, Application US/09435059
Patent No. 6323323
GENERAL INFORMATION:
APPLICANT: Sledziwski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/435,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,329
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: ZC1893
US-09-435-059-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 11 TGAGCGTCT 3

RESULT 157
US-09-354-947-619
Sequence 619, Application US/09354947
Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Fenobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618

```

; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
US-09-354-947-619

```

```

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 10 TTCATCCTT 18
Db 1 TTCCTCCTT 9

```

RESULT 158

```

US-09-249-155A-4/c
; Sequence 4, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-4

```

```

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GTGAGCCGAC 9
Db 9 GTGAGCCAC 1

```

RESULT 159

```

US-09-249-155A-163/c
; Sequence 163, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound

```

```

; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-163

```

```

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GTGAGCCGAC 9
Db 9 GTGAGCCAC 1

```

RESULT 160

```

US-09-249-155A-267/c
; Sequence 267, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-267

```

```

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

```

RESULT 161

```

US-09-249-155A-317/c
; Sequence 317, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737

```

;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/097,937
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: US 60/102,051
;; PRIOR FILING DATE: 1998-09-28
;; NUMBER OF SEQ ID NOS: 346
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 317
;; LENGTH: 11
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-249-155A-317

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCCAC 9
Db 9 GTGAGCCAC 1

RESULT 162
PCT-US93-12388-619
; Sequence 619, Application PC/TUS9312388
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12388
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
PCT-US93-12388-619

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TTTCATCCTT 18
||| |||||
Db 1 TTTCCTCCTT 9

RESULT 163
PCT-US94-07107A-8/c
; Sequence 8, Application PC/TUS9407107A
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of
; APPLICANT: America, as represented by the Secretary,
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07107A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,043
; FILING DATE: 29-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-156-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-07107A-8

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||||
Db 9 CTTTCCTCCT 1

RESULT 164
US-08-859-954-85
; Sequence 85, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.

```
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-85

Query Match 38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTATC 15
Db 2 CTTATC 8

RESULT 165
US-08-859-954-111
; Sequence 111, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-859-954-111

Query Match 38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 2 CATCCTT 8

RESULT 166
US-08-859-954-365
; Sequence 365, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-859-954-111
```



```
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
US-08-859-954-365

Query Match      38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 2 CATCCTT 8

RESULT 167
US-09-432-020B-14/c
; Sequence 14, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 14
; LENGTH: 9
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CR13m probe hybridizes with V520F mutation site;
; OTHER INFORMATION: the 5'-terminal guanidine is derivatized to carry
; OTHER INFORMATION: a primary amino group which covalently binds to the
; OTHER INFORMATION: epoxysilane glass
US-09-432-020B-14

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 168
US-09-163-485-23/c
; Sequence 23, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILLMORE, HELEN
; APPLICANT: BROADBUSH, WILLIAM
; APPLICANT: GILLIES, GEORGE
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
; FILE REFERENCE: VCU1P4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases

US-09-163-485-23

Query Match      38.9%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 2 CATCCTT 8

RESULT 167
US-09-432-020B-14/c
; Sequence 14, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriguez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 14
; LENGTH: 9
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CR13m probe hybridizes with V520F mutation site;
; OTHER INFORMATION: the 5'-terminal guanidine is derivatized to carry
; OTHER INFORMATION: a primary amino group which covalently binds to the
; OTHER INFORMATION: epoxysilane glass
US-09-432-020B-14

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 168
US-09-163-485-23/c
; Sequence 23, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILLMORE, HELEN
; APPLICANT: BROADBUSH, WILLIAM
; APPLICANT: GILLIES, GEORGE
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
; FILE REFERENCE: VCU1P4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases

US-09-163-485-23

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 9 YTTCTCTCCT 1

RESULT 169
US-09-153-242-38/c
; Sequence 38, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide H8
US-09-153-242-38

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
Db 8 GTGAGCG 2

RESULT 170
US-09-989-789-2472/c
; Sequence 2472, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2472
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2472

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTTCATCC 16
Db 9 TTTCATCC 3
```

```
RESULT 171
US-09-989-789-2477/c
; Sequence 2477, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2477
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2477

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
Db 9 TTCATCC 3

RESULT 172
US-08-441-887A-306/c
; Sequence 306, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-306

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 9 TCATCCTT 2

RESULT 173
US-08-522-384-116
; Sequence 116, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2459-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-116

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTT 17
Db 1 TCATCCTT 7

RESULT 174
US-09-305-408-21
; Sequence 21, Application US/09305408
; Patent No. 6194155
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jeffrey
; TITLE OF INVENTION: Computerized Method of Identifying and Locating
; TITLE OF INVENTION: Resonating, Self-Hybridizing Nucleic Acid Elements
; FILE REFERENCE: 2275.2.1
; CURRENT APPLICATION NUMBER: US/09/305,408
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ebola virus
```

US-09-305-408-21

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 4 CTTTCATC 10

RESULT 175

US-09-305-408-22/c
; Sequence 22, Application US/09305408
; Patent No. 6194155
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jeffrey
; TITLE OF INVENTION: Computerized Method of Identifying and Locating
; FILE REFERENCE: 2275.2.1
; CURRENT APPLICATION NUMBER: US/09/305.408
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ebola virus
US-09-305-408-22

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 7 CTTTCATC 1

RESULT 176

US-09-305-408-31
; Sequence 31, Application US/09305408
; Patent No. 6194155
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jeffrey
; TITLE OF INVENTION: Computerized Method of Identifying and Locating
; FILE REFERENCE: 2275.2.1
; CURRENT APPLICATION NUMBER: US/09/305.408
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ebola virus
US-09-305-408-31

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 4 CTTTCATC 10

RESULT 177

US-08-927-165A-32/c
; Sequence 32, Application US/08927165A
; Patent No. 6410226
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.

; APPLICANT: Holloman, William K.
; APPLICANT: Rice, Michael C.
; APPLICANT: Smith, Sheryl T.
; APPLICANT: Shu, Zhigang
; TITLE OF INVENTION: Mammalian and Human Rec2
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pheasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927.165A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansburg, Daniel
; REGISTRATION NUMBER: 36156
; REFERENCE/DOCKET NUMBER: 7991-010-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-504-4444
; TELEFAX: 215-504-4545
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-927-165A-32

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 9 TCATCCT 3

RESULT 178

US-09-508-753B-34/c
; Sequence 34, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508.753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 34
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-34

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 10 CATCCTT 4
|||||

RESULT 179
US-09-508-753B-132/c
; Sequence 132, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 132
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-132

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTATCCT 16
Db 8 TTATCCT 2
|||||

RESULT 180
US-09-508-753B-209
; Sequence 209, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 209
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-209

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 1 CATCCTT 7
|||||

RESULT 181
US-09-508-753B-299
; Sequence 299, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 299
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-299

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
Db 4 GTGAGCG 10
|||||

RESULT 182
US-10-032-307-41
; Sequence 41, Application US/10032307
; Patent No. 6683173
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Gall, Alexander A.
; APPLICANT: Likhov, Sergey G.
; APPLICANT: Afonina, Irina A.
; APPLICANT: Singer, Michael J.
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: T-m Leveling Methods
; FILE REFERENCE: 17682A-003630US
; CURRENT APPLICATION NUMBER: US/10/032,307
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/054,830
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/054,832
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/431,385
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: US 60/186,046
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 09/640,953
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/724,959
; PRIOR FILING DATE: 2000-11-28

;; PRIOR APPLICATION NUMBER: US 09/796,988
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 90
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:duplex
;; OTHER INFORMATION: complement 6
US-10-032-307-41

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
|||
Db 4 AGCGACT 10

RESULT 183
US-08-078-662A-12/c
; Sequence 12, Application US/08078662A
; Patent No. 5523221
; GENERAL INFORMATION:
; APPLICANT: Weiner, Michael
; TITLE OF INVENTION: METHOD FOR THE DIRECTIONAL
; TITLE OF INVENTION: CLONING OF DNA
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: STRATAG.010A
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-078-662A-12

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGGACTTC 12
|||
Db 10 GAAGGACTTC 1

RESULT 184
US-08-335-565A-17/c
; Sequence 17, Application US/08335565A
; Patent No. 5527671
; GENERAL INFORMATION:
; APPLICANT: Li, Kening
; APPLICANT: Rouse, Douglas I.
; APPLICANT: German, Thomas L.
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: 1 South Pinckney St., PO BOX 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.93065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-335-565A-17

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTGATCCTT 18
|||
Db 10 CGTCATCCAT 1

RESULT 185
US-08-440-787A-83/c
; Sequence 83, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-440-787A-83

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGACGGACTT 11
Db 10 TCAGCGAATT 1

RESULT 186
US-08-545-253A-15/c
; Sequence 15, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELE: 575102
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-545-253A-15

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
Db 10 GGGAGTGAAT 1

RESULT 187
US-08-780-835B-3/c
; Sequence 3, Application US/08780835B
; Patent No. 5922688
; GENERAL INFORMATION:
; APPLICANT: Hung, Mien-Chie
; APPLICANT: King, Xiangming
; TITLE OF INVENTION: PE43 is a Tumor Suppressor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,835B
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSC500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-835B-3

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 10 ACTTCCTGCT 1

RESULT 188
US-08-481-658B-23
; Sequence 23, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
```

;; TITLE OF INVENTION: MN Gene and Protein
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Leona L. Lauder
;; STREET: 6 Mariposa Court
;; CITY: Tiburon
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94920
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/481.658B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/260,190
;; FILING DATE: 15-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lauder, Leona L.
;; REGISTRATION NUMBER: 30,863
;; REFERENCE/DOCKET NUMBER: D-0021.3E
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-435-2034
;; TELEFAX: 415-435-0727
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; DESCRIPTION: Initiator consensus sequence
;; US-08-481-658B-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 YYCAVYVY 10

RESULT 189
US-08-053-451B-156
; Sequence 156, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053.451B
; FILING DATE: 26-APR-1993

;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Halluin, Albert P.
;; REGISTRATION NUMBER: 25,227
;; REFERENCE/DOCKET NUMBER: 7606-033-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-854-3660
;; TELEFAX: 415-854-3694
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 156:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA
;; US-08-053-451B-156

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 CTTCAAGCTT 10

RESULT 190
US-08-477-504A-23
; Sequence 23, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; US-08-477-504A-23

```
Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCACTCTT 18
Db 1 YYCAYYYY 10

RESULT 191
US-08-486-756A-23
; Sequence 23, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-486-756A-23

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCACTCTT 18
Db 1 YYCAYYYY 10

RESULT 192
US-08-485-862B-23
; Sequence 23, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
```

```
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-485-862B-23

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCACTCTT 18
Db 1 YYCAYYYY 10

RESULT 193
US-08-388-353-189/c
; Sequence 189, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```


APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-189

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 10 ACCTCTCCT 1

RESULT 194
US-08-388-353-261
; Sequence 261, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-261

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
Db 1 TTAGCCACTT 10

RESULT 195
US-08-388-353-455/c
; Sequence 455, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 455:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-455

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 10 CTTTCATCCTT 1

RESULT 196
US-08-488-551B-189/c
; Sequence 189, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

```
;
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-189

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 10 ACCTCTTCCT 1

RESULT 197
US-08-488-551B-261
; Sequence 261, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-261

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
Db 1 TTAGCCACTT 10

RESULT 198
US-08-488-551B-455/c
; Sequence 455, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
```

; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 455:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-455

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
|||||
Db 10 CTTTCATCCTT 1

RESULT 199
US-08-787-739-23
; Sequence 23, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,739
; FILING DATE: 24-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,756
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,658
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,862
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-787-739-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
::|||:::
Db 1 YYCAYYYY 10

RESULT 200
US-08-787-739-24
; Sequence 24, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,739
; FILING DATE: 24-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,756
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,658
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,862
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863

```
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: consensus sequence for AP1
; DESCRIPTION: transcription factor
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Locker and Buzard
; JOURNAL: DNA Sequencing and Mapping
; VOLUME: 1
; PAGES: 3-11
; DATE: 1990
; US-08-787-739-24

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
   |||||
Db 1 TGTGAGACTT 10

RESULT 201
US-08-719-337-15/c
; Sequence 15, Application US/08719337
; Patent No. 6054634
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 6054634th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,337
; FILING DATE: 25-SEP-1996
; CLASSIFICATION: 047
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,567
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-719-337-15

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACT 10
   |||||
Db 10 GGGAGTCACT 1 .

RESULT 202
US-08-487-077A-23
; Sequence 23, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; US-08-487-077A-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
   ::|||::
Db 1 YYCAVYYY 10

RESULT 203
US-08-485-863A-23
; Sequence 23, Application US/08485863A
```

Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-485-863A-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTTCATCCTT 18
:::||||:::
Db 1 YYCAYYYY 10

RESULT 204
US-09-063-450-30/c
; Sequence 30, Application US/09063450
; Patent No. 6109776
; GENERAL INFORMATION:
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Method and System for Computationally Identifying
; FILE OF INVENTION: Clusters Within a Set of Sequences
; FILE REFERENCE: 77001.002
; CURRENT APPLICATION NUMBER: US/09/063,450
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example
; OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-30

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTTTCATCCTT 18
||| |||||
Db 10 CTGCTCTCCTT 1

RESULT 205
US-08-522-384-77
; Sequence 77, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; FILE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-77

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ACTTCATCCTT 17
||| |||||
Db 1 ACTACTTCCTT 10

RESULT 206
US-08-564-100-8/c
; Sequence 8, Application US/08564100
; Patent No. 6153379
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Shumaker, John
; APPLICANT: Metspalu, Andres
; TITLE OF INVENTION: PARALLEL PRIMER EXTENSION APPROACH TO
; FILE OF INVENTION: NUCLEIC ACID SEQUENCE ANALYSIS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/564,100
; APPLICATION NUMBER: US/08/564,100
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reynolds, Leo R.
; REGISTRATION NUMBER: 20,884
; REFERENCE/DOCKET NUMBER: BCM94-01A
; TELECOMMUNICATION INFORMATION:

Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
|||||
Db 10 ACTTCCTGCT 1

RESULT 210

US-09-178-115-23
; Sequence 23, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; PUBLICATION INFORMATION:
; AUTHORS: Locker and Buzard,
; JOURNAL: DNA Sequencing and Mapping
; VOLUME: 1
; PAGES: 3-11
; DATE: 1990
US-09-178-115-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
:::|:::
Db 1 YYCAYYYY 10

RESULT 211

US-09-178-115-24
; Sequence 24, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A

; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; PUBLICATION INFORMATION:
; AUTHORS: Locker and Buzard,
; JOURNAL: DNA Sequencing and Mapping
; VOLUME: 1
; PAGES: 3-11
; DATE: 1990
US-09-178-115-24

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
|||||
Db 1 TGTGAGACTT 10

RESULT 212

US-09-177-776-23
; Sequence 23, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07

```

; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
US-09-177-776-23

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 91;
Matches      2; Conservative      8; Mismatches      0; Indels      0; Gaps      0;

Qy      9 CTTTCATCCTT 18
Db      1 YYCAYYYY 10
      ::|||:::
      1 YYCAYYYY 10

RESULT 213
US-09-177-776-24
; Sequence 24, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177.776A
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN

```

```

; PUBLICATION INFORMATION:
; AUTHORS: Locker and Buzard,
; JOURNAL: DNA Sequencing and Mapping
; VOLUME: 1
; PAGES: 3-11
; DATE: 1990
US-09-177-776-24

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      2 TGAGCGACTT 11
Db      1 TGTGAGACTT 10
      ||| |||||
      1 TGTGAGACTT 10

RESULT 214
US-09-140-084-15
; Sequence 15, Application US/09140084A
; Patent No. 6300065
; GENERAL INFORMATION:
; APPLICANT: Kieke, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: D6061CIP2
; CURRENT APPLICATION NUMBER: US/09/140,084A
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer
; OTHER INFORMATION: towards Gal promoter
US-09-140-084-15

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      3 GAGCGACTTC 12
Db      1 GATCGAATTC 10
      ||| |||||
      1 GATCGAATTC 10

RESULT 215
US-08-618-834C-46
; Sequence 46, Application US/08618834C
; Patent No. 6361937
; GENERAL INFORMATION:
; APPLICANT: Stryer, Lubert
; TITLE OF INVENTION: Computer-Aided Nucleic Acid
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: CA
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,834C
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```



```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: APTFP002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-618-834C-46

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 1 ACATCACCCT 10

RESULT 216
US-09-498-608A-11
; Sequence 11, Application US/09498608A
; Patent No. 6403314
; GENERAL INFORMATION:
; APPLICANT: Agilent Technologies
; TITLE OF INVENTION: Computational Method And System for Predicting Fragmented Hybridization
; FILE REFERENCE: Agilent 10992048
; CURRENT APPLICATION NUMBER: US/09/498,608A
; CURRENT FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A hypothetical target sequence
US-09-498-608A-11

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 1 GGGACTTTAT 10

RESULT 217
US-09-724-297-15
; Sequence 15, Application US/09724297
; Patent No. 6423538
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Wittrup, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: 97-99C
; CURRENT APPLICATION NUMBER: US/09/724,297
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 10
```

```
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: PCR primer towards Gal promoter
US-09-724-297-15

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
Db 1 GATCGAATTC 10

RESULT 218
US-09-154-750A-33
; Sequence 33, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: P53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-33

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
Db 1 AGCCACTGCA 10

RESULT 219
US-09-508-753B-77/c
; Sequence 77, Application US/09508753B
; Patent No. 6547736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 77
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-77

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
| | | | | | | |
Db 10 GGCTTCATTC 1

RESULT 220

US-09-508-753B-154
; Sequence 154, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 154
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-154

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
| | | | | | | |
Db 1 GGCTTCATTC 10

RESULT 221

US-09-508-753B-247/c
; Sequence 247, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 247
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-247

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
| | | | | | | |
Db 10 CGAACTCATC 1

RESULT 222

US-09-508-753B-282
; Sequence 282, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 282
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-282

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
| | | | | | | |
Db 1 CGAACTCATC 10

RESULT 223

US-09-508-753B-411/c
; Sequence 411, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 411
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-411

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 10 CTACATCCGT 1

RESULT 224

US-08-894-454-132/c
; Sequence 132, Application US/08894454
; Patent No. 6544784
; GENERAL INFORMATION:
; APPLICANT: VAN DEN VEN, W.J.M.
; APPLICANT: SCHOENMAKERS, H.F.P.M.
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRANT GROWTH
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Webb Law Firm
; STREET: 700 Koppers Building, 436 Seventh Avenue
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,454
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP/00716
; FILING DATE: 19-FEB-1996
; APPLICATION NUMBER: 95200390.3
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: 95201951.1
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Barbara E
; REGISTRATION NUMBER: 31,198
; REFERENCE/DOCKET NUMBER: 702-971100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 412-471-8815
; TELEFAX: 412-471-4094
; TELEX:
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-894-454-132

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 10 GAGACTCCAT 1

RESULT 225

US-09-769-482-30
; Sequence 30, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO

; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995-0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-30

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
Db 1 CAACTCAAC 10

RESULT 226

US-09-884-363-5/c
; Sequence 5, Application US/09884363
; Patent No. 6582725
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-884-363-5

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
Db 10 ACTTCCTGCT 1

RESULT 227

US-09-989-789-1268/c
; Sequence 1268, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 10

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1268

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
||| ||| |||
Db 10 GCGACTCTT 1

RESULT 228
US-09-989-789-1630
; Sequence 1630, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1630

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GAGGGAGTTC 10

RESULT 229
US-09-989-789-1631
; Sequence 1631, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1631

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GAGGGAGTTC 10

RESULT 230
5175268-10
; Patent No. 5175268
; APPLICANT: IWASA, SUSUMU; FUJII, TOMOKO; MARUMOTO, RYUJI;
; IGARASHI, KOICHI
; TITLE OF INVENTION: DNA ENCODING RECOMBINANT HUMAN
; LYMPHOTOXIN
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/416,657
; FILING DATE: 03-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,029
; FILING DATE: 21-DEC-1987
; SEQ ID NO:10:
; LENGTH: 10
5175268-10

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
||| ||| ||| |||
Db 1 GAATTCATGC 10

RESULT 231
US-08-232-144-9
; Sequence 9, Application US/08232144
; Patent No. 5571695
; GENERAL INFORMATION:
; APPLICANT: SELBIE, Lisa
; APPLICANT: HERZOG, Herbert
; APPLICANT: SHINE, John
; TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: 555 13th St, N.W., Suite 701-East
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,144
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-107A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-232-144-9

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGACTTCA 13
 |||||
 Db 1 CGACGTCA 8

RESULT 232

US-08-509-858-3
 ; Sequence 3, Application US/08509858
 ; Patent No. 5780613
 ; GENERAL INFORMATION:
 ; APPLICANT: Letsinger, Robert L.
 ; APPLICANT: Herrlein, Mathias K.
 ; TITLE OF INVENTION: COVALENT LOCK FOR SELF-ASSEMBLED
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE CONSTRUCTS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 5780613thwestern Hwy.
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/509,858
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: 0570.00037
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (248) 539-5050
 ; TELEFAX: (248) 539-5055
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-509-858-3

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
 |||||
 Db 1 TTCCTCT 8

RESULT 233

US-08-859-954-42/c
 ; Sequence 42, Application US/08859954
 ; Patent No. 6083695
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramin
 ; APPLICANT: Hardin, Paul E.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 1301 McKinney, Suite 5100
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.A.
 ZIP: 77010-3095
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,954
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/632,782
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 ; US-08-859-954-42

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
 |||||
 Db 8 ACTTCACC 1

RESULT 234

US-08-859-954-95/c
 ; Sequence 95, Application US/08859954
 ; Patent No. 6083695
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramin
 ; APPLICANT: Hardin, Paul E.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,954
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/632,782
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 95:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 US-08-859-954-95

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
 |||||
 Db 8 ACTTCAGC 1

RESULT 235
 US-08-859-954-146/c
 ; Sequence 146, Application US/08859954
 ; Patent No. 6083695
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramin
 ; APPLICANT: Hardin, Paul E.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,954
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/632,782
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 146:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 US-08-859-954-146

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
 |||||
 Db 8 ACTCCATC 1

RESULT 236
 US-08-859-954-152/c
 ; Sequence 152, Application US/08859954
 ; Patent No. 6083695
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramin
 ; APPLICANT: Hardin, Paul E.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,954
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/632,782
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 152:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 US-08-859-954-152

Query Match 35.6%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATC 15
 |||||
 Db 8 ACTGCATC 1

RESULT 237

US-08-859-954-155/c
; Sequence 155, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5246
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

US-08-859-954-155
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATC 15
Db 8 ACCTCATC 1

RESULT 238
US-08-859-954-197
; Sequence 197, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 ACTTCATC 15
Db 8 ACCTCATC 1

RESULT 239
US-08-859-954-213
; Sequence 213, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:

STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

US-08-859-954-197
Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCGACTTC 12
Db 1 GAGACTTC 8

RESULT 239
US-08-859-954-213
; Sequence 213, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:

STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-213

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCAT 14
Db 1 GACTCCAT 8

RESULT 240
US-08-859-954-217
; Sequence 217, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-217

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTC 12
Db 8 GTGACTTC 1

RESULT 242
US-08-859-954-446/c
```

```
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-217

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCAT 14
Db 1 GACTTCAT 8

RESULT 241
US-08-859-954-247/c
; Sequence 247, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-247

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTC 12
Db 8 GTGACTTC 1

RESULT 242
US-08-859-954-446/c
```


; Sequence 446, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-446

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 8 TCATCCTT 1

RESULT 243
US-08-859-954-539/c
; Sequence 539, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.

; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 539:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-859-954-539

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGA 8
Db 8 GTGAGAGA 1

RESULT 244
US-08-859-954-543/c
; Sequence 543, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.

```

; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 543:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
;
US-08-859-954-543

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 8 TCAGCCTT 1

RESULT 245
US-08-859-954-544/c
; Sequence 544, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 544:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

```

```

US-08-859-954-544

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
Db 8 TCCTCCTT 1

RESULT 246
US-09-041-675-26/c
; Sequence 26, Application US/09041675A
; Patent No. 6100032
; GENERAL INFORMATION:
; APPLICANT: Kern, Scott
; APPLICANT: Zewel, Leigh
; APPLICANT: Dai, Jia Le
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Human SMAD3 and SMAD4 are
; TITLE OF INVENTION: sequence-specific transcription activators
; FILE REFERENCE: 01107.74098
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic random oligonucleotides selected for
; OTHER INFORMATION: binding to human SMAD3 or human SMAD4
;
US-09-041-675-26

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGAC 9
Db 8 TGAGGGAC 1

RESULT 247
US-09-256-340-6
; Sequence 6, Application US/09256340
; Patent No. 6255476
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Mullah, Khairuzzaman B.
; APPLICANT: Rosenblum, Barnett B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/09/256,340
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
;
US-09-256-340-6

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 248

US-09-256-340-7
; Sequence 7, Application US/09256340
; Patent No. 6255476
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Mullah, Khairuzzaman B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/09/256,340
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
US-09-256-340-7

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 249

US-09-813-378-6
; Sequence 6, Application US/09813378
; Patent No. 6316610
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Mullah, Khairuzzaman B.
; APPLICANT: Rosenblum, Barnett B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/09/813,378
; CURRENT FILING DATE: 2001-03-20
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
US-09-813-378-6

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 250

US-09-813-378-7
; Sequence 7, Application US/09813378
; Patent No. 6316610
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Mullah, Khairuzzaman B.
; APPLICANT: Rosenblum, Barnett B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/09/813,378
; CURRENT FILING DATE: 2001-03-20
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
US-09-813-378-7

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 251

US-09-232-000B-27
; Sequence 27, Application US/09232000B
; Patent No. 6432642
; GENERAL INFORMATION:
; APPLICANT: LIVAK, Kenneth J.
; APPLICANT: EGHOLM, Michael W.
; APPLICANT: HUNKAPILLER, Michael W.
; TITLE OF INVENTION: BINARY PROBE AND CLAMP COMPOSITION AND METHODS FOR TARGET
; TITLE OF INVENTION: HYBRIDIZATION DETECTION
; FILE REFERENCE: 4419US
; CURRENT APPLICATION NUMBER: US/09/232,000B
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Labelled PNA
US-09-232-000B-27

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 252

US-09-232-000B-30
; Sequence 30, Application US/09232000B
; Patent No. 6432642
; GENERAL INFORMATION:

; APPLICANT: LIVAK, Kenneth J.
; APPLICANT: EGHOLM, Michael
; APPLICANT: HUNKAPILLER, Michael W.
; TITLE OF INVENTION: BINARY PROBE AND CLAMP COMPOSITION AND METHODS FOR TARGET
; TITLE OF INVENTION: HYBRIDIZATION DETECTION
; FILE REFERENCE: 4419US
; CURRENT APPLICATION NUMBER: US/09/232.000B
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Labelled PNA
US-09-232-000B-30

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 253
US-09-232-000B-40
; Sequence 40, Application US/09232000B
; Patent No. 6432642
; GENERAL INFORMATION:
; APPLICANT: LIVAK, Kenneth J.
; APPLICANT: EGHOLM, Michael
; APPLICANT: HUNKAPILLER, Michael W.
; TITLE OF INVENTION: BINARY PROBE AND CLAMP COMPOSITION AND METHODS FOR TARGET
; TITLE OF INVENTION: HYBRIDIZATION DETECTION
; FILE REFERENCE: 4419US
; CURRENT APPLICATION NUMBER: US/09/232.000B
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Labelled 2' OMe RNA
US-09-232-000B-40

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 254
US-10-010-717-6
; Sequence 6, Application US/10010717
; Patent No. 6525183
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Rosenblum, Barnett B.
; APPLICANT: Mullah, Khairuzzaman B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/10/010.717
; CURRENT FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 09/256,340
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
US-10-010-717-6

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 255
US-10-010-717-7
; Sequence 7, Application US/10010717
; Patent No. 6525183
; GENERAL INFORMATION:
; APPLICANT: Vinayak, Ravi S.
; APPLICANT: Lee, Linda G.
; APPLICANT: Mullah, Khairuzzaman B.
; APPLICANT: Rosenblum, Barnett B.
; TITLE OF INVENTION: Methods and Compositions for Synthesis of Labelled
; TITLE OF INVENTION: Oligonucleotides and Analogs on Solid-Supports
; FILE REFERENCE: 4407
; CURRENT APPLICATION NUMBER: US/10/010.717
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/256,340
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Test Sequence
US-10-010-717-7

Query Match 35.6%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCCTCCTT 8

RESULT 256
US-09-194-842A-13
; Sequence 13, Application US/09194842A
; Patent No. 6416948
; GENERAL INFORMATION:
; APPLICANT: Pilarski, Linda M.
; APPLICANT: Belch, Andrew R.
; APPLICANT: Szczepek, Agnieszka J.
; TITLE OF INVENTION: METHODS FOR DETECTION OF REARRANGED DNA
; FILE REFERENCE: STI-008USCPA
; CURRENT APPLICATION NUMBER: US/09/194.842A
; CURRENT FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: US 60/019,106
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US97/09534
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-842A-13

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGAC 9
||| |||||
Db 1 TGTGCGAC 8

RESULT 257
US-09-194-842A-24
; Sequence 24, Application US/09194842A
; Patent No. 6416948
; GENERAL INFORMATION:
; APPLICANT: Pilarski, Linda M.
; APPLICANT: Belch, Andrew R.
; APPLICANT: Szczepiek, Agnieszka J.
; TITLE OF INVENTION: METHODS FOR DETECTION OF REARRANGED DNA
; FILE REFERENCE: STI-008USCPA
; CURRENT APPLICATION NUMBER: US/09/194,842A
; CURRENT FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: US 60/019,106
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US97/09534
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-842A-24

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGAC 9
||| |||||
Db 1 TGTGCGAC 8

RESULT 258
US-09-194-842A-27
; Sequence 27, Application US/09194842A
; Patent No. 6416948
; GENERAL INFORMATION:
; APPLICANT: Pilarski, Linda M.
; APPLICANT: Belch, Andrew R.
; APPLICANT: Szczepiek, Agnieszka J.
; TITLE OF INVENTION: METHODS FOR DETECTION OF REARRANGED DNA
; FILE REFERENCE: STI-008USCPA
; CURRENT APPLICATION NUMBER: US/09/194,842A
; CURRENT FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: US 60/019,106
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US97/09534
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-842A-27

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGAC 9
||| |||||
Db 1 TGTGCGAC 8

RESULT 259
US-09-989-789-2014/c
; Sequence 2014, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2014
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2014

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
||| |||||
Db 8 TCACCCCTT 1

RESULT 260
US-09-989-789-2167/c
; Sequence 2167, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2167
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2167

Query Match 35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTT 11
||| |||||
Db 8 AGCGCCTT 1

RESULT 261
US-09-989-789-2236/c

```
; Sequence 2236, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2236
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2236

Query Match      35.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 AGCGACTT 11
      |||||
Db      8 AGCGCCTT 1

RESULT 262
PCT-US91-03680-53
; Sequence 53, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
```

```
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 3
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 6..7
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 9
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "7-(N-methyl-8-oxo-2'-deoxyadenine
; OTHER INFORMATION: that have xylose sugar linked via the
; OTHER INFORMATION: o-xylene ring)"
PCT-US91-03680-53

Query Match      34.4%; Score 6.2; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTTTCATC 15
      |||:|
Db      3 CTTTMTTC 9

RESULT 263
US-08-436-145-6
; Sequence 6, Application US/08436145
; Patent No. 5681943
; GENERAL INFORMATION:
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Gryaznov, Sergei M.
; TITLE OF INVENTION: METHOD OF FORMING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,145
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-323 (NW)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-145-6

Query Match      33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 11 TCATCC 16
|||||
Db 3 TCATCC 8

RESULT 264

US-08-480-173A-27
; Sequence 27, Application US/08480173A
; Patent No. 6072049
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans A
; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Popovich & Wiles, P.A.
; STREET: 80 S. 8th Street, Suite 1902
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.173A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Popovich, Thomas E
; REGISTRATION NUMBER: 30,099
; REFERENCE/DOCKET NUMBER: MED1003USD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-334-8991
; TELEFAX: 612-334-8994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..4
; OTHER INFORMATION: /note= "Nucleotides 1-4 form a
; OTHER INFORMATION: single-stranded "sticky end"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5..8
; OTHER INFORMATION: /note= "Adapter sequence results
; OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-8 of
; OTHER INFORMATION: SEQ ID NO: 28"
US-08-480-173A-27

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATCCTT 18
|||||
Db 2 ATCCTT 7

RESULT 265

US-08-859-954-60
; Sequence 60, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin

; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-60

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATCCTT 18
|||||
Db 3 ATCCTT 8

RESULT 266

US-08-859-954-168
; Sequence 168, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-168

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ATCCTT 18
|||||
Db 2 ATCCTT 7

RESULT 267
US-08-859-954-184/c
Sequence 184, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246

INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-184

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCT 17
|||||
Db 7 CATCCT 2

RESULT 268
US-08-859-954-245/c
Sequence 245, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-245

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-346

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 8 ACTTCA 13
| | | | |
Db 8 ACTTCA 3

RESULT 272
US-08-859-954-549/c
Sequence 549, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 549:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-549

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 11 TCATCC 16

LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-549

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GTGAGC 6
| | | | |
Db 8 GTGAGC 3

RESULT 273
US-08-859-954-561
Sequence 561, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 561:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-561

Query Match 33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

```
Db      1  TCACTC 6

RESULT 274
US-08-484-408A-27
; Sequence 27, Application US/08484408A
; Patent No. 6117653
; GENERAL INFORMATION:
; APPLICANT: Thoma, Hans A
; TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Popovich & Wiles, P.A.
; STREET: 80 S. 8th Street, Suite 1902
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,408A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Popovich, Thomas E
; REGISTRATION NUMBER: 30,099
; REFERENCE/DOCKET NUMBER: MED1003USD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-334-8991
; TELEFAX: 612-334-8994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4
; OTHER INFORMATION: /note= "Nucleotides 1-4 form a
; OTHER INFORMATION: single-stranded "sticky end"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5..8
; OTHER INFORMATION: /note= "Adapter sequence results
; OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-8 of
; OTHER INFORMATION: SEQ ID NO: 28"
US-08-484-408A-27

Query Match      33.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13  ATCCTT 18
Db      2  ATCCTT 7

RESULT 275
US-08-097-349-11/c
; Sequence 11, Application US/08097349
; Patent No. 5437697
; GENERAL INFORMATION:
; APPLICANT: Hanafey, Michael K.
; APPLICANT: Sebastian, Scott A.
; APPLICANT: Tingey, Scott V.
; TITLE OF INVENTION: A Method to Identify Genetic Markers

; TITLE OF INVENTION: That Are Linked to Agronomically
; TITLE OF INVENTION: Important Genes
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM
; OPERATING SYSTEM: Microsoft Windows Version 3.0
; SOFTWARE: Microsoft Word Version 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,349
; FILING DATE: JULY 23, 1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrissey, Bruce W.
; REGISTRATION NUMBER: 30,663
; REFERENCE/DOCKET NUMBER: BB-1038-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4927
; TELEFAX: 302-774-0164
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-097-349-11

Query Match      33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8  ACTTCA 13
Db      7  ACTTCA 2

RESULT 276
US-08-586-329-10/c
; Sequence 10, Application US/08586329
; Patent No. 5658736
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon C.
; TITLE OF INVENTION: OLIGONUCLEOTIDE POPULATION PREPARATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,329
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5266
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-586-329-10
Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCT 17
Db 9 CATCCT 4

RESULT 277
US-08-503-671-11/c
; Sequence 11, Application US/08503671
; Patent No. 5746023
; GENERAL INFORMATION:
; APPLICANT: Hanafey, Michael K
; APPLICANT: Sebastian, Scott A
; APPLICANT: Tingey, Scott V
; TITLE OF INVENTION: A Method to Identify Genetic Markers
; TITLE OF INVENTION: That Are Linked to Agronomically Important Genes
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Co.
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/503,671
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrissey, Bruce W
; REGISTRATION NUMBER: 30,663
; REFERENCE/DOCKET NUMBER: BB-1038-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4927
; TELEFAX: 302-892-7949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-503-671-11
Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCA 13
Db 7 ACTTCA 2

RESULT 278
```

```
US-08-318-947A-12/c
; Sequence 12, Application US/08318947A
; Patent No. 5798245
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-318-947A-12
Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTT 11
Db 6 CGACTT 1

RESULT 279
US-08-605-163-19/c
; Sequence 19, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verdy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
```

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,163
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05986.0005-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-605-163-19

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Oy 8 ACTTCA 13
Db 6 ACTTCA 1

RESULT 280
US-08-795-303-12/c
Sequence 12, Application US/08795303
Patent No. 5948656
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
ADDRESSEE: Tian, Qingheng
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, NW Suite 800
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060
TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-795-303-12

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Oy 6 CGACTT 11
Db 6 CGACTT 1

RESULT 281
US-09-383-630-18
Sequence 18, Application US/09383630A
Patent No. 6265632
GENERAL INFORMATION:
APPLICANT: Avner Yayon et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
CHONDRODYSPLASIA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCII file

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A

FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-383-630-18

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

```
Qy 12 CATCCT 17
      |||||
Db 3 CATCCT 8

RESULT 282
US-09-194-842A-12/c
; Sequence 12, Application US/09194842A
; Patent No. 6416948
; GENERAL INFORMATION:
; APPLICANT: Pilarski, Linda M.
; APPLICANT: Belch, Andrew R.
; APPLICANT: Szczepek, Agnieszka J.
; TITLE OF INVENTION: METHODS FOR DETECTION OF REARRANGED DNA
; FILE REFERENCE: STI-008USCPA
; CURRENT APPLICATION NUMBER: US/09/194,842A
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: US 60/019,106
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US97/09534
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-842A-12

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGC 6
      |||||
Db 9 GTGAGC 4

RESULT 283
US-09-989-789-455/c
; Sequence 455, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-455

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTC 12
      |||||
Db 6 GACTTC 1

RESULT 284
US-09-989-789-456/c
; Sequence 456, Application US/09989789
; Patent No. 6588746
```

```
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-456

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTC 12
      |||||
Db 6 GACTTC 1

RESULT 285
US-09-989-789-577/c
; Sequence 577, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 577
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-577

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTC 12
      |||||
Db 6 GACTTC 1

RESULT 286
US-09-989-789-2103/c
; Sequence 2103, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2103
; LENGTH: 9
```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2103

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCC 16
| | | | |
Db 8 TCATCC 3

RESULT 287
US-09-989-789-2231
; Sequence 2231, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2231
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2231

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGC 6
| | | | |
Db 3 GTGAGC 8

RESULT 288
US-09-989-789-2232
; Sequence 2232, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2232
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2232

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGC 6
| | | | |
Db 3 GTGAGC 8

RESULT 289
US-09-989-789-2246/c
; Sequence 2246, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2246
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2246

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCT 17
| | | | |
Db 7 CATCCT 2

RESULT 290
US-09-989-789-2498
; Sequence 2498, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2498
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2498

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGC 6
| | | | |
Db 3 GTGAGC 8

RESULT 291
PCT-US91-03680-43
; Sequence 43, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven

;; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
;; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
;; TITLE OF INVENTION: DUPLEX DNA
;; NUMBER OF SEQUENCES: 158
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morrison & Foerster
;; STREET: 545 Middlefield Road, Suite 200
;; CITY: Menlo Park
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94025
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/03680
;; FILING DATE: 19910524
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 4610-0011.40
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-327-7250
;; TELEFAX: 415-327-2951
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 2
;; OTHER INFORMATION: /mod_base= OTHER
;; OTHER INFORMATION: /note= "5-methylcytosine"
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 5
;; OTHER INFORMATION: /mod_base= OTHER
;; OTHER INFORMATION:
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 6
;; OTHER INFORMATION: /mod_base= OTHER
;; OTHER INFORMATION: /note= "5-methylcytosine"
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 9
;; OTHER INFORMATION: /mod_base= OTHER
;; OTHER INFORMATION: /note= "5-methylcytosine-5-methylcytosine,
;; OTHER INFORMATION: linking group o-xyloso (nucleotides that have
;; OTHER INFORMATION: xylose sugar linked via the o-xylyene ring)"
PCT-US91-03680-43

Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTT 18
|||
Db 1 TCTTMCCT 8

RESULT 292
5256568-5
;Patent No. 5256568
; APPLICANT: Panayotatos, Nikos
; TITLE OF INVENTION: VECTORS AND TRANSFORMED MOST CELLS FOR
; RECOMBINANT PROTEIN PRODUCTION WITH REDUCED EXPRESSION OF

;; SELECTABLE MARKERS
;; NUMBER OF SEQUENCES: 9
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/468,338
;; FILING DATE: 12-FEB-1990
;; SEQ ID NO: 5
;; LENGTH: 9
5256568-5
Query Match 33.3%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 ATCCTT 18
|||||
Db 4 ATCCTT 9
Search completed: September 9, 2004, 11:28:58
Job time : 1 secs

| | | | | | | |
|---|-----|-----------------|----|---|-----------------|-------------------|
| c 180 | 6.8 | 37.8 | 10 | 1 | US-10-816-079-1 | Sequence 1, Appli |
| ALIGNMENTS | | | | | | |
| RESULT 1 | | | | | | |
| US-09-731-457B-61/c | | | | | | |
| ; Sequence 61, Application US/09731457B | | | | | | |
| ; Patent No. US20020103146A1 | | | | | | |
| ; GENERAL INFORMATION: | | | | | | |
| ; APPLICANT: Ian Popoff | | | | | | |
| ; APPLICANT: Jacqueline Wyatt | | | | | | |
| ; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P1 | | | | | | |
| ; TITLE OF INVENTION: EXPRESSION | | | | | | |
| ; FILE REFERENCE: RTS-0182 | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/731,457B | | | | | | |
| ; CURRENT FILING DATE: 2000-12-06 | | | | | | |
| ; NUMBER OF SEQ ID NOS: 87 | | | | | | |
| ; SEQ ID NO 61 | | | | | | |
| ; LENGTH: 20 | | | | | | |
| ; TYPE: DNA | | | | | | |
| ; ORGANISM: Artificial Sequence | | | | | | |
| ; FEATURE: | | | | | | |
| ; OTHER INFORMATION: Antisense Oligonucleotide | | | | | | |
| US-09-731-457B-61 | | | | | | |
| Query Match 74.4%; Score 13.4; DB 1; Length 20; | | | | | | |
| Best Local Similarity 93.3%; Pred. No. 10; | | | | | | |
| Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | | | | |
| Qy | 3 | GAGCGACTTCATCCT | 17 | | | |
| Db | 17 | GGGCGACTTCATCCT | 3 | | | |
| RESULT 2 | | | | | | |
| US-09-504-231A-456/c | | | | | | |
| ; Sequence 456, Application US/09504231A | | | | | | |
| ; Patent No. US20020013458A1 | | | | | | |
| ; GENERAL INFORMATION: | | | | | | |
| ; APPLICANT: Blatt, Lawrence | | | | | | |
| ; APPLICANT: McSwiggen, James | | | | | | |
| ; APPLICANT: Roberts, Beth | | | | | | |
| ; APPLICANT: Pavco, Pamela | | | | | | |
| ; APPLICANT: Macejak, Dennis | | | | | | |
| ; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE | | | | | | |
| ; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION | | | | | | |
| ; FILE REFERENCE: fpi 247/282 | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/504,231A | | | | | | |
| ; CURRENT FILING DATE: 2000-02-15 | | | | | | |
| ; PRIOR APPLICATION NUMBER: 09/274,553 | | | | | | |
| ; PRIOR FILING DATE: 1999-03-23 | | | | | | |
| ; PRIOR APPLICATION NUMBER: 09/257,608 | | | | | | |
| ; PRIOR FILING DATE: 1999-02-24 | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/100,842 | | | | | | |
| ; PRIOR FILING DATE: 1998-09-18 | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/083,217 | | | | | | |
| ; PRIOR FILING DATE: 1998-04-27 | | | | | | |
| ; NUMBER OF SEQ ID NOS: 3242 | | | | | | |
| ; SOFTWARE: PatentIn version 3.0 | | | | | | |
| ; SEQ ID NO 456 | | | | | | |
| ; LENGTH: 15 | | | | | | |
| ; TYPE: RNA | | | | | | |
| ; ORGANISM: Artificial Sequence | | | | | | |
| ; FEATURE: | | | | | | |
| ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target | | | | | | |
| US-09-504-231A-456 | | | | | | |
| Query Match 68.9%; Score 12.4; DB 1; Length 15; | | | | | | |
| Best Local Similarity 92.9%; Pred. No. 9.6; | | | | | | |
| Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | | | | |

Qy 1 GTGAGCGACTTCAT 14
|||||
Db 14 GTGAGCGACTTCAT 1

RESULT 3

US-09-274-553D-456/c
; Sequence 456, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 456
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-456

Query Match 68.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.6;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCAT 14
|||||
Db 14 GTGAGCGACTTCAT 1

RESULT 4

US-10-230-006-681
; Sequence 681, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fornaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
; FILE REFERENCE: 400/056 (MBHH01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 681
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-681

Query Match 67.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCATCCT 17
|:||||| |:| |:

Db 1 GUGAGCGCCUUCUCCCU 17

RESULT 5

US-09-949-041A-19
; Sequence 19, Application US/09949041A
; Publication No. US20030104387A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rif
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-949-041A-19

Query Match 63.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 15;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
|||||
Db 3 TGAGCGAATTCAT 15

RESULT 6

US-10-230-006-682
; Sequence 682, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fornaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
; FILE REFERENCE: 400/056 (MBHH01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 682
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-682

Query Match 62.2%; Score 11.2; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCATCCT 17
:||||| |:| |:
Db 1 UGAGCGCCUUCUCCCU 16

RESULT 7

US-09-949-039-23/c
; Sequence 23, Application US/09949039
; Publication No. US20030166160A1
; GENERAL INFORMATION:
; APPLICANT: HANLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

```
; FILE REFERENCE: 057220/1301
; CURRENT APPLICATION NUMBER: US/09/949,039
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
US-09-949-039-23

Query Match          60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTGAGCGACTTCAT 14
Db      14 GGGAGCGGCTTCAT 1

RESULT 8
US-09-949-039-25/c
; Sequence 25, Application US/09949039
; Publication No. US20030166160A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; FILE REFERENCE: 057220/1301
; CURRENT APPLICATION NUMBER: US/09/949,039
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
US-09-949-039-25

Query Match          60.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTGAGCGACTTCAT 14
Db      14 GGGAGCGGCTTCAT 1

RESULT 9
US-10-033-145-1293/c
; Sequence 1293, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1293
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-033-145-1293

Query Match          55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGAGCGGACTT 11
Db      10 TGAGCGGACTT 1

RESULT 10
US-09-504-231A-457/c
; Sequence 457, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 457
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-457

Query Match          55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGAGCGGACT 10
Db      10 GTGAGCGGACT 1

RESULT 11
US-09-274-553D-457/c
; Sequence 457, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
```

;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3148
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 457
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-457

Query Match 55.6%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACT 10
Db 10 GTGAGCGGACT 1
|||||

RESULT 12
US-08-591-486B-33/c
; Sequence 33, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsenslepen, Georg F
; APPLICANT: Schlingsenslepen, Reimar
; APPLICANT: Schlingsenslepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-33

Query Match 54.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 29;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCATCC 16
Db 13 AGCAACTTCAACC 1
|||||

RESULT 13
US-09-504-231A-283
; Sequence 283, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: ID# 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 283
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-283

Query Match 54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGGACTTCA 13
Db 3 GUGAUCGACUGCA 15
|:|:|:|:|:|:|

RESULT 14
US-09-274-553D-283
; Sequence 283, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: ID# 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27

```

; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 283
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-283

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCA 13
Db 3 GUGAUCGACUGCA 15

RESULT 15
US-09-949-041A-7
; Sequence 7, Application US/09949041A
; Publication No. US20030104387A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rf
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-949-041A-7

Query Match      54.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCAT 14
Db 3 TGAGCCAATTCAT 15

RESULT 16
US-10-320-210A-6
; Sequence 6, Application US/10320210A
; Publication No. US20030203378A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Thilo
; APPLICANT: Borovjagin, Anton
; TITLE OF INVENTION: METHODS TO SCREEN FOR ANTIBIOTIC AGENTS AND THEIR USE IN
; TITLE OF INVENTION: TREATMENT OF OPPORTUNISTIC INFECTIONS
; FILE REFERENCE: 3564/2032
; CURRENT APPLICATION NUMBER: US/10/320,210A
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/20520
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,572
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Hansenula wingei

```

```

US-10-320-210A-6

Query Match      51.1%; Score 9.2; DB 1; Length 14;
Best Local Similarity 64.3%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCATCC 16
Db 1 GAGCCACUGAAUCC 14

RESULT 17
US-09-943-531A-7
; Sequence 7, Application US/09943531A
; Publication No. US20030059774A1
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Rieinger, Karl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP2C19 POLYMORPHISMS
; FILE REFERENCE: 52459-20020.00
; CURRENT APPLICATION NUMBER: US/09/943,531A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-7

Query Match      50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
Db 2 ACTTCATCC 10

RESULT 18
US-09-943-531A-25/c
; Sequence 25, Application US/09943531A
; Publication No. US20030059774A1
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Rieinger, Karl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP2C19 POLYMORPHISMS
; FILE REFERENCE: 52459-20020.00
; CURRENT APPLICATION NUMBER: US/09/943,531A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-25

Query Match      50.0%; Score 9; DB 1; Length 11;

```

Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
|||||||
Db 10 ACTTCATCC 2

RESULT 19
US-10-446-201-24
; Sequence 24, Application US/10446201
; Publication No. US20040029160A1
; GENERAL INFORMATION:
; APPLICANT: Britja, Ramon
; APPLICANT: Garcia, Ramon G.
; TITLE OF INVENTION: Parallel Stranded Duplexes of Deoxyribonucleic Acid and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 020415
; CURRENT APPLICATION NUMBER: US/10/446,201
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: test sequence
US-10-446-201-24

Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17
|||||||
Db 1 CTTCATCCT 9

RESULT 20
US-10-055-732-21
; Sequence 21, Application US/10055732
; Publication No. US20030135040A1
; GENERAL INFORMATION:
; APPLICANT: Britja, Ramon
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US20030135040A1
; TITLE OF INVENTION: Structures
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/197,559
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-21

Query Match 50.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17

Db 1 CTTCATCCT 9
|||||||

RESULT 21
US-10-001-670-79/c
; Sequence 79, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/10/001,670
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/231,303
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 08/663,824
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-79

Query Match 48.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCAGCGACTTCA 13
|||||||
Db 12 TCAGCGACTGCA 1

RESULT 22
US-09-879-813-78
; Sequence 78, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: D45
; OTHER INFORMATION: The sequence GTTATGGTGGGT is deleted
US-09-879-813-78

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17

```
Qy 2 TGAGCGACTTCA 13
    ||||| |||||
Db 2 TGGCGGCTTCA 13
    ||||| |||||

RESULT 23
US-10-146-505-78
; Sequence 78, Application US/10146505
; Publication No. US2003010889A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: D45
; OTHER INFORMATION: The sequence GTTTATGTTGGGT is deleted
US-10-146-505-78

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTCA 13
    ||||| |||||
Db 2 TGGCGGCTTCA 13
    ||||| |||||

RESULT 24
US-10-627-561-6/c
; Sequence 6, Application US/10627561
; Publication No. US20040086918A1
; GENERAL INFORMATION:
; APPLICANT: LOEWY, ZVI
; APPLICANT: CHAUNG, WAYNE
; APPLICANT: POTTATHIL, RAVEENDRAN
; TITLE OF INVENTION: MACROMOLECULAR PROTECTION ASSAY
; FILE REFERENCE: 517427-2007.1
; CURRENT APPLICATION NUMBER: US/10/627,561
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/398,685
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide
US-10-627-561-6

Query Match 48.9%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTC 12
    ||||| |||||
Db 13 GTGATCGACATC 2
    ||||| |||||

RESULT 25
US-10-033-145-740
; Sequence 740, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 740
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-033-145-740

Query Match 46.7%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
    ||||| |||||
Db 1 ACTTCCTCCT 10
    ||||| |||||

RESULT 26
US-10-450-797-1017/c
; Sequence 1017, Application US/10450797
; Publication No. US2004014233A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1017
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-450-797-1017

Query Match 46.7%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
    ||||| |||||
```



```
Db      11 ACTTCAACT 2

RESULT 27
US-09-751-561-27/c
; Sequence 27, Application US/09751561
; Patent No. US20010007985A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: -18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-751-561-27

Query Match      46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      1 GTGAGCGGACT 10
Db      10 GTCAGCGGACT 1

RESULT 28
US-09-989-364-31/c
; Sequence 31, Application US/09989364
; Publication No. US2003003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21

Query Match      46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      1 GTGAGCGGACT 10
Db      10 GTCAGCGGACT 1

RESULT 29
US-10-001-670-84
; Sequence 84, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/10/001,670
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/231,303
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 08/663,824
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-84

Query Match      46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      5 GCGACTTCAT 14
Db      2 GCGCTTCAT 11

RESULT 30
US-10-001-670-99
; Sequence 99, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/10/001,670
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/231,303
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 08/663,824
```

```
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-99

Query Match      46.7%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
    ||| |||||
Db 2 GCGGCTTCAT 11

RESULT 31
US-10-302-547-31
; Sequence 31, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HP1V1) FROM cDNA AND USE OF RECOMBINANT HP1V1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
; CURRENT APPLICATION NUMBER: US/10/302,547
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/331,961
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 31
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Bovine parainfluenza virus 3
US-10-302-547-31

Query Match      44.4%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCCT 17
    :|||:|
Db 3 UUCAUCCU 10

RESULT 32
US-10-055-732-22
; Sequence 22, Application US/10055732
; Publication No. US2003013504A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US200301350
; TITLE OF INVENTION: Structures
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/197,559
```

```
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: "n" = propanediol
US-10-055-732-22

Query Match      44.4%; Score 8; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
    ||||| |||
Db 1 CTTTCATCCT 9

RESULT 33
US-09-774-021-13
; Sequence 13, Application US/09774021
; Patent No. US20020102556A1
; GENERAL INFORMATION:
; APPLICANT: Laken, Steven J.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Genotyping by Mass Spectrometric Analysis of Short DNA
; TITLE OF INVENTION: Fragments
; FILE REFERENCE: 01107.73601
; CURRENT APPLICATION NUMBER: US/09/774,021
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/198,340
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-774-021-13

Query Match      43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCATC 15
    ||| |||||
Db 1 GCGCTTCTTC 11

RESULT 34
US-10-450-797-117
; Sequence 117, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-117

Query Match 43.3%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTTC 12
||| ||| ||| |||
Db 1 TGTGCGGCTTC 11

RESULT 35

US-09-751-561-10
; Sequence 10, Application US/09751561
; Patent No. US20010007985A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
; APPLICANT: Simpson, John
; TITLE OF INVENTION: Method for the Determination and
; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/547,214
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-015-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; TELEFAX: (212)-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-751-561-10

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| ||| ||| |||
Db 1 AGTGCCTTCAT 11

RESULT 36
US-09-844-493-13
; Sequence 13, Application US/09844493
; Patent No. US20020076711A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: LI, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: METHODS FOR DESIGNING EXOGENOUS REGULATORY MOLECULES
; FILE REFERENCE: 8325-0016
; CURRENT APPLICATION NUMBER: US/09/844,493
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,605
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible
; OTHER INFORMATION: end
US-09-844-493-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| ||| ||| |||
Db 1 GATCGAATTCA 11

RESULT 37

US-09-844-501-13
; Sequence 13, Application US/09844501
; Patent No. US20020081603A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: LI, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: DATABASES OF REGULATORY SEQUENCES; METHODS OF MAKING AND USING SA
; FILE REFERENCE: 8325-0015
; CURRENT APPLICATION NUMBER: US/09/844,501
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,556
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible
; OTHER INFORMATION: end

US-09-844-501-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| ||| |||
Db 1 GATCGAATTCA 11

RESULT 38

US-09-844-265-13
; Sequence 13, Application US/09844265
; Patent No. US20020127559A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: LJ, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: PHARMACOGENOMICS AND IDENTIFICATION OF DRUG TARGETS BY
; TITLE OF INVENTION: RECONSTRUCTION OF SIGNAL TRANSDUCTION PATHWAYS BASED ON
; TITLE OF INVENTION: SEQUENCES OF ACCESSIBLE REGIONS
; FILE REFERENCE: 8325-0017
; CURRENT APPLICATION NUMBER: US/09/844,265
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,608
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible
; OTHER INFORMATION: end
US-09-844-265-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
||| ||| |||
Db 1 GATCGAATTCA 11

RESULT 39

US-09-989-364-14
; Sequence 14, Application US/0989364
; Publication No. US20030003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-14

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
||| ||| |||
Db 1 AGTGGCTTCAT 11

RESULT 40

US-10-149-553-10
; Sequence 10, Application US/10149553
; Publication No. US20040072159A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences
; APPLICANT: Bio-oriented Technology Research Advancement Insti
; TITLE OF INVENTION: bZIP TRANSCRIPTION FACTOR THAT CONTROLS EXPRESSION OF
; TITLE OF INVENTION: THE STORAGE PROTEIN IN THE RICE PLANT
; FILE REFERENCE: SHIMIZU-07053
; CURRENT APPLICATION NUMBER: US/10/149,553
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2000-311295
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-149-553-10

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTT 11
||| ||| |||
Db 2 GTGAGTCACCT 12

RESULT 41

US-10-140-763A-11/c
; Sequence 11, Application US/10140763A
; Publication No. US2003010420A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Methods and Compositions for Modulating
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression
; FILE REFERENCE: SIER-012
; CURRENT APPLICATION NUMBER: US/10/140,763A
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,641
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-140-763A-11

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy 1 GTGAGCGGACTT 11
    ||| ||| |||
Db 11 GTGGCGGAATT 1

RESULT 42
US-10-001-670-96
; Sequence 96, Application US/10001670
; Publication No. US20030119002A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: IDENTIFICATIONS THAT OCCUR IN POPULATIONS AND
; TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/10/001,670
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/231,303
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 08/663,824
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-96

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCAT 14
    ||| ||| |||
Db 1 AGCTGCTTCAT 11

RESULT 43
US-10-083-682-13
; Sequence 13, Application US/10083682
; Publication No. US20030129603A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: LI, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: DATABASES OF REGULATORY SEQUENCES; METHODS OF MAKING AND USING SA
; FILE REFERENCE: 8325-0015
; CURRENT APPLICATION NUMBER: US/10/083,682
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/844,501
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,556
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible

US-10-083-682-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    ||| ||| |||
Db 1 GATCGAATTCA 11

RESULT 44
US-10-434-947-13
; Sequence 13, Application US/10434947
; Publication No. US20030190664A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan
; APPLICANT: URNOV, Fyodor
; APPLICANT: GUSCHIN, Dmitry
; APPLICANT: COLLINGWOOD, Trevor
; APPLICANT: LI, Xiao-Yong
; APPLICANT: JOHNSTONE, Brian
; TITLE OF INVENTION: PHARMACOGENOMICS AND IDENTIFICATION OF DRUG TARGETS BY
; TITLE OF INVENTION: RECONSTRUCTION OF SIGNAL TRANSDUCTION PATHWAYS BASED ON
; TITLE OF INVENTION: RECONSTRUCTIONS OF ACCESSIBLE REGIONS
; FILE REFERENCE: 8325-0017
; CURRENT APPLICATION NUMBER: US/10/434,947
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/844,265
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/214,674
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/228,608
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: adapter
; OTHER INFORMATION: oligonucleotide containing a Sau 3AI-compatible

US-10-434-947-13

Query Match 43.3%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTCA 13
    ||| ||| |||
Db 1 GATCGAATTCA 11

RESULT 45
US-10-113-877-47/c
; Sequence 47, Application US/10113877
; Publication No. US20020177218A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Yu
; APPLICANT: Wang, Xiao-Yang
; APPLICANT: Turpin, Pierre
; TITLE OF INVENTION: Methods of detecting multiple DNA
; TITLE OF INVENTION: binding protein and DNA interactions in a sample, and
; TITLE OF INVENTION: devices, systems and kits for practicing the same.
; FILE REFERENCE: CLON-071
; CURRENT APPLICATION NUMBER: US/10/113,877
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,658
; PRIOR FILING DATE: 2001-03-30
```

; PRIOR APPLICATION NUMBER: 60/314,330
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-113-877-47

Query Match 41.1%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
| | | | |
Db 9 ACTTCCTCC 1

RESULT 46
US-08-935-377-21/c
; Sequence 21, Application US/08935377
; Publication No. US20030133917A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: T Cells Specific for Target Antigens and
; TITLE OF INVENTION: Vaccines Based Thereon
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,377
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-935-377-21

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
| | | | |
Db 9 GACTTGATC 1

RESULT 47
US-09-822-250-21/c

; Sequence 21, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-21

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
| | | | |
Db 9 GACTTGATC 1

RESULT 48
US-09-810-936-103
; Sequence 103, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-810-936-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 1 CTTTCACCT 9

RESULT 49
US-09-738-973-48
; Sequence 48, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.

; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algathe, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Carol R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-48

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||
Db 1 CTTCAACCT 9

RESULT 50
US-09-429-755-103
; Sequence 103 Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-429-755-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||
Db 1 CTTCAACCT 9

RESULT 51
US-09-924-400-103
; Sequence 103 Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.

; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer for amplification from breast cancer
; OTHER INFORMATION: tumor cDNA
US-09-924-400-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||
Db 1 CTTCAACCT 9

RESULT 52
US-09-854-133-48
; Sequence 48 Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-48

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
||| |||
Db 1 CTTCAACCT 9

RESULT 53
US-09-875-453-70/C
; Sequence 70 Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:

```
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135.30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-70

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
| | | | | | |
Db 9 ACTTCATTC 1

RESULT 54
US-09-884-363-7/c
; Sequence 7, Application US/09884363
; Publication No. US2003004392A1
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-884-363-7

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACTTCATCC 16
| | | | | | |
Db 10 ACTTCCTCC 2

RESULT 55
US-09-884-363-8/c
; Sequence 8, Application US/09884363
; Publication No. US2003004392A1
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
```

```
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Promoter
US-09-884-363-8

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCACTCCTT 18
| | | | | | |
Db 9 TTCTCTCCTT 1

RESULT 56
US-09-821-694A-25/c
; Sequence 25, Application US/09821694A
; Publication No. US20030134277A1
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINE NUCLEIC ACID
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder
; OTHER INFORMATION: Binding sequence
US-09-821-694A-25

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
| | | | | | |
Db 10 GACTTCCTC 2

RESULT 57
US-09-821-694A-25/c
; Sequence 25, Application US/09821694A
; Publication No. US20040121319A9
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINE NUCLEIC ACID
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```


; OTHER INFORMATION: Description of Artificial Sequence: Decoder
; OTHER INFORMATION: binding sequence
US-09-821-694A-25

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 10 GACTTCTTC 2

RESULT 58

US-09-821-694A-29
; Sequence 29, Application US/09821694A
; Publication No. US20030134277A1
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder probe
; OTHER INFORMATION: sequence
US-09-821-694A-29

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 1 GACTTCTTC 9

RESULT 59

US-09-821-694A-29
; Sequence 29, Application US/09821694A
; Publication No. US20040121319A9
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder probe
; OTHER INFORMATION: sequence
US-09-821-694A-29

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
|||||
Db 1 GACTTCTTC 9

RESULT 60

US-10-079-137B-103
; Sequence 103, Application US/10079137B
; Publication No. US20040073016A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Mishner, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C13
; CURRENT APPLICATION NUMBER: US/10/079,137B
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer for amplification from breast cancer
; OTHER INFORMATION: tumor cDNA
US-10-079-137B-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17
|||||
Db 1 CTTCACCT 9

RESULT 61

US-10-293-222-174
; Sequence 174, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-174

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 2 CGTCATCCT 10

RESULT 62

US-10-293-222-229
; Sequence 229, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 229
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-229

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 1 CTTAATCCT 9

RESULT 63

US-10-293-222-285
; Sequence 285, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 285
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-285

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 10 TTTCATCCTT 18
| | | | |
Db 1 TTCTCTCCTT 9

RESULT 64

US-10-293-222-288
; Sequence 288, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 288
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-288

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTTCATCCTT 18
| | | | |
Db 1 TTCTCTCCTT 9

RESULT 65

US-10-293-222-337/c
; Sequence 337, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 337
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-337

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
| | | | |
Db 10 TGAGAGACT 2

RESULT 66

US-10-257-021-86/c
; Sequence 86, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:

; APPLICANT: Morin, Patrice J.
 ; APPLICANT: Sherman-Baust, Cheryl A.
 ; APPLICANT: Pizer, Ellen S.
 ; APPLICANT: Hough, Colleen D.
 ; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
 ; FILE REFERENCE: 14014.036902
 ; CURRENT APPLICATION NUMBER: US/10/257,021
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: PCT/US01/10947
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/194,336
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 86
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-257-021-86

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 9 CTTTCCTCT 17
 |||||
 Db 10 CTTTCCTCT 2

RESULT 67

US-10-033-145-57/c
 ; Sequence 57, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 57
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-57

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 9 CTTTCCTCT 17
 |||||
 Db 10 CTTTCCTCT 2

RESULT 68

US-10-033-145-124/c
 ; Sequence 124, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800

; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 124
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-124

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 10 TTTCATCCTT 18
 |||||
 Db 10 TTTCATCCT 2

RESULT 69

US-10-033-145-498
 ; Sequence 498, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 498
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-498

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 GTGAGCCGAC 9
 |||||
 Db 2 GTGAGCCAC 10

RESULT 70

US-10-033-145-1179/c
 ; Sequence 1179, Application US/10033145
 ; Publication No. US2002015151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENZYME CORPORATION
 ; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1179
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1179

Query Match 41.1%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 48;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 10 CGTCATCCT 2

RESULT 71

US-10-033-145-2127
; Sequence 2127, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT FILING DATE: 2001-11-05
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2127
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2127

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGACTTCA 13
| | | | |
Db 2 GTGACTTCA 10

RESULT 72

US-10-108-164-112/c
; Sequence 112, Application US/10108164
; Publication No. US20030104356A1
; GENERAL INFORMATION:
; APPLICANT: Berger, Shelley L.
; APPLICANT: Fraser, Nigel W.
; APPLICANT: Tal-Singer, Ruth
; APPLICANT: Leary, Jeffrey J.
; TITLE OF INVENTION: Compounds And Methods For Treating And
; Screening Viral Reactivation
; FILE REFERENCE: P50682C1
; CURRENT APPLICATION NUMBER: US/10/108,164
; CURRENT FILING DATE: 2002-03-26
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 09/424,348
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: PCT/US98/13733
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: 60/051,633
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: 60/054,515
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 60/080,352
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-108-164-112

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
| | | | |
Db 9 GACTTGATC 1

RESULT 73

US-10-227-001-6/c
; Sequence 6, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-triggered Fluorescent
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: US 09/428,236
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
; OTHER INFORMATION: conjugate
US-10-227-001-6

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCGACTTC 12
| | | | |
Db 9 AGCACTTC 1

RESULT 74

US-10-144-649A-48
; Sequence 48, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-144-649A-48

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
| | | | |
Db 1 CTTCAACT 9

```
RESULT 75
US-10-212-679-103
; Sequence 103, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer for amplification from breast cancer
; OTHER INFORMATION: tumor cDNA
US-10-212-679-103

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 9 CTTCACTCT 17
Db 1 CTTCACTCT 9

RESULT 76
US-10-329-465-102/c
; Sequence 102, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-102

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 10 TTCACTCTT 18
Db 10 TTCACTCAT 2

RESULT 77
US-10-330-627-735/c
; Sequence 735, Application US/10330627
```

```
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 735
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-735

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 2 TGAGCGACT 10
Db 10 TGAGAGACT 2

RESULT 78
US-10-330-627-880/c
; Sequence 880, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 880
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-880

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 9 CTTCACTCT 17
Db 10 CTTCTCTCT 2

RESULT 79
US-10-330-627-921/c
; Sequence 921, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
```

; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 921
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-921

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
||| ||| |||
Db 9 GTGAGCCAC 1

RESULT 80

US-10-330-627-922/c
; Sequence 922, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 922
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-922

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
||| ||| |||
Db 9 GTGAGCCAC 1

RESULT 81

US-10-330-627-1166/c
; Sequence 1166, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1166

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
||| ||| |||
Db 9 GTGAGCCAC 1

RESULT 82
US-10-343-710-130/c
; Sequence 130, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: WETZELS, Ingrid
; APPLICANT: WENNDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M. K. H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343,710
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-343-710-130

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
||| ||| |||
Db 9 GACTTGATC 1

RESULT 83

US-10-034-350-21/c
; Sequence 21, Application US/10034350
; Publication No. US20040151730A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens
; FILE REFERENCE: 1821.0010002
; CURRENT APPLICATION NUMBER: US/10/034,350
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-034-350-21

Query Match 41.1%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GACTTCATC 15
||| ||| |||
Db 9 GACTTGATC 1

RESULT 84

```
US-09-955-363-20/c
; Sequence 20, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; Bell, Lillian A.
; Kindevogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: N
; ANTI-SENSE: N
; IMMEDIATE SOURCE:
; CLONE: ZC1893
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-955-363-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
Db 11 TGAGCGTCT 3

RESULT 85
US-09-249-155-4/c
; Sequence 4, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1998-02-12
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-4
```

```
Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 86
US-09-249-155-163/c
; Sequence 163, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1998-02-12
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-163

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGAC 9
Db 9 GTGAGCCAC 1

RESULT 87
US-09-943-531A-4
; Sequence 4, Application US/09943531A
; Publication No. US20030059774A1
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Risinger, Karl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP2C19 POLYMORPHISMS
; FILE REFERENCE: 52459-20020.00
; CURRENT APPLICATION NUMBER: US/09/943,531A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: GB 0021286.0
```

```
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-4

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy      8 ACTTCATCC 16
      ||||| |||||
Db      2 ACTTTATCC 10

RESULT 88
US-09-943-531A-24/c
; Sequence 24, Application US/09943531A
; Publication No. US20030059774A1
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Rieger, Karl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP2C19 POLYMORPHISMS
; FILE REFERENCE: 52459-20020.00
; CURRENT APPLICATION NUMBER: US/09/943,531A
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-24

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy      8 ACTTCATCC 16
      ||||| |||||
Db      10 ACTTTATCC 2

RESULT 89
US-09-933-346-619
; Sequence 619, Application US/09993346
; Publication No. US20030124530A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; Cantor, Charles R.
; Andrews, Beth M.
; Turin, Lisa M.
; Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA

; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-4

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy      8 ACTTCATCC 16
      ||||| |||||
Db      2 ACTTTATCC 10

RESULT 88
US-09-943-531A-24/c
; Sequence 24, Application US/09943531A
; Publication No. US20030059774A1
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Rieger, Karl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP2C19 POLYMORPHISMS
; FILE REFERENCE: 52459-20020.00
; CURRENT APPLICATION NUMBER: US/09/943,531A
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide of polymorphic site 1060
US-09-943-531A-24

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy      8 ACTTCATCC 16
      ||||| |||||
Db      10 ACTTTATCC 2

RESULT 89
US-09-933-346-619
; Sequence 619, Application US/09993346
; Publication No. US20030124530A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; Cantor, Charles R.
; Andrews, Beth M.
; Turin, Lisa M.
; Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA

; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,346
; FILING DATE: 13-Jun-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,947
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/171,389
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brady, John F.
; REGISTRATION NUMBER: 39,118
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 619:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: a sample distamycin target sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 619:
US-09-993-346-619

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TTCATCCTT 18
      ||||| |||||
Db      1 TTCCTCCTT 9

RESULT 90
US-10-446-201-2
; Sequence 2, Application US/10446201
; Publication No. US20040029160A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon G.
; TITLE OF INVENTION: Parallel Stranded Duplexes of Deoxyribonucleic Acid and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 020415
; CURRENT APPLICATION NUMBER: US/10/446,201
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Linked to other strands to form hairpins
US-10-446-201-2
```


Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCTCTCT 9

RESULT 91
US-10-446-201-14/c
; Sequence 14, Application US/10446201
; Publication No. US20040029160A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon G.
; TITLE OF INVENTION: Parallel Stranded Duplexes of Deoxyribonucleic Acid and Methods
; FILE REFERENCE: 020415
; CURRENT APPLICATION NUMBER: US/10/446,201
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: test sequence
US-10-446-201-14

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 11 CTTCTCTCT 3

RESULT 92
US-10-446-201-22
; Sequence 22, Application US/10446201
; Publication No. US20040029160A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon G.
; TITLE OF INVENTION: Parallel Stranded Duplexes of Deoxyribonucleic Acid and Methods
; FILE REFERENCE: 020415
; CURRENT APPLICATION NUMBER: US/10/446,201
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: test strand
US-10-446-201-22

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCTCTCT 9

RESULT 93

US-10-446-201-23
; Sequence 23, Application US/10446201
; Publication No. US20040029160A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon G.
; TITLE OF INVENTION: Parallel Stranded Duplexes of Deoxyribonucleic Acid and Methods
; FILE REFERENCE: 020415
; CURRENT APPLICATION NUMBER: US/10/446,201
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: test sequence
US-10-446-201-23

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
Db 1 CTTCTCTCT 9

RESULT 94
US-10-223-126-189/c
; Sequence 189, Application US/10223126
; Publication No. US20030092662A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Molecular Interaction Sites of 16S Ribosomal RNA and Methods of
; FILE REFERENCE: Modulating the Same
; FILE REFERENCE: IBIS-0424
; CURRENT APPLICATION NUMBER: US/10/223,126
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/313,890
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 189
; LENGTH: 11
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is any nucleotide
US-10-223-126-189

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 11 GACGTCNTCC 2

RESULT 95
US-10-055-732-2
; Sequence 2, Application US/10055732
; Publication No. US20030135040A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon Guimil

; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US200301350
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/197,559
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-2

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 1 CTTCTCCT 9

RESULT 96

US-10-055-732-9
; Sequence 9, Application US/10055732
; Publication No. US20030135040A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US200301350
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/197,559
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-9

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 1 CTTCTCCT 9

RESULT 97

US-10-055-732-20
; Sequence 20, Application US/10055732
; Publication No. US20030135040A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon Guimil
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US200301350
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: US 60/197,559
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-20

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTTTCATCCT 17
|||||
Db 1 CTTCTCCT 9

RESULT 98

US-10-314-322-4/c
; Sequence 4, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-4

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
|||||
Db 9 GTGAGCCAC 1

RESULT 99

US-10-314-322-163/c
; Sequence 163, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-163

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
|||||
Db 9 GTGAGCCAC 1

RESULT 100

US-10-314-322-267/c
; Sequence 267, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-267

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

Qy 2 TCAGCGACT 10
|||||
Db 10 TGAGAGACT 2

RESULT 101

US-10-450-797-98/c

; Sequence 98, Application US/10450797

; Publication No. US20040142335A1

; GENERAL INFORMATION:

US-10-314-322-317/c
; Sequence 317, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-317

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

Qy 1 GTGAGCGCAC 9
|||||
Db 9 GTGAGCCAC 1

RESULT 102

US-10-700-118-12
; Sequence 12, Application US/10700118
; Publication No. US20040137431A1
; GENERAL INFORMATION:
; APPLICANT: Lopez, Martin J.
; APPLICANT: Ericja, Ramon
; TITLE OF INVENTION: Target Sequences for the Detection of the West Nile Virus
; FILE REFERENCE: 030570
; CURRENT APPLICATION NUMBER: US/10/700,118
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: US 60/423508
; PRIOR FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: hairpin component
US-10-700-118-12

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

Qy 9 CTTCATCCT 17
|||||
Db 1 CTTCCTCT 9

RESULT 103

US-10-450-797-98/c
; Sequence 98, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:

```
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-98

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 AGCGACTTC 12
Db      9 AGCGACTGC 1

RESULT 104
US-10-450-797-142/c
; Sequence 142, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-142

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GACTTCATC 15
Db     11 GACTTCAAC 3

RESULT 105
US-10-450-797-250
; Sequence 250, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
```

```
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 250
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-250

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTTTCATCCT 17
Db      2 CTTTCCTCCT 10

RESULT 106
US-10-450-797-757/c
; Sequence 757, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 757
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-757

Query Match      41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCGACTTCA 13
Db     11 GCGCCTTCA 3

RESULT 107
US-10-450-797-1211
; Sequence 1211, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1211
```

; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1211

Query Match 41.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAGCGACT 10
|||||
Db 3 TGAGCAACT 11

RESULT 108

US-10-450-797-1326/c
; Sequence 1326, Application US/10450797
; Publication No. US20040142335A1

; GENERAL INFORMATION:

; APPLICANT: Petersohn, Dirk

; APPLICANT: Conradt, Marcus

; APPLICANT: Hofmann, Kay

; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

; FILE REFERENCE: HENK-0041

; CURRENT APPLICATION NUMBER: US/10/450,797

; PRIOR FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: PCT/EP01/15178

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: DE 101 00 121.5

; PRIOR FILING DATE: 2001-01-03

; NUMBER OF SEQ ID NOS: 1435

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1326

; LENGTH: 11

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-450-797-1326

Query Match

Best Local Similarity 41.1%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TTCATCCTT 18
|||||
Db 10 TTCATCCAT 2

RESULT 109

US-09-989-789-2472/c

; Sequence 2472, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2472

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-2472

Query Match

Best Local Similarity 38.9%; Score 7; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
|||||
Db 9 TTCATCC 3

RESULT 110

US-09-989-789-2477/c

; Sequence 2477, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2477

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-2477

Query Match

Best Local Similarity 38.9%; Score 7; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
|||||
Db 9 TTCATCC 3

RESULT 111

US-09-990-186-2472/c

; Sequence 2472, Application US/09990186

; Publication No. US20030068675A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2472

; LENGTH: 9

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-990-186-2472

Query Match

Best Local Similarity 38.9%; Score 7; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCATCC 16
|||||
Db 9 TTCATCC 3

RESULT 112

US-09-990-186-2477/c

; Sequence 2477, Application US/09990186

; Publication No. US20030068675A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2477
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2477

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCAATCC 16
Db 9 TTCAATCC 3

RESULT 113
US-09-989-994-2472/c
; Sequence 2472, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2472
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2472

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCAATCC 16
Db 9 TTCAATCC 3

RESULT 114
US-09-989-994-2477/c
; Sequence 2477, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2477
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2477

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TTCAATCC 16
Db 9 TTCAATCC 3

RESULT 115
US-10-182-327-156
; Sequence 156, Application US/10182327
; Publication No. US20040043468A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: THE NEUROSCIENCE INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: CHAPPELL, Stephen A.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: PINKSTAFF, Jason K.
; APPLICANT: KRUSHEL, Leslie
; APPLICANT: ZHOU, Wei
; TITLE OF INVENTION: SYNTHETIC INTERNAL RIBOSOME ENTRY SITES AND METHODS OF IDENTIFYING
; FILE REFERENCE: SCRIPI360-1
; CURRENT APPLICATION NUMBER: US/10/182,327
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: PCT/US 01/02586
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: random 9 nt sequence
US-10-182-327-156

Query Match 38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCG 7
Db 3 GTGAGCG 9

RESULT 116
US-10-076-047A-75
; Sequence 75, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: Proteins, Genes and their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer

```
; FILE REFERENCE: 2543-1-026
; CURRENT APPLICATION NUMBER: US/10/076,047A
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB 9919258.5
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: GB 0007754.5
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/GB00/03143
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-047A-75

Query Match      38.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CGACTTC 12
      |||||
Db      3 CGACTTC 9

RESULT 117
US-08-935-377-14
; Sequence 14, Application US/08935377
; Publication No. US20030133917A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: T Cells Specific for Target Antigens and
; TITLE OF INVENTION: Vaccines Based Thereon
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,377
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-935-377-14

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GACTTCA 13
      |||||
Db      4 GACTTCA 10

US-08-935-377-14
```

```
Db      4 GACTTCA 10

RESULT 118
US-09-772-105-68/C
; Sequence 68, Application US/09772105
; Patent No. US20010029015A1
; GENERAL INFORMATION:
; APPLICANT: Ozelius, Laurie J.
; APPLICANT: Breakefield, Xandra O.
; TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND
; TITLE OF INVENTION: METHODS OF DETECTING NEURONAL DISEASES
; FILE REFERENCE: 0838.1001009
; CURRENT APPLICATION NUMBER: US/09/772,105
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/218,363
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/099,454
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/050,244
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exon/intron of DYTI
US-09-772-105-68

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 CATCCTT 18
      |||||
Db      9 CATCCTT 3

RESULT 119
US-09-822-250-14
; Sequence 14, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-14

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GACTTCA 13
      |||||
Db      4 GACTTCA 10

RESULT 120
US-10-398-885A-5
; Sequence 5, Application US/10398885A
; Publication No. US20040053282A1
```

; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahashi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-5

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGA 8
Db 4 TGAGCGA 10
|||||

RESULT 121
US-10-033-145-117/c
; Sequence 117, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-117

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CGACTTC 12
Db 7 CGACTTC 1
|||||

RESULT 122
US-10-033-145-125
; Sequence 125, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE

; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-125

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 3 CATCCTT 9
|||||

RESULT 123
US-10-033-145-925/c
; Sequence 925, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 925
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-925

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CATCCTT 18
Db 7 CATCCTT 1
|||||

RESULT 124
US-10-033-145-1356/c
; Sequence 1356, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1356
; LENGTH: 10


```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1356

```

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels

Qy 9 CTTTCATC 15
|||
Db 10 CTTTCATC 4

```

RESULT 125
US-10-033-145-1948/c
; Sequence 1948, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1948
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1948

```

| | | | | |
|-----------------------|---------|---------------|-------|---------------|
| Query Match | 38.9%; | Score 7; | DB 1; | Length 10; |
| Best Local Similarity | 100.0%; | Pred. No. 58; | | |
| Matches | 7; | Conservative | 0; | Mismatches 0; |
| | | | | Indels |

Qy 12 CATCCTT 18
|||
Db 10 CATCCTT 4

RESULT 126
US-10-006-542B-8
; Sequence 8, Application US/10006542B
; Publication No. US20020178459A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: McNeish, John D.
; APPLICANT: Soeller, Walter C.
; APPLICANT: Thompson, John F.
; TITLE OF INVENTION: MODULATING RAMP ACTIVITY
; FILE REFERENCE: PC10897ANIS
; CURRENT APPLICATION NUMBER: US/10/006,542B
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/250,965
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mus Musculus
US-10-006-542B-8

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels

Qy 12 CATCCTT 18

Db 1 CATCCTT 7

```

RESULT 127
US-10-329-465-230/c
; Sequence 230, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,4
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 230
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligon
US-10-329-465-230

```

```
Query Match          38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 6 CGACTTC 12
| | | | |
pb 7 CGACTTC 1

```

RESULT 128
US-10-330-627-20/c
; Sequence 20, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Kelulescu, Victor E.
; APPLICANT: Kizler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 00107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-20

```

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels

Qy 11 TCATCCT 17
| | | | |
Db 9 TCATCCT 3

RESULT 129
US-10-330-627-37
; Sequence 37, Application US/10330627
; Publication No. US2003017577A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.

```
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-37

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9

RESULT 130
US-10-330-627-39
; Sequence 39, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-39

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9

RESULT 131
US-10-330-627-474/c
; Sequence 474, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-474

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9

RESULT 132
US-10-330-627-504/c
; Sequence 504, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 504
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-504

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 7 TCATCCT 1

RESULT 133
US-10-330-627-812
; Sequence 812, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 812
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-812

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9

RESULT 134
US-10-330-627-812
; Sequence 812, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 812
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-812

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATC 15
Db 3 CTTTCATC 9
```

RESULT 134

US-10-091-281-289
; Sequence 289, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative CREBB/HLF.01 motif
US-10-091-281-289

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCAT 14
|||||
Db 4 ACTTCAT 10

RESULT 135

US-10-091-281-290
; Sequence 290, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 290
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative VBPF/VBP.01 motif
US-10-091-281-290

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCAT 14
|||||
Db 4 ACTTCAT 10

RESULT 136

US-10-197-019-91
; Sequence 91, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan

; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: PatentIn version 3.1
US-10-197-019-91

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACTTCAT 14
|||||
Db 2 ACTTCAT 8

RESULT 137

US-10-176-972A-41
; Sequence 41, Application US/10176972A
; Publication No. US20030235822A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Gall, Alexander A.
; APPLICANT: Likhov, Sergey G.
; APPLICANT: Afonina, Irina A.
; APPLICANT: Singer, Michael J.
; APPLICANT: Kutayavin, Igor V.
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Systems and Methods for Predicting Oligonucleotide Melting
; FILE REFERENCE: 17682A-003640US
; CURRENT APPLICATION NUMBER: US/10/176,972A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/054,830
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/054,832
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 09/431,385
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: US 09/640,953
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/724,959
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/796,988
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:duplex
; OTHER INFORMATION: complement 6
US-10-176-972A-41

Query Match 38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCGACT 10
|||||
Db 4 AGCGACT 10

```
RESULT 138
US-10-193-507-68/c
; Sequence 68, Application US/10193507
; Publication No. US200400018493A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Kazemi, Amir
; APPLICANT: Lachowicz, Michael F.
; APPLICANT: Pabon, Vicente
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFERENCE: MMH-2790US
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-507-68

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCT 17
Db 10 TCATCCT 4

RESULT 139
US-10-627-561-7
; Sequence 7, Application US/10627561
; Publication No. US20040086918A1
; GENERAL INFORMATION:
; APPLICANT: LOEWY, ZVI
; APPLICANT: CHAUNG, WAYNE
; APPLICANT: POTTATHIL, RAVEENDRAN
; TITLE OF INVENTION: MACROMOLECULAR PROTECTION ASSAY
; FILE REFERENCE: 517427-2007.1
; CURRENT APPLICATION NUMBER: US/10/627,561
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/398,685
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-627-561-7

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAGCGAC 9
Db 2 GAGCGAC 8

RESULT 140
US-10-034-350-14
; Sequence 14, Application US/10034350
; Publication No. US20040151730A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; FILE REFERENCE: 1821.00100002
; CURRENT APPLICATION NUMBER: US/10/034,350
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-034-350-14

Query Match      38.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GACTTCA 13
Db 4 GACTTCA 10

RESULT 141
US-08-935-377-13/c
; Sequence 13, Application US/08935377
; Publication No. US20030131917A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: T Cells Specific for Target Antigens and
; TITLE OF INVENTION: Vaccines Based Thereon
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,377
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CWB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-935-377-13

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
Db 7 GACTTCATCC 16
```

Db 10 GACTTGGTCC 1

RESULT 142

US-09-822-250-13/c
; Sequence 13, Application US/09822250
; Patent No. US2002001878A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-13

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 7 GACTTTCATCC 16
|||||
Db 10 GACTTGGTCC 1

RESULT 143

US-09-785-632A-4/c
; Sequence 4, Application US/09785632A
; Patent No. US20020061512A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Young Do
; APPLICANT: Kim, Hyun-Won
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
; IDENTIFYING SAME
; FILE REFERENCE: 12279-002001
; CURRENT APPLICATION NUMBER: US/09/785,632A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-632A-4

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 8 ACTTCATCCT 17
|||||
Db 10 ACTCCACCT 1

RESULT 144

US-09-989-789-1268/c
; Sequence 1268, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1268

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
|||||
Db 10 GCGACTCCTT 1

RESULT 145

US-09-989-789-1630
; Sequence 1630, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1630

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
|||||
Db 1 GAGGGAGTTC 10

RESULT 146

US-09-989-789-1631
; Sequence 1631, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1631

US-09-989-789-1631

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GAGGGAGTTC 10

RESULT 147

US-09-772-719-23

; Sequence 23, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-09-772-719-23

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 63;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
::: ||| :::::
Db 1 YYCAYYYY 10

RESULT 148

US-09-842-777-25

; Sequence 25, Application US/09842777
; Publication No. US20020182668A1
; GENERAL INFORMATION:

; APPLICANT: Surani, Azim
; APPLICANT: Szeto, Yuk Y
; TITLE OF INVENTION: Human PEG3 Gene and Uses Thereof
; FILE REFERENCE: 41657
; CURRENT APPLICATION NUMBER: US/09/842,777
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EcoRI linker
US-09-842-777-25

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GATCGAATTC 10

RESULT 149

US-09-884-363-5/c

; Sequence 5, Application US/09884363
; Publication No. US20030044392A1
; GENERAL INFORMATION:

; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UMSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-884-363-5

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
||| ||| |||
Db 10 ACTTCCTGCT 1

RESULT 150

US-09-967-237-23

; Sequence 23, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:

; APPLICANT: Pastorek, Jaromir
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10

```
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
US-967-237-23

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 20.0%; Pred. No. 63;
Matches 2; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
Db 1 YYCAYYYY 10

RESULT 151
US-967-237-24
; Sequence 24, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; PUBLICATION INFORMATION:
; AUTHORS: Locker and Buzard,
; JOURNAL: DNA Sequencing and Mapping
; VOLUME: 1
; PAGES: 3-11
; DATE: 1990
;
US-967-237-24

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 2 TGAGCGACTT 11
Db 1 TGTGAGACTT 10

RESULT 152
US-990-186-1268/c
; Sequence 1268, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;
```

```
US-990-186-1268

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
Db 10 GCGACTCCTT 1

RESULT 153
US-990-186-1630
; Sequence 1630, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

US-990-186-1630

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
Db 1 GAGGGAGTTC 10

RESULT 154
US-990-186-1631
; Sequence 1631, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

US-990-186-1631

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 3 GAGCGACTTC 12
Db 1 GAGGGAGTTC 10
```

RESULT 155

US-09-748-710-29/c
; Sequence 29, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; TITLE OF INVENTION: FROM SAGE TAGS FOR GENE IDENTIFICATION
; FILE REFERENCE: ARCD:343US
; CURRENT APPLICATION NUMBER: US/09/748,710
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-748-710-29

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 10 GAGCGCTCTC 1

RESULT 156

US-09-989-994-1268/c
; Sequence 1268, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1268

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 5 GCGACTTCAT 14
||| ||| |||
Db 10 GCGACTCTCT 1

RESULT 157

US-09-989-994-1630
; Sequence 1630, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1630

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GAGCGACTTC 10

RESULT 158

US-09-989-994-1631
; Sequence 1631, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1631

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GAGCGACTTC 12
||| ||| |||
Db 1 GAGCGACTTC 10

RESULT 159

US-10-228-876-1/c
; Sequence 1, Application US/10228876
; Publication No. US20040038400A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Allan C.
; APPLICANT: Loros, Jennifer J.
; APPLICANT: Duniap, Jay C.
; TITLE OF INVENTION: METHODS FOR REGULATING GENE EXPRESSION USING LIGHT
; FILE REFERENCE: DC-0194
; CURRENT APPLICATION NUMBER: US/10/228,876
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10


```
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-228-876-1

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
   |||||
Db 10 AGCGGCATCA 1

RESULT 160
US-10-653-677-1
; Sequence 1, Application US/10653677
; Publication No. US20040053981A1
; GENERAL INFORMATION:
; APPLICANT: University of No. US20040053981A1alth Carolina at Chapel Hill
; APPLICANT: Wilson, W. David
; APPLICANT: Boykin, David W
; APPLICANT: Tidwell, Richard R
; TITLE OF INVENTION: NOVEL COMPOUNDS THAT EXHIBIT SPECIFIC MOLECULAR RECOGNITION OF
; TITLE OF INVENTION: MIXED NUCLEIC ACID SEQUENCES AND BIND IN THE DNA MINOR GROOVE AS
; TITLE OF INVENTION: A DIMER
; FILE REFERENCE: 421/60/16/2/2
; CURRENT APPLICATION NUMBER: US/10/653,677
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 09/745,004
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: US 60/172,863
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Top strand of self-annealing oligo 1
US-10-653-677-1

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
   |||||
Db 1 CGAATTCGTC 10

RESULT 161
US-10-033-145-202
; Sequence 202, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 202
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-202
```

```
Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 ACTTCATCCT 17
   |||||
Db 1 ACTCCTTCCT 10

RESULT 162
US-10-033-145-849
; Sequence 849, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 849
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-849

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
   |||||
Db 1 TGGGCGCCTT 10

RESULT 163
US-10-033-145-1437
; Sequence 1437, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1437
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1437

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGCGACTTCA 13
   |||||
Db 1 AGCCACCTCA 10

RESULT 164
US-10-254-828-8/c
```

```
; Sequence 8, Application US/10254828
; Publication No. US20030082613A1
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. Thomas
; APPLICANT: Shumaker, John M.
; APPLICANT: Metespalu, Andres
; TITLE OF INVENTION: PARALLEL PRIMER EXTENSION APPROACH TO
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ANALYSIS
; FILE REFERENCE: 2875.1001-008
; CURRENT APPLICATION NUMBER: US/10/254,828
; CURRENT FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 08/564,100
; PRIOR FILING DATE: 1994-06-22
; PRIOR APPLICATION NUMBER: PCT/US94/07086
; PRIOR FILING DATE: 1994-06-22
; PRIOR APPLICATION NUMBER: SE 9302152-5
; PRIOR FILING DATE: 1993-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-254-828-8

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy      1 GTGAGCGACT 10
Db      10 GTAAGCGATT 1

RESULT 165
US-10-329-465-116/c
; Sequence 116, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-116

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy      2 TGAGCGACTT 11
Db      10 TGAGCGCTT 1

RESULT 166
US-10-329-465-139/c
; Sequence 139, Application US/10329465
```

```
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-139

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
Db      10 CTTTCCTCTT 1

RESULT 167
US-10-329-465-181/c
; Sequence 181, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-181

Query Match          37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 CTTTCATCCTT 18
Db      10 CTGCATTCTT 1

RESULT 168
US-10-223-765-4/c
; Sequence 4, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
```

```
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-765-4

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 ACTTCATCCT 17
        ||| ||| |||
Db      10 ACTCACCT 1

RESULT 169
US-10-390-045-30
; Sequence 30, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995-0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-390-045-30

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 CGACTTCATC 15
        ||| ||| |||
Db      1 CAACCTCAAC 10

RESULT 170
US-10-330-627-754
; Sequence 754, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 754
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-754

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 GAGCGACTTC 12
        ||| ||| |||
Db      1 GAGCGGCTC 10

RESULT 171
US-10-330-627-769/c
; Sequence 769, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 769
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-769

Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TGACCGACTT 11
        ||| ||| |||
Db      10 TGAATGACTT 1

RESULT 172
US-10-330-627-770/c
; Sequence 770, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-330-627-770

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 TGAGCGACTT 11
||| |||||
Db 10 TGAATGACTT 1

RESULT 173

US-10-330-627-885
; Sequence 885, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptsomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 885
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-885

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 4 AGCGACTTCA 13
||| |||||
Db 1 AGCCACTGCA 10

RESULT 174

US-10-330-627-940
; Sequence 940, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptsomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 940
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-940

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 TGAGCGACTT 11
||| |||||
Db 1 TGGGCGCCTT 10

RESULT 175

US-10-330-627-1345/c
; Sequence 1345, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptsomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1345

Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
||| |||||
Db 10 CATCTTCCTT 1

RESULT 176

US-10-352-615-132/c
; Sequence 132, Application US/10352615
; Publication No. US20030190285A1
; GENERAL INFORMATION:
; APPLICANT: VAN DEN VEN, W.J.M.
; SCHOENMAKERS, H.F.P.M.
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
; GENES
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Webb Law Firm
; STREET: 700 Koppers Building, 436 Seventh Avenue
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,615
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,454
; FILING DATE: 15-AUG-1997
; APPLICATION NUMBER: PCT/EP/00716
; FILING DATE: 19-FEB-1996
; APPLICATION NUMBER: 95200390.3
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: 95201951.1
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Barbara E
; REGISTRATION NUMBER: 31,198
; REFERENCE/DOCKET NUMBER: 702-971100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 412-471-8815
; TELEFAX: 412-471-4094

```
;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-352-615-132
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCGACTTCAT 14
| | | | |
Db 10 GAGACTCCAT 1

RESULT 177
US-10-434-479-30
; Sequence 30, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-30
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGACTTCATC 15
| | | | |
Db 1 CAACTTCAAC 10

RESULT 178
US-10-302-547-35
; Sequence 35, Application US/10302547
; Publication No. US20040142448A1
; GENERAL INFORMATION:
; APPLICANT: MUREPHY, BRIAN R.
; APPLICANT: COLLINS, PETER L.
; APPLICANT: SKIADOPOULOS, MARIO H.
; APPLICANT: NEWMAN, JASON T.
; TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
; TITLE OF INVENTION: 1 (HPiV1) FROM CDNA AND USE OF RECOMBINANT HPiV1 IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
; TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 2303-37-3
US-10-302-547-35
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTTTCATCCTT 18
| : : | : | :
Db 1 CUUUAUCCCU 10

RESULT 179
US-10-034-350-13/c
; Sequence 13, Application US/10034350
; Publication No. US20040151730A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens
; FILE REFERENCE: 1821.0010002
; CURRENT APPLICATION NUMBER: US/10/034,350
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-034-350-13
Query Match 37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GACTTCATCC 16
| | | | |
Db 10 GACTTGGTCC 1

RESULT 180
US-10-816-079-1/c
; Sequence 1, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GA0129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-1
```

```
Query Match      37.8%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 63;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      9 CTTGCTCCTT 18
      ||| |||||
Db      10 CTTGCTCCTT 1
```

```
Search completed: September 9, 2004, 11:30:56
Job time : 0.001 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2004, 11:32:37 ; Search time 0.001 Seconds
(without alignments)
0.720 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18

Sequence: 1 gtgagcgacttcattcctt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 20 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2 summaries

Database : rst32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 7.4 | 41.1 | 11 | 1 | CF310854 |
| 2 | 6.4 | 35.6 | 9 | 1 | CF309109 |

ALIGNMENTS

RESULT 1
CF310854
LOCUS
DEFINITION ABP--05-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-M02, mRNA sequence.
ACCESSION CF310854
VERSION CF310854
KEYWORDS EST.
SOURCE CF310854.1 GI:33682615
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

RESULT 2
CF309109
LOCUS
DEFINITION ABF--03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-C20, mRNA sequence.
ACCESSION CF309109
VERSION CF309109.1
KEYWORDS EST.
SOURCE CF309109.1 GI:33680870
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-M02"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 41.1%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Oy 1 GTGAGCGCAG 9

Db 3 GTAGCGCAG 11

RESULT 2

CF309109

LOCUS

DEFINITION

ABF--03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-C20, mRNA sequence.

ACCESSION

CF309109

VERSION

CF309109.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 9)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .9

source

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--03-C20"

/tissue_type="leaf"

/dev_stages="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 35.6%; Score 6.4; DB 1; Length 9;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 10 TTCTTCCT 17
||| |||
Db 2 TTCTTCCT 9

Search completed: September 9, 2004, 11:32:38
Job time : 0.001 secs